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(54) Title: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers or other diseases, or are otherwise regulated in disease. Related methods and compositions that can be used for diagnosis, prognosis, and treatment of those medical conditions are disclosed. Also described herein are methods that can be used to identify modulators of these selected conditions.



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METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

5 CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority to USSN 60/340,376, filed December 14, 2001; Attorney Docket Number 018501-006400US, filed February 8, 2002; USSN 60/347,211, filed January 8, 2002; USSN 60/334,393, filed November 29, 2001; USSN 60/335,394, filed November 15, 2001; USSN 60/347,349, filed January 10, 2002; USSN 60/368,809, filed March 29, 2002; USSN 60/409,450, filed September 9, 2002; USSN 60/359,077, filed February 20, 2002; USSN 60/386,614, filed June 5, 2002; USSN 60/356,714, filed February 13, 2002; USSN 60/397,775 filed July 22, 2002; USSN 60/332,464, filed November 21, 2001; USSN 60/397,845, filed July 22, 2002; USSN 60/370,110, filed April 4, 2002; USSN 60/396,839, filed July 16, 2002; USSN 60/350,666, filed November 13, 2001; and USSN 60/372,246, filed April 15 12, 2002; each of which is incorporated herein by reference for all purposes. The application also incorporates by reference PCT/US02/29560; PCT/US02/02242; and PCT/US02/17594.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in cancer and other 20 diseases; and to the use of such expression profiles and compositions in the diagnosis, prognosis, and therapy of these conditions. The invention further relates to methods for identifying and using agents and/or targets that modulate these conditions.

BACKGROUND OF THE INVENTION

Cancer is a major cause of morbidity in the United States. For example, in 1996, the 25 American Cancer Society estimated that 1,359,150 people were diagnosed with a malignant neoplasm and 554,740 died from one of these diseases. Cancer is responsible for 23.9 percent of all American deaths and is exceeded only by heart disease as a cause of mortality (33 percent). Unfortunately, cancer mortality is increasing and sometime early in this century, cancer is expected to become the leading cause of mortality in the United States as it already is 30 in Japan.

Cancers share the characteristic of disordered control over normal cell division, growth, and differentiation. Their initial clinical manifestations are extremely heterogeneous, with over

70 types of cancer arising in virtually every organ and tissue of the body. Moreover, some of those similarly classified cancer types may represent multiple different molecular diseases. Unfortunately, some cancers may be virtually asymptomatic until late in the disease course, when treatment is more difficult, and prognosis grim.

5 Treatment for cancer typically includes surgery, chemotherapy, and/or radiation therapy. Although nearly 50 percent of cancer patients can be effectively treated using these methods, the current therapies all induce serious side effects which diminish quality of life. The identification of novel therapeutic targets and diagnostic markers will be important for improving the diagnosis, prognosis, and treatment of cancer patients.

10 Recent advances in molecular medicine have increased the interest in tumor-specific antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues, preferably accessible from the vasculature and at the cell surface, and ideally not expressed in normal adult tissues. Expression in tissues that are dispensable for life, however, may be
15 tolerated, e.g., reproductive organs, especially those absent in one sex. Examples of antigens that are currently available for the detection and treatment of certain cancers include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. See Ross and Fletcher (1998) Stem Cells 16:413-428. Similarly, anti-CD20 monoclonal antibodies
20 (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. See Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is valuable for improving the current treatment of cancer patients. Accordingly, provided herein are molecular targets for therapeutic
25 intervention in various defined cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate cancer.

SUMMARY OF THE INVENTION

The present invention provides methods for determining the presence or absence of a
30 pathological cell in a patient, the method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a biological sample from the patient, thereby determining the presence or absence of the pathological cell.

In certain embodiments of the method, the pathology is described in Table 1, including a cancer; the biological sample comprises isolated nucleic acids; the nucleic acids are mRNA; the biological sample is tissue from an organ which is affected by the pathology of Table 1, including a cancer; a further step is used of amplifying nucleic acids before the step of detecting the nucleic acid; the detecting is of a protein encoded by the nucleic acid; the nucleic acid comprises a sequence as described in Tables 2A-80; the detecting step is carried out by using a labeled nucleic acid probe, utilizing a biochip comprising a sequence at least 80% identical to a sequence as described in Tables 2A-80, or detecting a polypeptide encoded by the nucleic acid; or the patient is undergoing a therapeutic regimen to treat the pathology of Table 1, or is suspected of having the pathology or cancer.

Compositions are also provided, e.g., an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-80, including, e.g., those which are labeled; an expression vector comprising such nucleic acid; a host cell comprising such expression vector; an isolated polypeptide which is encoded by such a nucleic acid molecule comprising a sequence as described in Tables 2A-80; or an antibody that specifically binds the polypeptide. In particular embodiments, the antibody is: conjugated to an effector component, is conjugated to a detectable label (including, e.g., a fluorescent label, a radioisotope, or a cytotoxic chemical), an antibody fragment, or is a humanized antibody.

Additional methods are provided, including methods for specifically targeting a compound to a pathological cell in a patient, the method comprising administering to the patient an antibody, as described, thereby providing the targetting. Others include, e.g., methods for determining the presence or absence of a pathological cell in a patient, the methods comprising contacting a biological sample with an antibody, as described. In more particular methods, the antibody is: conjugated to an effector component, or to a fluorescent label; or the biological sample is a blood, serum, urine, or stool sample.

Further methods include those for identifying a compound that modulates a pathology-associated polypeptide, the method comprising steps of: contacting the compound with a pathology-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80; and determining the functional effect of the compound upon the polypeptide. Another drug screening assay method comprises steps of: administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and comparing the level of gene expression

of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-80 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of the pathology.

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DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for various disorders, e.g., angiogenesis, fibrosis, and various defined forms of cancer, including metastatic cancer, as well as methods for screening for compositions which modulate such conditions. Also provided are methods for treating such disorders or cancers. See, e.g., American Society of Clinical Oncology (ed. 2001) ASCO Curriculum: Symptom Management Kendall/Hunt, ISBN: 0787277851; Bonadonna, et al. (2001) Textbook of Breast Cancer (2d ed.) Dunitz Martin, ISBN: 1853178241; Devita and Hellman (eds. 2001) Cancer Principles and Practice of Oncology (2 vols.), Lippincott Williams, ISBN: 0781723876; Howell, et al. (2001) Breast Cancer Isis Medical Media, ISBN: 1901865584; Kaye and Laws (2001) Brain Tumours: An Encyclopedic Approach (2d ed.) Churchill Livingstone, ISBN: 0443064261; Mihm, et al. (2001) The Melanocytic Proliferation: A Comprehensive Textbook of Pigmented Lesions Wiley-Liss, ISBN: 0471252719; Montgomery and Aaron (2001) Clinical Pathology of Soft-Tissue Tumors Marcel Dekker, ISBN: 0824702905; Petrovich, et al. (eds. 2001) Combined Modality of Central Nervous System Tumors (Medical Radiology) Springer Verlag, ISBN: 3540660534; Rosen (2001) Rosen's Breast Pathology Lippincott Williams and Wilkins, ISBN: 0781723795; Shah, et al. (2001) Oral Cancer Isis Medical Media, ISBN: 189906687X; Weiss and Goldblum (2001) Enzinger and Weiss's Soft Tissue Tumors (4th ed.) Mosby, ISBN: 0323012000; Abeloff, et al. (eds. 2000) Clinical Oncology (2d ed.) Churchill Livingstone, ISBN: 044307545X; American Society of Clinical Oncology (ed. 2000) Cancer Genetics and Cancer Predisposition Testing Kendall/Hunt, ISBN: 0787276154; Fletcher (2000) Diagnostic Histopathology of Tumors (2 vols. 2d ed.) Churchill Livingstone, ISBN: 0443079927; Vogelzang (ed. 2000) Comprehensive Textbook of Genitourinary Oncology (2d ed.) Lippincott Williams and Wilkins, ISBN: 0683306456; Holland, et al. (eds. 2000) Holland-Frei Cancer Medicine (Book with CD-ROM 5th ed.) Decker, ISBN: 1550091131; Turrisi, et al. (2000) Lung Cancer Isis Medical Media, ISBN: 1901865428; Bartolozzi and Lencioni (eds. 1999) Liver Malignancies: Diagnostic and Interventional Radiology (Medical Radiology) Springer Verlag, ISBN: 3540647562; Gasparini

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- (ed. 1999) Prognostic Variables in Node-Negative and Node-Positive Breast Cancer Kluwer, ISBN: 0792384474; Hansen (ed. 1999) The LASLC Textbook of Lung Cancer: International Association for the Study of Lung Cancer Dunitz Martin, ISBN: 1853177083; Raghavan, et al. (eds. 1999) Textbook of Uncommon Cancer (2nd ed.) Wiley, ISBN: 0471929212; Thawley, et al. (eds. 1999) Comprehensive Management of Head and Neck Tumors (2 vols.) Saunders, ISBN: 0721655823; Whittaker and Holmes (eds. 1999) Leukemia and Related Disorders (3d ed.) Blackwell Science, ISBN: 0865426074; Aapro (ed. 1998) OncoMedia: Medical Oncology (CD-ROM) Elsevier Science, ISBN: 0080427480; Abeloff (1998) Clinical Oncology (Library Version 2 CD-ROM Individual Version 2.0 Windows and Macintosh) Harcourt Brace, ISBN: 0443075557; Benson (ed. 1998) Gastrointestinal Oncology (Cancer Treatment and Research, CTAR 98) Kluwer, ISBN: 0792382056; Brambilla and Brambilla (eds. 1998) Lung Tumors: Fundamental Biology and Clinical Management (Vol 124) Marcel Dekker, ISBN: 0824701607; Canellos, et al. (eds. 1998) The Lymphomas Saunders, ISBN: 0721650309; Greenspan and Remagen (1998) Differential Diagnosis of Tumors and Tumor-Like Lesions of Bones and Joints Lippincott Williams and Wilkins Publishers, ISBN: 0397517106; Hiddemann (ed. 1998) Acute Leukemias VII: Experimental Approaches and Novel Therapies (Haematologie Und Bluttransfusion, Vol 39), Springer Verlag, ISBN: 3540635041; Husband and Reznick (1998) Imaging in Oncology (2 vols.) Mosby, ISBN: 1899066489; Leibel and Phillips (eds. 1998) Textbook of Radiation Oncology Saunders, ISBN: 0721653367; Maloney and Miller (eds. 1998) Cutaneous Oncology: Pathophysiology, Diagnosis, and Management Blackwell Science, ISBN: 0865425175; Mittal, et al. (eds. 1998) Advances in Radiation Therapy Kluwer, ISBN: 0792399811; Oldham (ed. 1998) Principles of Cancer Biotherapy (3d ed.) Kluwer, ISBN: 0792335074; Ozols (ed. 1998) Gynecologic Oncology Kluwer, ISBN: 0792380703; Parkin, et al. (eds. 1998) Cancer Incidence in Five Continents (Iarc Scientific Publications, No 143) Oxford University Press, ISBN: 9283221435; Perez and Brady (eds. 1998) Principles and Practice of Radiation Oncology Lippincott Williams and Wilkins, ISBN: 0397584164; Black, et al. (eds. 1997) Cancer of the Nervous System Blackwell Science, ISBN: 0865423849; Bonadonna, et al. (1997) Textbook of Breast Cancer: A Clinical Guide to Therapy Blackwell Science, ISBN: 1853173487; Pollock (ed. 1997) Surgical Oncology Kluwer, ISBN: 0792399005; Sheaves, et al. (eds. 1997) Clinical Endocrine Oncology Blackwell Science, ISBN: 086542862X; Vahrson (1997) Radiation Oncology of Gynecological Cancers Springer Verlag, ISBN: 0387567682; Walterhouse and Cohn (eds. 1997) Diagnostic and Therapeutic

- Advances in Pediatric Oncology Kluwer, ISBN: 0792399781; Aisner (ed. 1996) Comprehensive Textbook of Thoracic Oncology Lippincott, Williams and Wilkins, ISBN: 0683000624; Bertino, et al. (eds. 1996) Encyclopedia of Cancer (3 vols.) Academic, ISBN: 012093230X; Cavalli, et al. (1996) Textbook of Medical Oncology Dunitz Martin, ISBN: 1853172901;
- 5 Peckham, et al. (eds. 1995) Oxford Textbook of Oncology (2-Vols.) Oxford University Press, ISBN: 0192616854; and Freireich and Kantarjian (eds. 1996) Molecular Genetics and Therapy of Leukemia (Cancer Treatment and Research, V. 84) Kluwer, ISBN: 0792339126.

In particular, identification of markers selectively expressed on defined cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the

10 invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g.,

15 using antisense or RNAi. The markers may be useful for molecular characterization of subsets of the diseases, e.g., as provided in Table 1, which subsets may actually require very different treatments. Moreover, the markers may also be important in related diseases to the specific disorders and cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also

20 be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

25 Tables 2B-76B provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in diseased samples (see Tables 1-3), particularly sequences involved in angiogenesis, arthritis, prostate cancer, breast cancer, colorectal cancer, cervical cancer, bladder cancer, head and neck cancer, esophageal cancer, lung cancer, ovarian cancer, pancreatic cancer, renal cancer, stomach cancer, skin

30 cancer, testicular cancer, uterine cancer, glioblastoma, Ewing sarcoma, soft tissue sarcoma, and lung fibrosis. Tables 2A-80 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

The term "cancer protein" or "cancer polynucleotide" or "cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably about 92%, 94%, 96%, 97%, 98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-80; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-80, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-80 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, preferably 90%, 91%, 93%, 95%, 97%, 98%, or 99% or greater amino sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-80. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "cancer polypeptide" and a "cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" cancer protein or nucleic acid refers to a cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains elements normally contained in one or more naturally occurring, wild type cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing, including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, frozen sections taken for histologic purposes, archival samples, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is

typically obtained from a eukaryotic organism, most preferably a mammal such as a primate, e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish. Livestock and domestic animals are of interest.

5 "Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

10 The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 93%, 95%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over
15 a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes
20 sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is about 50-100 amino acids or nucleotides in length.

25 For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison
30 algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from about 20 to 600, usually about 50 to 200, more usually about 100 to 150, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Wiley).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-

scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1992) Proc. Natl. Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787.

One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its

native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from
5 some open reading frames that naturally flank the gene and encode proteins other than protein encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing
10 at least one contaminant or component from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally
15 occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as
20 those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g.,
25 norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetic refers to a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter
30 symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variant" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts,

et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide.

"Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkahge, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein;

- Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986) Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucleic Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am. Chem. Soc. 111:2321-2322), O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach, Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-1897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature 365:566-568; Carlsson, et al. (1996) Nature 380:207, all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Natl. Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141, and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Letsinger, et al. (1994) Nucleoside and Nucleotide 13:1597; Chapters 2 and 3 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176). Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in at least two advantages. The PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively

insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The depiction of a single strand
5 also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically
10 refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

15 A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags; and c) colored or fluorescent dyes. The labels may be incorporated into the cancer nucleic acids,
20 proteins, and antibodies. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , electron-dense reagents, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be
25 made detectable such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase. Methods are known for conjugating the antibody to the label. See, e.g., Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound
30 (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including

radioactive compounds, fluorescent compounds, enzymes or substrates, tags such as epitope tags, toxins; activatable moieties, chemotherapeutic agents; lipases; antibiotics; chemoattracting moieties, immune modulators (micA/B), or radioisotopes, e.g., emitting "hard" beta, radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, e.g., covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, methods using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein, or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is

achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. The protein may be isolated or purified away from some or most of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. An isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a cancer protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid

sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental
5 and developmental conditions. An "inducible" promoter is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

10 An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed in operable linkage to a promoter.

15 The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe
20 will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with
25 Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the
30 target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01-1.0 M sodium ion concentration (or other salts) at pH 7.0 to

8.3 and the temperature is at least about 30° C for short probes (e.g., about 10-50 nucleotides) and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times
5 background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although annealing temperatures may vary between about 32°-48° C depending on primer length. For
10 high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec, and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high
15 stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press, NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy
20 permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is typically at least twice background. Alternative hybridization and wash conditions can be utilized to provide conditions of similar
25 stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. (eds. 1991 and supplements) Current Protocols in Molecular Biology Wiley.

The phrase "functional effects" in the context of assays for testing compounds that modulate activity of a cancer protein includes the determination of a parameter that is indirectly
30 or directly under the influence of the cancer protein or nucleic acid, e.g., a physiological, functional, physical, or chemical effect, such as the ability to decrease cancer. It includes ligand binding activity; cell viability; cell growth on soft agar; anchorage dependence; contact

inhibition and density limitation of growth; cellular proliferation; cellular transformation; growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing metastasis; and other characteristics of cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the cancer protein, measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring growth, cellular proliferation, cell viability, cellular transformation, growth factor or serum dependence, tumor specific marker levels, invasiveness into Matrigel, tumor growth and metastasis in vivo, mRNA and protein expression, and other characteristics of cancer cells. The functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators," and "modulators" of cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Such assays for

inhibitors and activators include, e.g., expressing the cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of cancer can also be identified by incubating cancer cells with the test compound and determining increases or decreases in the expression of 1 or more cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more cancer proteins, such as cancer proteins encoded by the sequences set out in Tables 2A-80.

Samples or assays comprising cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is about 110%, more preferably 150%, more preferably 200-500% (e.g., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (2d ed.) Wiley-Liss.

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes.

5 Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven.

10 An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these
15 light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H - C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild
20 conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant
25 DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies,
30 many techniques known. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985) pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in

Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783.

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, effector function, chemoattractant, immune modulator, etc.; or (b) the variable region, or a portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of cancer-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic cancerous tissue, or cancer tissue or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different cancer states, information regarding which genes are important (including both up-and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

The identification of sequences that are differentially expressed in cancer versus non-cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis

and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression
5 profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the cancer expression profile. This may be done by making biochips comprising sets of the important cancer genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the cancer proteins can be
10 evaluated for diagnostic purposes or to screen candidate agents. In addition, the cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are
15 differentially expressed in cancer relative to normal tissues and/or non-malignant disease, or in different types of related diseases, herein termed "cancer sequences." As outlined below, cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred embodiment, the cancer sequences are from humans; however, cancer sequences from other
20 organisms may be useful in animal models of disease and drug evaluation; thus, other cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Cancer sequences from other organisms may be obtained using the techniques outlined below.

25 Cancer sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the skin cancer sequences are recombinant nucleic acids. These nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips comprising nucleic acid probes or PCR microtiter plates with selected probes to the cancer
30 sequences.

A cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the cancer sequences outlined herein. Such homology can be based

upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, e.g., using homology programs or hybridization conditions.

For identifying cancer-associated sequences, the cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and
5 non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing cancer samples with metastatic cancer samples from other cancers, such as lung, stomach, gastrointestinal cancers, etc. Samples of different stages of cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are
10 applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

In one embodiment, the genes showing changes in expression as between normal and
15 disease states are compared to genes expressed in other normal tissues, including, and not limited to lung, heart, brain, liver, stomach, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the cancer screen that are expressed in a significant amount in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not
20 necessary (e.g., where organs may be dispensible, e.g., female or male specific). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs were there expression.

In a preferred embodiment, cancer sequences are those that are up-regulated in cancer; that is, the expression of these genes is higher in the cancer tissue as compared to non-cancer or
25 non-malignant tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Uniformity among relevant samples is also preferred.

Unigene cluster identification numbers and accession numbers herein are for the
30 GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is available, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7; and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases,

e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH. See Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have
5 been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, cancer sequences are those that are down-regulated in the cancer; that is, the expression of these genes is lower in cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher
10 being preferred.

Informatics

The ability to identify genes that are over or under expressed in cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development,
15 and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with cancer or related diseases. See Tables 1-3. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA).
20 Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access
25 to the database, such as a personal computer, but is preferably distributed on a wide area
30 network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. Similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or
5 absolute abundance of a variety of molecular and macromolecular species from a biological sample representing cancer, e.g., the identification of cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others.
10 Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is available. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued
15 and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval
20 system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S.
25 Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with
30 navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures. See also Baxevanis, et al. (2001) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins Wiley; Mount (2001)

- Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999)
Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge University Press; Baxeavanis and Oeullette (eds. 1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler (1999)
- 5 Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et al. (eds. 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford University Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the
- 10 Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps, Sequences, and Genomes Chap and Hall.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

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In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

20

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention

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provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method
5 for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount
10 of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed,
15 Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line,
20 wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes
25 generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a
30 query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute

the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

5 The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can
10 be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal
15 comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

 The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be
20 stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values. See, e.g., Ewens and Grant (2001) Statistical Methods in Bioinformatics: An Introduction Springer-Verlag. Mathematical approaches can also be used to conclude whether similarities or differences in the gene expression exhibited by different
25 samples are significant. See, e.g., Golub, et al. (1999) Science 286:531-537; Duda, et al. (2001) Pattern Classification Wiley; and Hastie, et al. (2001) The Elements of Statistical Learning: Data Mining, Inference, and Prediction Springer-Verlag. One approach to determine whether a sample is more similar to or has maximum similarity with a given condition between the sample and one or more pools representing different conditions for comparison; the pool with the
30 smallest vector angle is then chosen as the most similar to the biological sample among the pools compared.

Characteristics of cancer-associated proteins

Cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the cancer protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus.

- 5 Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the Cell (3d ed.) Garland). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase
- 10 activity, polymerase activity, and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

- An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In
- 15 addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH
- 20 domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. These motifs can be identified on the basis of amino acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.
- 25 One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420 ; Bateman, et al. (1999) Nuc.
- 30 Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may

have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors, and the like. Extracellular domains also bind to cell-associated

molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

5 Cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are
10 typically permeabilized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment. Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

It will also be appreciated that a transmembrane protein can be made soluble by
15 removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal
20 sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion
25 into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or altering numerous aspects of physiology. Cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic
30 markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL mechanisms.

Use of cancer nucleic acids

As described above, cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally
5 determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

As detailed elsewhere, percent identity can be determined using an algorithm such as BLAST. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. Alignment
10 may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids described, the percentage of homology may be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, e.g., homology of sequences shorter than those of the sequences identified will be determined using the number of nucleosides in the
15 shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, e.g., nucleic acids which hybridize under high stringency to a described nucleic acid, or its complement, or is also found on naturally occurring mRNAs is considered a cancer sequence. In another embodiment, less stringent hybridization conditions are used; e.g.,
20 moderate or low stringency conditions may be used; see Ausubel, supra, and Tijssen, supra.

The cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-80, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, using the sequences provided herein, extended sequences, in either direction, of
25 the cancer genes can be obtained, using techniques well known for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent
30 parts recombined to form the entire cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant cancer nucleic acid can

be further used as a probe to identify and isolate other cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant cancer nucleic acids and proteins.

The cancer nucleic acids of the present invention are used in several ways. In one embodiment, nucleic acid probes to the cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, cancer nucleic acids that include coding regions of cancer proteins can be put into expression vectors for the expression of cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8-100 bases long, with from about 10-80 bases being preferred, and from about 30-50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

Nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or
5 binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, e.g., streptavidin to the support and
10 the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds, and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid
15 support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

20 The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often, the substrate may contain discrete individual sites appropriate for individual partitioning and identification. The number of possible substrates is very large, and include, but
25 are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably
30 fluoresce. See WO 0055627.

Generally the substrate is planar, although other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube for flow-

through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is
5 derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups, and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers; e.g., homo-or hetero-bifunctional linkers as are well known
10 (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or
15 attachment may be via linkage to an internal nucleoside. In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface. For example,
20 photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix
25 GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative
30 amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of cancer-associated RNA. Methods of quantitative amplification are well known.

Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569, Landegren, et al. (1988) Science 241:1077-1080, and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Natl. Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of cancer proteins from nucleic acids

In a preferred embodiment, cancer nucleic acids, e.g., encoding cancer proteins, are used to make a variety of expression vectors to express cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in

the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the cancer protein. Numerous types of appropriate expression vectors and suitable regulatory sequences are known for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known, and are useful in the present invention.

An expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, *supra*; and Kitamura, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:9146-9150.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known and will vary with the host cell used.

The cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a cancer protein, under the appropriate conditions to induce or cause expression of the cancer protein. Conditions appropriate for cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line), and various other human cells and cell lines.

In a preferred embodiment, the cancer proteins are expressed in mammalian cells. Mammalian expression systems may be used, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, supra). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, are available, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-
5 bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the cancer protein in bacteria. The protein is either secreted into the growth media (gram-
10 positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable
15 markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques such as calcium chloride treatment, electroporation, and others.

20 In one embodiment, cancer proteins are produced in insect cells using, e.g., expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors.

In a preferred embodiment, a cancer protein is produced in yeast cells. Yeast expression systems are well known, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillerimondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.
25

The cancer protein may also be made as a fusion protein, using available techniques. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the cancer
30 protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the cancer protein is a cancer peptide, the nucleic acid encoding the peptide may

be linked to other nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His6, myc, HA, etc.

In a preferred embodiment, the cancer protein is purified or isolated after expression. Cancer proteins may be isolated or purified in a variety of ways depending on what other
5 components are present in the sample and the requirements for purified product, e.g., natural conformation or denatured. Standard purification methods include ammonium sulfate precipitations, electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the cancer protein may be purified using a standard anti-
10 cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, e.g., Walsh (2002) Proteins: Biochemistry and Biotechnology Wiley; Hardin, et al. (eds. 2001) Cloning, Gene Expression and Protein Purification Oxford Univ. Press; Wilson, et al. (eds. 2000) Encyclopedia of Separation Science Academic Press; and Scopes (1993) Protein Purification Springer-Verlag. The degree of
15 purification necessary will vary depending on the use of the cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription
20 or translation inhibitors, etc.

Variants of cancer proteins

Also included within one embodiment of cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than
25 about 80%, even more preferably greater than about 85%, and most preferably greater than 90%. In some embodiments the homology will be as high as about 93-95% or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques, as are outlined above for nucleic acid homologies.

30 Cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of cancer proteins are portions or fragments of the wild type sequences herein. In addition, as

outlined above, the cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence.

In one embodiment, the cancer proteins are derivative or variant cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative
5 cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at many residue positions within the cancer peptide.

Also included within one embodiment of cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes:
10 substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis
15 using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as a naturally occurring analogue, although variants can also be selected which have modified characteristics.

20 While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined
25 sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1-20 amino acids, although considerably larger insertions may be tolerated. Deletions generally range from about 1-20 residues, although in some cases deletions
30 may be much larger.

Substitutions, deletions, insertions, or combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the

alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships described.

The variants typically exhibit essentially the same qualitative biological activity and will
5 elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of cancer proteins as needed. Alternatively, the variant may be designed such that a biological activity of the cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Substantial changes in function or immunological identity are sometimes made by
10 selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which generally are expected to produce the greatest changes in the polypeptide's
15 properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain,
20 e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Variants typically exhibit a similar qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to
25 modify the characteristics of the skin cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of
30 a cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking cancer polypeptides to a water-

insoluble support matrix or surface for use in a method for purifying anti-cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutamyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of serinyl, threonyl, or tyrosyl residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1992) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the cancer polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence cancer polypeptide. Glycosylation patterns can be altered in many ways. Different cell types to express cancer-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence cancer polypeptide (for O-linked glycosylation sites). The cancer amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g., WO 87/05330; pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for

amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) Arch. Biochem. Biophys. 259:52-57 and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases.

5 See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of cancer comprises linking the cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

10 Cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-

15 terminus of the cancer polypeptide. The presence of such epitope-tagged forms of a cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a cancer polypeptide

20 with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are available. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol.

25 Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science

30 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Natl. Acad. Sci. USA 87:6393-6397).

Also included are other cancer proteins of the cancer family, and cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related cancer proteins from humans or other organisms. Particularly useful probe and/or PCR primer
5 sequences include the unique areas of the cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for PCR reaction have been well described (e.g., Innis, PCR Protocols, supra).

In addition, cancer proteins can be made that are longer than those encoded by the
10 nucleic acids of the Tables, e.g., by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Cancer proteins may also be identified as being encoded by cancer nucleic acids. Thus, cancer proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

15 Antibodies to cancer proteins

In a preferred embodiment, when the cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell
20 receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from a protein sequence set out in the tables.

25 Methods of preparing polyclonal antibodies exist (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 2A-80 or
30 fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum

albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). Various immunization protocols may be used.

- 5 The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent.
- 10 Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line
- 15 using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine, or human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or
- 20 more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.
- 25 In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for another antigen, and
- 30 preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to cancer protein are capable of reducing or eliminating a biological function of a cancer protein, in a naked form or conjugated to an effector moiety, as is described below. That is, the addition of anti-cancer protein antibodies (either polyclonal or preferably monoclonal) to cancer tissue (or cells containing cancer) may
5 reduce or eliminate the cancer. Generally, at least a 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.)
10 Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the
15 recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized
20 antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human
25 immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be essentially performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeven, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding
30 sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human antibodies can also be produced using phage display libraries (Hoogenboom and Winter (1992) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95).

- 5 Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-851; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

- 15 By immunotherapy is meant treatment of cancer with an antibody raised against cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

- 25 In a preferred embodiment the cancer proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted cancer protein, e.g., in autocrine signaling.

- In another preferred embodiment, the cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may bind the extracellular domain of the cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane cancer protein. The antibody may be a competitive, non-
- 30

competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the cancer protein. The antibody may also be an antagonist of the cancer protein. Further, the antibody may prevent activation of the transmembrane cancer protein, or may induce or suppress a particular cellular pathway. In one aspect, when the antibody prevents the binding of
5 other molecules to the cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane
10 protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, cancer may be treated by administering to a patient antibodies directed against the transmembrane cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, target a drug loaded liposome, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The
15 effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a cancer protein. In another aspect the therapeutic moiety may modulate the activity of molecules associated with or in close proximity to a cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or
20 collagenase or protein kinase activity associated with cancer, or be an attractant of other cells, such as NK cells. See, e.g., USSN 09/544,494.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with cancer. Cytotoxic agents
25 are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, croton, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against cancer proteins, or binding of a
30 radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane cancer proteins not only serves to increase the local concentration of therapeutic moiety in the cancer afflicted area, but also serves to reduce

deleterious side effects that may be associated with the untargeted therapeutic moiety.

Antibody fragments may be used to target toxin loaded liposomes.

In another preferred embodiment, the cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein
5 which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto may contain a signal for that target localization, e.g., a nuclear localization signal.

10 The cancer antibodies of the invention specifically bind to cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related sequences is often also important.

15 Detection of cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing cancer) and in cancer tissue (and in some cases, for varying severities of cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide
20 expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including
25 both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and
30 among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus

permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene
5 expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to,
10 quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene
15 expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to cancer genes, e.g., those identified as
20 being important in a cancer or disease phenotype, can be evaluated in a cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. The assays
25 are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the cancer protein are detected. Although DNA or RNA encoding the cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a cancer protein is detected. Probes to detect mRNA can
30 be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA, or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after

immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method, detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably
5 labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl
10 phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane, or intracellular proteins) are used in diagnostic assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in diagnostic assays. This can be performed on an individual gene or
15 corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of cancer, e.g., for prognostic or
20 diagnostic purposes. Detection of these proteins in putative cancer tissue allows for detection, prognosis, or diagnosis of cancer or similar disease, and for selection of therapeutic strategy. In one embodiment, antibodies are used to detect cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following
25 separation of proteins, the cancer protein is detected, e.g., by immunoblotting with antibodies raised against the cancer protein.

In another preferred method, antibodies to the cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai, et al. (eds. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. In this method, cells are contacted with
30 from one to many antibodies to the cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a

detectable label. In another method the primary antibody to the cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of cancer proteins.

5 Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

10 In another preferred embodiment, antibodies find use in diagnosing cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of cancer proteins. Antibodies can be used to detect a cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous cancer protein.

15 In a preferred embodiment, in situ hybridization of labeled cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, a diagnosis, a prognosis, or a prediction may be based on the findings. It is further understood that the genes
20 which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in prognosis assays. As above, gene
25 expression profiles can be generated that correlate to cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, cancer probes may be attached to biochips for the detection and quantification of cancer sequences in a tissue or patient. The assays proceed as outlined
30 above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in drug screening assays or
5 by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-88; Heid (1996) Genome Res. 6:986-994.

10 In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the cancer phenotype or an identified physiological function of a cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of
15 drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be
20 performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal
25 versus tissue undergoing cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

30 The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be

monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically
5 involve a plurality of those entities described herein.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for
10 each well.

Modulators of cancer

Expression monitoring can be performed to identify compounds that modify the expression of one or more cancer-associated sequences, e.g., a polynucleotide sequence set out
15 in the tables. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate cancer, modulate cancer proteins, bind to a cancer protein, or interfere with the binding of a cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical
20 equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator
25 suppresses a cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

30 Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or

less than 1500, or less than 1000, or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or
5 heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a cancer protein. By "neutralize"
10 is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity,
15 creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis. See, e.g., Janzen (2002) High Throughput Screening: Methods and Protocols Humana; Devlin (ed. 1997) High Throughput Screening: The Discovery of Bioactive Substances Dekker; and Mei and Czarnik (eds. 2002) Integrated Drug Discovery Techniques
20 Dekker.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired
25 characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical
30 library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be

synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37:1233-1251).

Preparation and screening of combinatorial chemical libraries is well known. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6909-6913, vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-1305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33 Baum (Jan 18, 1993) C&EN; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and

implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of cancer gene transcription, inhibition, or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test

compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines, or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eukaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc.; with purification and/or amplification such as PCR performed as appropriate. For example, an in

vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target
5 sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which
10 specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

These assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702,
15 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246, and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

20 A variety of hybridization conditions may be used in the present invention, including high, moderate, and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration,
25 salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components
30 of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used

to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

5 The assay data are analyzed to determine the expression levels, and changes in expression levels as between states of individual genes, forming a gene expression profile.

 Screens are performed to identify modulators of the cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another
10 embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially
15 expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

 In addition, screens can be done for genes that are induced in response to a candidate agent or treatment process. After identifying a modulator based upon its ability to suppress a cancer expression pattern leading to a normal expression pattern (or its converse), or to
20 modulate a single cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated cancer tissue reveals genes that are not expressed in normal tissue or cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be
25 identified and used by methods described herein for cancer genes or proteins. In particular, these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics, e.g., toxin loaded liposomes, to the treated cancer tissue sample.

 Thus, in one embodiment, a test compound is administered to a population of cancer
30 cells that have an associated cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell

surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

5 Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

 Thus, e.g., cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on cancer activity. By defining such a signature for the cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein
15 need to change.

 In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes
20 are sometimes referred to herein as "cancer proteins" or a "cancer modulatory protein". The cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the cancer modulatory protein is a fragment. In a preferred embodiment, the cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of the Tables. In another
25 embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

 Preferably, the cancer modulatory protein is a fragment of about 14-24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a
30 non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.

In one embodiment the cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the cancer protein is conjugated to BSA.

Measurements of cancer polypeptide activity, or of cancer or the cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5-48 hours. In one embodiment, the cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA, and the like with an antibody that selectively binds to the cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or

the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins." The cancer protein may be a fragment, or alternatively, the full length protein to a fragment shown herein.

5 In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

10 In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the cancer proteins can be used in the assays.

15 Thus, in a preferred embodiment, the methods comprise combining a cancer protein and a candidate compound, and determining the binding of the compound to the cancer protein. Preferred embodiments utilize the human cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative cancer proteins may be used.

20 Generally, in a preferred embodiment of the methods herein, the cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface
25 of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes, and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular
30 manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not

sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked
5 through incubation with bovine serum albumin (BSA), casein, or other innocuous protein or other moiety.

In a preferred embodiment, the cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the cancer protein is added. Novel binding agents include specific antibodies, non-natural
10 binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.), and the like.

15 The determination of the binding of the test modulating compound to the cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and
20 washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

25 In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (e.g., a cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test
30 compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between about 4–40° C. Incubation

periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1-1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

5 In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent.

10 Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the cancer protein with a higher affinity. Thus, if the test
15 compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the cancer proteins. In one embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second
20 sample comprises a test compound, a cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

25 Alternatively, differential screening is used to identify drug candidates that bind to the native cancer protein, but cannot bind to modified cancer proteins. The structure of the cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

30 Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein.

Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

5 A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may
10 be added in an order that provides for the requisite binding.

 In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a
15 cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

 In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including
20 chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

 In this way, compounds that modulate cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the
25 compound.

 In one embodiment, a method of inhibiting cancer cell division is provided. The method comprises administration of a cancer inhibitor. In another embodiment, a method of inhibiting cancer is provided. The method may comprise administration of a cancer inhibitor. In a further embodiment, methods of treating cells or individuals with cancer are provided, e.g., comprising
30 administration of a cancer inhibitor.

 In one embodiment, a cancer inhibitor is an antibody as discussed above. In another embodiment, the cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are available, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described, e.g., in Freshney (1998) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss; Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss; and Garkavtsev, et al. (1996) Nature Genet. 14:415-20.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (2000), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1998), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879); Freshney, supra. This is in part due to release of various growth

5 factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released
10 from human glioma at a higher level than from normal brain cells (see, e.g., Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem. Cancer Biol. 3:89-96.

15 Various techniques which measure the release of these factors are described in Freshney (1998), supra. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum; Freshney (1985)
20 Anticancer Res. 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate cancer-associated sequences.

Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into
25 Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other
30 extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved,

or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), *supra*.

Tumor growth in vivo

Effects of cancer-associated sequences on cell growth can be tested in transgenic or
5 immune-suppressed mice. Knock-out transgenic mice can be made, in which the cancer gene is disrupted or in which a cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the
10 endogenous cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the
15 chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288-1292). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

20 Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected
25 into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably about 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction
30 (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a cancer-associated protein is down-regulated, or entirely inhibited, by the use of an inhibitory or antisense polynucleotide, e.g., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. Analogs are comprehended by this invention so long as they function effectively to hybridize with the cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for cancer molecules. A preferred antisense molecule is for a cancer sequences in the Tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14-30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific manner. See, e.g., Brumelkamp, et al. (2002) Scienceexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be

effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

5 In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general
10 review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparation are described in, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-
15 45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

Polynucleotide modulators of cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface
20 receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of cancer may be introduced into a cell containing the
25 target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating cancer in cells or organisms are
30 provided. In one embodiment, the methods comprise administering to a cell an anti-cancer antibody that reduces or eliminates the biological activity of an endogenous cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic

acid encoding a cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the cancer sequence is down-regulated in cancer, such state may be reversed by increasing the amount of cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous cancer gene or administering a gene
5 encoding the cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/0386. Alternatively, e.g., when the cancer sequence is up-regulated in cancer, the activity of the endogenous cancer gene is decreased, e.g., by the administration of a cancer antisense or other
10 inhibitor, e.g., RNAi.

In one embodiment, the cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to cancer proteins. Similarly, the cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify cancer antibodies useful for production, diagnostic, or therapeutic
15 purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The cancer antibodies may be coupled to standard affinity chromatography columns and used to purify cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the cancer protein.

20 Methods of identifying variant cancer-associated sequences

Without being bound by theory, expression of various cancer sequences is correlated with cancer. Accordingly, disorders based on mutant or variant cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant cancer genes, e.g., determining all or part of the sequence of at least one
25 endogenous cancer gene in a cell. In a preferred embodiment, the invention provides methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced cancer gene to
30 a known cancer gene, e.g., a wild-type gene.

The sequence of all or part of the cancer gene can then be compared to the sequence of a known cancer gene to determine if any differences exist. This can be done using known

homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the cancer gene of the patient and the known cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

5 In a preferred embodiment, the cancer genes are used as probes to determine the number of copies of the cancer gene in the genome.

In another preferred embodiment, the cancer genes are used as probes to determine the chromosomal localization of the cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the cancer gene locus.

10 Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable using known techniques. See, e.g., Ansel, et al. (1999) 15 Pharmaceutical Dosage Forms and Drug Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceut. Assn.; and Pickar (1998) Dosage Calculations Thomson. Adjustments for cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as 20 the age, body weight, general health, sex, diet, time of administration, drug interaction, and the severity of the condition may be necessary. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in cancer.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and 25 veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, 30 vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts, and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are available.

The compositions for administration will commonly comprise a cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by
5 conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents, and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, and the like. The concentration of active agent in these formulations can vary widely, and will be
10 selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., (1980) Remington's Pharmaceutical Science (18th ed.) Mack, and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill.

Thus, a typical pharmaceutical composition for intravenous administration would be
15 about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent.

20 The compositions containing modulators of cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend
25 upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a
30 mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender,

administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present cancer protein-modulating compounds can be administered alone or in combination with additional cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the Tables, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA, or other foreign genetic material into a host cell (see, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the cancer coding regions) can be administered in a gene therapy application. These cancer genes can include inhibitory applications, e.g., as inhibitory RNA, gene therapy (e.g., for incorporation into the genome), or antisense compositions.

Cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can

include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341-349), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in
5 immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p.
10 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al.
15 (1995) Nature Med. 1:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de
20 Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance
25 designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham,
30 Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron, or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes;

biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient.

5 This approach is described, for instance, in Wolff et. al. (1990) Science 247:1465-1468, as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S.
10 Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode cancer polypeptides or polypeptide
15 fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors are available for therapeutic
20 administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing a
25 cancer gene or portion of a cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a cancer patient. The cancer gene used for DNA vaccines can encode full-length cancer proteins, but more preferably encodes portions of the cancer proteins including peptides derived from the cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a
30 cancer gene. For example, cancer-associated genes or sequence encoding subfragments of a cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure

provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the cancer polypeptide encoded by the DNA vaccine. Additional or
5 alternative adjuvants are available.

In another preferred embodiment, cancer genes find use in generating animal models of cancer. When the cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein inhibitory or antisense RNA directed to the cancer gene will
10 also diminish or repress expression of the gene. Animal models of cancer find use in screening for modulators of a cancer-associated sequence or modulators of cancer. Similarly, transgenic animal technology, including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the cancer protein. When desired, tissue-specific expression or knockout of the
15 cancer protein may be necessary.

It is also possible that the cancer protein is overexpressed in cancer. As such, transgenic animals can be generated that overexpress the cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a
20 determination of the expression level of the transgene. Animals generated by such methods will find use as animal models of cancer and are additionally useful in screening for modulators to treat cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are
25 also provided by the invention. In diagnostic and research applications, such kits may include at least one of the following: assay reagents, buffers, cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative cancer polypeptides or polynucleotides, small molecule inhibitors of cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically
30 acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials

typically comprise written or printed materials, they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to, electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may
5 include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing cancer-associated
10 activity. Optionally, the kit contains biologically active cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will typically be selected based on correlations with important parameters in disease which may be identified in historical or
15 outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and
20 analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Table 1 lists medical conditions, abnormalities, or organs affected by diseases, referred to in Tables 2A and 3A, for which markers have been identified, and other related medical conditions (including various stages and/or metastases) in which those markers will also be useful, e.g., in therapeutic, diagnostic, prognostic, subsetting, vaccine, and other uses.

- 5 blood vessels/angiogenesis: hemangiomas, lymphangiomas, angiosarcoma, lymphangiosarcoma, Kaposi's sarcoma, wound healing, tissue remodeling, psoriasis, ischemic heart disease, inflammatory diseases (e.g., arthritis, asthma, chronic bronchitis), atherosclerosis, endometriosis, presumed ocular histoplasmosis syndrome, hypoxia, solid tumors, lymphomas, lymphadenitis, lymphangitis, autoimmune diseases (e.g., RA, SLE, juvenile chronic arthritis, pigmented villonodular synovitis, etc.), retinal neovascularization syndromes (e.g., diabetic retinopathy, macular degeneration, presumed ocular histoplasmosis syndrome, etc.), scleritis/conjunctivitis, hypertrophic scars (keloid), birth control, uterine fibroids
- 10 bladder: carcinoma in situ, papillary carcinomas, transitional cell carcinoma, squamous cell carcinoma
bone: Ewing sarcoma, sarcomas arising from skeletal and extraskelatal connective tissues, including the peripheral nervous system (e.g. chondrosarcoma, osteosarcoma)
brain: glioblastoma, oligodendroglioma, anaplastic astrocytoma, meningioma, medulloblastoma, neuroblastoma, ependymoma, schwannoma, craniopharyngioma, pineoblastoma, pheocytoma, neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors, granular cell tumors, plexosarcoma, ganglioneuroma, neuroepithelioma, neuroma, ganglioneuroma
- 15 breast: ductal carcinoma in situ, lobular carcinoma in situ
cervix: cancer of the cervix, vagina, or vulva
colon/rectum: precancerous colorectal disease (e.g., neoplastic polyps (adenomas), familial adenomatous polyposis, ulcerative colitis), colon cancer, e.g., epithelial tumor (e.g., adenocarcinoma, mucinous adenocarcinoma, signet-ring cell adenocarcinoma, squamous cell carcinoma, adenosquamous carcinoma, undifferentiated carcinoma, unclassified carcinoma), carcinoid tumor (e.g., argentaffin, nonargentaffin, composite), non-epithelial tumor (e.g., leiomyosarcoma, others), inflammatory bowel disease (e.g., ulcerative colitis, Crohn's disease (granulomatous colitis), dysplasia), rectal cancer, cancer of the anal region (e.g., squamous cell carcinoma, transitional carcinoma, adenocarcinoma, carcinoma, papillary villous carcinoma, mucinous adenocarcinoma, melanoma)
- 20 esophagus: premalignant or predisposing conditions (e.g., esophagitis), squamous cell cancers (e.g., cancers of the head and neck, lung, or cervix), gastroduigestive carcinomas (e.g., cancers of the stomach, colon, or rectum)
fibrosis: lung fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, cirrhosis (liver fibrosis), renal fibrosis, scleroderma, wound healing
- 25 head and neck: tumors of the nasal cavity, paranasal sinuses, nasopharynx, oral cavity, oral pharynx, lip, larynx, hypopharynx, salivary glands, paragangliomas, esophagus
kidney: clear cell (nonpapillary) carcinoma, papillary carcinoma, chromophobe renal carcinoma, hypernephroma, adenocarcinoma, sporadic renal carcinomas, hereditary renal carcinomas (von Hippel-Lindau disease), carcinoma of the renal pelvis, ureteral carcinoma, fibroma, papillary adenoma, angiolymphoma, oncocyoma
leukocytes: acute lymphoblastic leukemia/lymphoma, chronic lymphocytic leukemia, follicular lymphoma, large B-cell lymphoma, Burkitt lymphoma, plasma cell neoplasms, mantle cell lymphoma, lymphoplasmacytic lymphoma, peripheral T-cell lymphoma, adult T-cell leukemia/lymphoma, Hodgkin disease, acute myelogenous leukemia, chronic myelogenous leukemia, thymic hyperplasia, hairy cell leukemia, malignant transformation, inappropriate activation or abnormalities of leukocytes (e.g., immature, precursor B (pre-B) or precursor T (pre-T) lymphocytes, monocytes, neutrophils, eosinophils, basophils, dendritic cells, lymphoblasts), arthritis, inflammation, leukocytosis, lymphadenitis, lymphangitis, bacteremia, chronic nonspecific lymphadenitis, psoriasis, wound healing
- 30 liver: hepatitis (e.g., types A, B, C), benign epithelial tumors and tumor like conditions, primary malignant epithelial tumors, primary malignant mesenchymal tumors, tumors of the gallbladder or bile duct
- 35 lung: lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, esophageal cancer
ovary: ovarian carcinoma (e.g., epithelial (serous tumors, mucinous tumors, endometrioid tumors), germ cell (e.g., teratomas, choriocarcinomas, polyembryomas, embryonal carcinoma, endodermal sinus tumor, dysgerminoma, gonadoblastoma), stromal carcinomas (e.g., granulosa stromal cell tumors)), fallopian tube carcinoma, peritoneal carcinoma, leiomyoma
- 40 pancreas: adenocarcinoma, ductal adenocarcinoma, mucinous cyst adenocarcinoma, acinar cell carcinoma, unclassified large cell carcinoma, small cell carcinoma, pancreatoblastoma, duct-ectatic mucin-hypersecreting tumor, mucinous cyst adenoma, papillary cystic neoplasm, serous cyst adenoma, diabetes mellitus, chronic pancreatitis
prostate: epithelial neoplasms (e.g., adenocarcinoma, small cell tumors, transitional cell carcinoma, carcinoma in situ, and basal cell carcinoma), carcinosarcoma, non-epithelial neoplasms (e.g., mesenchymal and lymphoma), germ cell tumors, prostatic intraepithelial neoplasia (PIN), hormone independent prostate cancer, benign prostate hyperplasia, prostatitis
- 45 skin/melanoma: melanoma, lentigo (common benign localized hyperplasia of melanocytes), nevocellular nevi (congenital or acquired neoplasm of melanocytes), actinic keratosis (overgrowth of outer layers of skin), basal cell carcinoma, Merkel cell carcinoma, benign fibrous histiocytoma (dermal neoplasms of fibroblasts and histiocytes), dermatofibrosarcoma protuberans (well differentiated fibrosarcoma of the skin), xanthomas (tumor-like collections of foamy histiocytes within the dermis), dermal vascular tumors, seborrheic keratoses (benign tumor), acanthosis nigricans (benign or malignant hyperplasia and hyperpigmentation of skin), and squamous cell carcinomas of the skin, lung, cervix, esophagus, uterus, head, neck, or bladder
- 50 soft tissue: soft tissue tumors (e.g., fibrosarcoma, liposarcoma, leiomyosarcoma, histiocytoma, fibrohistiocytic sarcoma) smooth muscle tumors (e.g., rhabdomyoma, rhabdomyosarcoma) tumors of the blood and lymph vessels (e.g., angiosarcoma, lymphangiosarcoma, Kaposi's sarcoma), perivascular tumors (e.g., glomus tumors, hemangiopericytoma), synovial tumors (e.g., mesothelioma), neural tumors (e.g., neurofibroma, neurofibrosarcoma, malignant peripheral nerve sheath tumors, granular cell tumors, plexosarcoma, ganglioneuroma, neuroepithelioma, extraskelatal Ewing's sarcoma, schwannoma, neuroma, ganglioneuroma), paraganglioma, extraskelatal cartilaginous and osseous tumors (e.g., chondrosarcoma, osteosarcoma), pluripotent mesenchymal tumors, epithelioid sarcomas, rhabdoid tumors, desmoplastic small cell tumors, alveolar sarcoma
- 55 stomach: adenocarcinoma, squamous cell carcinoma, adenocanthoma, carcinoid, leiomyosarcoma, gastritis (chronic atrophic, H. pylori associated), hyperplastic polyps, lipoma, leiomyoma, esophageal adenocarcinomas
- 60 testicles: germ cell tumors (including seminomas, embryonal carcinomas, teratomas, choriocarcinomas, yolk sac tumors), sex chord stromal tumors (including Leydig cell tumors, Sertoli cell tumors, and Granulosa cell tumors), germ cell and gonadal stromal elements (e.g., gonadoblastomas), adnexal and paratesticular tumors (e.g., mesotheliomas, soft tissue sarcomas, and adnexal of the rete testes), miscellaneous neoplasms (including carcinoid, lymphoma, and cysts)
uterus: epithelial tumors (e.g., endometrioid, papillary endometrioid, papillary serous, clear cell, mucinous), mesenchymal tumors (e.g., endometrial stromal sarcoma, leiomyosarcoma, nonspecific sarcomas), mixed tumors (e.g., malignant mixed müllerian tumors, adenosarcoma)

70 Tables 2B-72B, 76B, and 79B list accession numbers for Pkeys lacking UnigeneID's for Tables 2A-72A, 76A, and 79A, respectively. For each probeset is listed gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

75 Tables 2C-72C, 76C, and 79C list genomic positioning for Pkeys lacking Unigene ID's and accession numbers in Tables 2A-72A, 76A, and 79A, respectively. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Table 2A, Disease Indications and Preferred Utilities for Selected Genes

80 Table 2A provides preferred disease indications and preferred utilities for about 413 selected genes. These genes were identified using Eos/Alfymetrix Genechip arrays.

Pkey:	Unique Eos probeset identifier number
ExAcct:	Exemplar Accession number
UnigeneID:	Unigene ID number

Unigene Title: Unigene gene title
 Disease: preferred diseases indicated for selected gene as described in table 1 and abbreviated as follows: blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), glio (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrosis diseases), headnk (head & neck diseases), lei (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), sarc (soft tissue and bone diseases), mela (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)
 Utility: preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)

Pkey; ExAccn; UnigeneID; Unigene Title; Disease; Utility

102892; BE440042; Hs.83326; matrix metalloproteinase 3 (st; headnk; mAb+diag+s.m.
 104865; T79340; Hs.22575; B-cell CLL/lymphoma 6, member ; angio; CTL
 104978; A1199268; Hs.19322; Homo sapiens, Similar to RIKEN; colon, lung, pros, blad, stom; CTL
 109424; NM_005329; Hs.85962; hyaluronan synthase 3; blad, lung; mAb+s.m.
 110765; AK000322; Hs.18457; hypothetical protein FLJ20315; colon, pros, stom, uter; mAb+diag
 110906; AA035211; Hs.17404; SOX7 SRY (sex determining reg; angio, blad; CTL
 115522; BE614387; Hs.333893; c-Myc target JPO1; colon, lung, blad, panc; CTL
 116176; AA311152; Hs.288708; hypothetical protein FLJ21562; colon; CTL
 118595; AK000465; Hs.50081; KIAA1199 protein; colon, lung; diag
 123049; BE047680; Hs.211869; dickkopf (Xenopus laevis) homo; EWS; mAb+diag
 131486; F06972; Hs.27372; endothelial tyrosine kinase (E; angio; CTL+s.m.
 133370; AF245505; Hs.72157; Adican; breast, lung, panc; diag
 310016; AW449812; Hs.152475; ESTs; colon; CTL
 322303; AJ357412; Hs.157601; ESTs; colon, pros, fibro, breast; CTL+diag
 400289; X07820; Hs.2258; matrix metalloproteinase 10 (s; angio, blad, lung, cerv, ovar, headnk, esoph; mAb+diag+s.m.
 400297; A127076; Hs.288381; hypothetical protein DKFp5640; breast, blad, colon, pros; mAb
 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulat; breast, ovar, pros, stom, uter, blad, lung, headnk; mAb
 400843; ; NM_003105; Homo sapiens sortil; blad; s.m.
 402075; ; ENSP00000251056; Plasma membra; blad, lung, headnk, cerv, mela, esoph; mAb+diag
 402901; ; NM_025206; Homo sapiens hypoth; blad ; CTL
 404287; ; FGENESH predicted novel CUB-dom; panc, lung, colon, uter, esoph; mAb+s.m.
 404682; ; ortholog of mouse polydomain p; panc; diag
 404875; ; NM_022819; Homo sapiens phosph; blad; CTL+s.m.
 404977; ; Insulin-like growth factor 2 (; blad, ovar, sarc; mAb+diag
 405033; ; C1002652; gij544327[sp]Q04799; blad; s.m.
 406400; ; kallikrein 8 (neuropsin/ovastin; ovar, uter; diag
 406964; M21305; ; FGENES predicted novel secrete; angio, blad, fibro, sarc; diag
 407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE:4299; glio, blad; CTL
 407792; A077715; Hs.39384; putative secreted ligand homol; ovar, uter, cerv, panc; mAb+diag
 407811; AW190902; Hs.40098; cysteine knot superfamily 1, B; blad, panc, stom, uter, lung, esoph; diag
 407836; T79340; Hs.22575; B-cell CLL/lymphoma 6, member ; angio; CTL
 407975; X89426; Hs.41716; endothelial cell-specific mole; angio, renal; diag
 408243; Y00787; Hs.624; interleukin 8; blad, stom, headnk, cerv, lung, angio, esoph, panc; diag
 408367; AK001178; Hs.44424; Homo sapiens orphan neurotrans; mela; mAb+s.m.
 408369; R38438; Hs.118747; SLC15A2 Solute carrier family ; pros, lung, fibro, uter, glio, cerv, ovar; mAb
 408380; AF123050; Hs.44532; diubiquitin; lung, blad, headnk, panc, stom, fibro, esoph, mela; CTL
 408482; NM_000576; Hs.45743; adenosine A2b receptor; lung, esoph, headnk, colon; mAb+s.m.
 408562; A1436323; Hs.31141; roundabout (axon guidance rece; uter, fibro, sarc; mAb+s.m.
 408790; AW580227; Hs.47860; neurotrophic tyrosine kinase, ; lung; mAb+s.m.
 408908; BE296227; Hs.250822; serine/threonine kinase 15; blad, lung, headnk, stom, colon; s.m.
 409041; AB033025; Hs.50081; Hypothetical protein, XP_05186; uter, ovar, lung, colon, stom, headnk, breast, panc; CTL+diag
 409079; W87707; Hs.82065; interleukin 6 signal transduce; breast, pros; mAb+s.m.
 409103; AF251237; Hs.112208; XAGE-1 protein; lung; CTL
 409178; BE393948; Hs.50915; kallikrein 5; ovar, breast, mela; diag
 409220; BE243323; Hs.51233; tumor necrosis factor receptor; angio, renal, colon, stom; mAb+s.m.
 409420; Z15008; Hs.54451; laminin, gamma 2 (nicotin 100k; lung, headnk, panc, stom, cerv, esoph, blad; diag
 409632; W74001; Hs.55279; serine (or cysteine) proteinase; lung, blad, headnk; diag
 409663; A1743750; Hs.98306; KIAA1862 protein; renal; CTL
 409757; NM_001898; Hs.123114; cystatin SN; panc, stom, lung, blad; diag
 409889; AW630041; Hs.56937; suppression of tumorigenicity ; colon, ovar, pros; mAb+s.m.
 409893; AW247090; Hs.57101; minichromosome maintenance def; lung, cerv, blad, test, esoph; CTL+s.m.
 409956; AW103364; Hs.727; inhibin, beta A (activin A, ac; breast, panc, ovar, colon, headnk, lung, blad, esoph; diag
 410001; AB041036; Hs.57771; kallikrein 11; ovar, pros, uter, cerv, lung ; diag
 410055; AJ250839; Hs.58241; gene for serine/threonine prot; renal; s.m.
 410153; BE311926; Hs.15830; hypothetical protein FLJ12691; renal, blad; CTL
 410274; AA381807; Hs.336402; hypoxia-inducible protein 2; lung, renal; CTL
 410309; BE043077; Hs.278153; alpha-2,8-sialyltransferase II; panc; s.m.
 410407; X66839; Hs.63287; carbonic anhydrase IX; renal, lung, colon, stom, ovar, uter, blad, sarc; mAb+s.m.
 410418; D31382; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 411274; NM_002776; Hs.69423; kallikrein 10; colon, ovar, uter, cerv, headk, panc; diag
 411411; AA345241; Hs.55950; ESTs, Weakly similar to KIAA13; renal; mAb+s.m.
 411773; NM_006799; Hs.72026; protease, serine, 21 (testisin; ovar; diag
 411975; A1916058; Hs.144583; 3'UTR of dead ringer (Drosoph; test, colon; CTL
 412078; X69699; Hs.73149; paired box gene 8; ovar; CTL
 412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like; lung, blad, headnk, breast, ovar, panc, angio, test, mela; s.m.
 412314; AA825247; Hs.356084; G protein-coupled receptor 27 ; ovar, uter, test; mAb+s.m.
 412609; Z48804; Hs.74124; ocular albinism 1 (Nettleship; mela; s.m.
 412628; A1972402; Hs.306051; hypothetical protein MGC2648; pros; diag
 412709; AL022327; Hs.74518; KIAA0027 protein; glio, sarc; mAb+s.m.
 412719; AW016610; Hs.816; ESTs; lung, headnk, blad, glio, cerv, sarc; s.m.
 412959; D87458; Hs.75090; KIAA0282 protein; glio; CTL+s.m.
 413048; M93221; Hs.75182; mannose receptor, C type 1; fibro, panc; mAb

- 413063; AL035737; Hs.75184; chitinase 3-like 1 (cartilage; glio, ovar, blad, lung; diag
 413278; BE553085; Hs.833; interferon-stimulated protein; panc, lung, blad, breast, cerv, ovar, headnk, esoph, mela; CTL+s.m.
 413324; V00571; Hs.75294; corticotropin releasing hormon; blad; diag
 413365; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxyg; blad, lung, mela, fibro, uter, sarc; s.m.
 413554; AA319146; Hs.75426; secretogranin II (chromogranin; panc, glio; diag
 413719; BE439580; Hs.75498; small inducible cytokine subfa; leuk, panc, lung, headnk, cerv, colon, uter, stom, esoph; diag
 414555; N98569; Hs.76422; phospholipase A2, group IIA (p; pros; s.m.
 414577; A056548; Hs.378938; hypothetical protein FLJ20992; angio; CTL+diag
 414774; X02419; Hs.72774; plasminogen activator, urokinase; lung, blad, headnk, panc, stom, ovar, esoph; diag
 414812; X72755; Hs.77367; monokine induced by gamma inta; breast, blad, lung, fibro, panc, colon, headnk, cerv, stom, renal, ovar, test, mela, esoph; diag
 414883; AA926960; Hs.348669; CDC28 protein kinase 1; lung, ovar, stom, colon, cerv, headnk, test; s.m.
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; blad, lung, ovar, test; s.m.
 414991; C17898; Hs.295944; tissue factor pathway inhibitor; angio, panc, stom, lung, uter; CTL+diag
 415138; C18356; Hs.72472; NAME OMITTED ... receptor kinase; breast; mAb+s.m.
 415539; A1733881; Hs.306814; Homo sapiens lysyl oxidase-like; mela; diag
 415668; AW957684; Hs.78589; serine (or cysteine) proteinase; lung; mAb+diag+s.m.
 415669; NM_005025; Hs.78589; serine (or cysteine) proteinase; lung; mAb+diag+s.m.
 415817; U88967; Hs.78867; protein tyrosine phosphatase; lung, glio, headnk, cerv, mela, esoph, fibro, mAb+s.m.
 415929; AA724373; Hs.304950; Homo sapiens mucopolin-3 (MCO3); mela; mAb
 416091; AF295370; Hs.283082; defensin, beta 3; headnk, esoph, mela; CTL+diag
 416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient; lung, headnk, colon, uter, stom; CTL+s.m.
 416250; AA581386; Hs.73452; Kremen 2; esoph, lung, cerv, ovar; mAb+s.m.
 416530; U62801; Hs.79361; kallikrein 6 (neurosin, zyma); ovar, uter; diag
 416638; N32538; Hs.42645; solute carrier family 16 (mono; breast, panc, uter, mela; mAb+s.m.
 416658; U03272; Hs.79432; fibrinogen; lung, ovar, uter, blad, angio, test, sarc; diag
 416835; D54745; Hs.80247; cholecystokinin; pros, EWS, glio; diag
 416857; AA188775; Hs.292453; FGENSEH predicted TM containing; glio; mAb+s.m.
 416965; N26223; Hs.160436; MDAC1; fibro, ovar, uter; mAb
 417034; NM_006183; Hs.80962; neurotensin; lung, headnk, cerv; diag
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; blad, lung, headnk, cerv, esoph; diag
 417166; AA431323; Hs.42146; Paired box protein Pax-3; mela, sarc; CTL
 417389; BE260964; Hs.82045; midkine (neurite growth-promot; ovar, lung, blad, uter, cerv, panc, stom, mela, test, colon, sarc; mAb+diag
 417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glyco; panc, breast, blad, lung, headnk, cerv, uter, ovar, stom, renal; mAb
 417771; AA804698; Hs.82547; retinoic acid receptor respond; blad, cerv, panc, pros, ovar; mAb
 417868; AW067903; Hs.82772; collagen, type XI, alpha 1; lung, panc, breast, ovar, headnk, stom, sarc; CTL
 417931; W95642; Hs.82961; trefoil factor 3 (intestinal); ovar, panc, stom, colon, uter, pros; diag
 417933; X02308; Hs.82962; thymidylate synthetase; blad, lung, angio, colon, panc, esoph; s.m.
 418007; M13509; Hs.83169; matrix metalloproteinase 1 (in; lung, blad, fibro, headnk, panc, stom, colon, ovar, esoph, mela; mAb+diag+s.m.
 418030; BE207573; Hs.83321; neuromedin B; glio, panc; diag
 418064; BE387287; Hs.83384; S100 calcium-binding protein; mela; diag
 418281; U09550; Hs.1154; oviductal glycoprotein 1, 120k; uter, ovar; CTL+diag
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibi; lung, blad, ovar, headnk, panc, cerv, mela, sarc; s.m.
 418506; AA084248; Hs.372651; Unknown protein for MGC29643; angio, ovar, glio, uter, lung, blad, panc, mela, sarc; mAb+diag
 418526; BE019020; Hs.85833; solute carrier family 16 (mono; lung, blad, renal, panc, stom, colon, ovar; mAb+s.m.
 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via d; esoph, headnk; s.m.
 418578; NM_001327; Hs.87225; cancer/testis antigen (NY-ESO-1); lung, blad, stom, ovar, panc, esoph, cerv, sarc; CTL
 418738; AW388633; Hs.6682; solute carrier family 7 (cat; angio, lung, ovar, blad, colon, stom, panc, uter, leuk; mAb+s.m.
 418830; BE513731; Hs.348874; hypothetical protein MGC4816; lung; CTL
 418867; D31771; Hs.89404; msh (Drosophila) homeo box hom; blad; s.m.
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), recep; leuk, ovar, breast, blad, renal; mAb+s.m.
 419080; AW150835; Hs.18878; hypothetical protein FLJ21620; renal, lower uter, lung; CTL
 419121; AA374372; Hs.89626; parathyroid hormone-like hormo; lung, esoph, headnk, blad; diag
 419171; NM_002846; Hs.89655; protein tyrosine phosphatase; lung; mAb+s.m.
 419172; AW338625; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio, renal; mAb+s.m.
 419183; U60669; Hs.89663; cytochrome P450, subfamily XX; blad, lung, headnk, panc; CTL+s.m.
 419216; AU076718; Hs.164021; small inducible cytokine subfa; panc, lung, stom, cerv, pros, headnk, esoph; diag
 419235; AW470411; Hs.288433; neurotrophin; panc, fibro, headnk, lung; mAb+diag
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ovar, pros, lung, breast, uter, test, panc, stom, sarc; mAb+s.m.
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-fam1; glio, omuc, stom, lung, panc, colon, renal, uter; mAb+s.m.
 419556; U29615; Hs.91093; chitinase 1 (chitobiosidase); lung, fibro, test; mAb+diag
 419704; AA429104; Hs.45057; ESTs; glio; CTL+s.m.
 419723; AL120193; Hs.339810; longevity assurance (LAG1, S.; glio; mAb+diag
 419741; NM_007019; Hs.93002; ubiquitin carrier protein E2-C; blad, lung, colon, ovar, test, esoph, mela, sarc; CTL+s.m.
 419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-IRNA; fibro, stom, blad, esoph, uter; diag
 420159; AI572490; Hs.99785; Homo sapiens cDNA: FLJ21245 f; blad, stom; mAb
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; lung, mela, sarc; s.m.
 420370; Y13645; Hs.97234; uroplakin 2; blad; mAb
 420440; NM_002407; Hs.97644; mammaglobin 2; ovar, uter, cerv; diag
 420602; AF060877; Hs.99236; regulator of G-protein signal; headnk, glio, cerv, mela; CTL+s.m.
 420610; AI583183; Hs.99348; distal-less homeo box 5; uter, endo, lung; CTL
 420737; L08096; Hs.99899; CD70; tumor necrosis factor; renal; mAb+s.m.
 420876; AA918425; Hs.177744; FGENSE predicted novel protein; panc, blad; s.m.
 421056; AU076725; Hs.101408; branched chain aminotransferase; blad, lung; CTL+s.m.
 421110; AJ250717; Hs.1355; cathepsin E; blad, panc, stom, lung, fibro, ovar, esoph; sm+diag
 421340; F07783; Hs.1369; decay accelerating factor for; angio, panc, stom; diag
 421379; Y15221; Hs.103982; small inducible cytokine subfa; breast, panc, headnk, lung, stom, blad, cerv, colon, leuk, fibro, test, mela, esoph; diag
 421471; U80545; Hs.327179; solute carrier family 17 (sodi; renal; mAb+s.m.
 421474; U76362; Hs.104637; solute carrier family 1 (gluta; lung; mAb+s.m.
 421524; AA312082; Hs.105445; GDNF family receptor alpha 1; breast; mAb+s.m.
 421552; AF026692; Hs.105700; secreted frizzled-related prot; breast, ovar, panc, cerv, uter, pros, lung, stom, headnk; diag
 421563; NM_006433; Hs.105806; granulysin; fibro; diag
 421574; AJ000152; Hs.105924; defensin, beta 2; headnk, lung; CTL+diag
 421582; AI910275; Hs.350470; trefoil factor 1 (breast cancer; breast, panc, lung, omuc; diag

- 421659; NM_014459; Hs.106511; protocadherin 17; fibro; mAb
- 421753; BE314828; Hs.107911; ATP-binding cassette, sub-fam1; lung; mAb+s.m.
- 421817; AF146074; Hs.108560; ATP-binding cassette, sub-fam1; lung, cerv, headnk, blad; mAb+s.m.
- 421829; AB018330; Hs.108708; calcium/calmodulin-dependent p; pros; s.m.
- 422048; NM_012445; Hs.288126; spondin 2, extracellular matrx; panc, pros, sarc; diag
- 422083; NM_001141; Hs.111256; arachidonate 15-lipoxygenase, ; pros; s.m.
- 422109; S73265; Hs.1473; gastrin-releasing peptide; panc, lung, colon, fibro; diag
- 422158; L10343; Hs.112341; protease inhibitor 3, skin-der; headnk, blad, lung, cerv, stom, esoph; diag
- 422192; AA305159; Hs.113019; fls485; mela; s.m.
- 422260; AA315993; Hs.105484; regenerating gene type IV; colon, omuc, stom, panc; mAb+diag
- 422282; AF019225; Hs.114309; apolipoprotein L; blad, lung, headnk, renal; diag
- 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45); lung, blad, test, cerv, headnk, esoph; s.m.
- 422330; D30783; Hs.115263; epiregulin; panc, colon, blad; mAb+diag
- 422397; AJ223366; Hs.116051; MYEOV Myeloma overexpressed ge; panc, stom, colon, esoph, renal, blad; CTL+s.m.
- 422424; AJ186431; Hs.296638; prostate differentiation facto; blad, panc, pros, angio, colon, stom, lung, mela; diag
- 422578; AF239666; Hs.1545; caudal type homeo box transcr; colon; CTL
- 422627; BE336857; Hs.118787; transforming growth factor, be; colon, renal, sarc; mAb+diag
- 422765; AW409701; Hs.1578; baculoviral IAP repeat-contain; lung, blad; s.m.
- 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; blad, cer, lung, uter, angio, stom, test; s.m.
- 422867; L32137; Hs.1584; cartilage oligomeric matrix pr; breast, ovar, pros, panc, lung, colon, uter, sarc; diag
- 422956; BE545072; Hs.122579; ECT2 protein (Epithelial cell ; ovar, blad, panc, lung, headnk, colon, stom; CTL+s.m.
- 423161; AL049227; Hs.124776; downstream of cadherin 6 (by 3; renal, ovar, blad; mAb+s.m.
- 423184; NM_004428; Hs.1624; ephrin-A1; pros, panc, renal, colon; mAb+s.m.
- 423242; AL039402; Hs.125783; DEME-6 protein; breast, renal, ovar, pros, colon; CTL
- 423508; AW604297; Hs.129711; hepatitis A virus cellular rec; renal, colon; mAb
- 423583; AL122055; Hs.129836; KIAA1028 protein; pros; s.m.
- 423634; AW959908; Hs.1690; heparin-binding growth factor ; lung, blad, headnk, panc; diag
- 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (m; blad, lung, headnk, ovar, panc, colon, stom, uter, cerv, esoph, test; mAb+diag+s.m.
- 423936; U77629; Hs.135639; achaete-scute complex (Drosophila) colon, stom, ovar, CTL
- 423961; D13666; Hs.136348; perostin (OSF-2os); breast, colon, blad, lung, fibro, panc, headnk, ovar, mela, sarc; mAb+diag
- 424008; R02740; Hs.137555; putative chemokine receptor; G; blad, headnk, stom, cerv, esoph; mAb+s.m.
- 424046; AF027866; Hs.138202; serine (or cysteine) proteinase; headnk, lung, cerv; diag
- 424321; W74048; Hs.1765; lymphocyte-specific protein ty; mela, fibro; s.m.
- 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); lung, colon, test; s.m.
- 424411; NM_005209; Hs.146543; crystallin, beta A2; panc, sarc; s.m.
- 424502; AF242388; Hs.149585; lengsin; lung; s.m.
- 424503; NM_002205; Hs.149609; Integrin, alpha 5 (fibronectin; panc, pros, angio, blad, lung; mAb+s.m.
- 424620; AA101043; Hs.151254; kallikrein 7 (chymotryptic, st; ovar; diag
- 424687; J05070; Hs.151738; matrix metalloproteinase 9 (ge; headnk, panc, lung, blad, uter, cerv, colon, stom, test, mela, sarc; diag
- 424735; U31875; Hs.272499; short-chain alcohol dehydrogen; blad, breast; CTL+s.m.
- 424825; AF207069; Hs.153357; procollagen-lysine, 2-oxogluta; mela; CTL+s.m.
- 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a); ovar, blad, lung, headnk, panc, stom; s.m.
- 424917; A1636208; Hs.96901; hypothetical protein FLJ23049; fibro, uter, ovar; CTL
- 424943; AU077260; Hs.153924; death-associated protein kinase; fibro; s.m.
- 425009; X58288; Hs.154151; protein tyrosine phosphatase, ; renal, fibro; mAb+s.m.
- 425071; NM_013989; Hs.154424; deloninase, iodothyronine, typ; pros, colon, stom, uter, cerv, headnk, esoph, panc; diag
- 425115; R44564; Hs.123956; downstream of: G protein-coupl; gli; mAb+s.m.
- 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (s; breast, ovar, lung, colon, panc, headnk, stom, uter, cerv, blad, esoph, sarc; mAb+diag+s.m.
- 425263; NM_001197; Hs.155419; BCL2-interacting killer (apopt; pros; s.m.
- 425322; U63630; Hs.155637; protein kinase, DNA-activated; lung, headnk; s.m.
- 425535; AB007937; Hs.158287; syndecan 3; mela, gli; mAb+s.m.
- 425650; NM_001944; Hs.1925; desmoglein 3 (permpigius vulgar; lung, headnk, cerv, esoph, blad; mAb
- 425721; AC002115; Hs.159309; uroplakin 1A; blad; mAb
- 425723; NM_014420; Hs.159311; dickkopf (Xenopus laevis) homo; endo, uter, colon; CTL+diag
- 425734; AF056209; Hs.159396; peptidylglycine alpha-amidatn; lung; s.m.
- 425776; U25128; Hs.159499; parathyroid hormone receptor 2; ovar, uter, lung; mAb+diag
- 425842; AJ587490; Hs.159623; NK-2 (Drosophila) homolog B; panc, gli; s.m.
- 425852; AK001504; Hs.159651; death receptor 6, TNF superfam; blad, lung, headnk; mAb+s.m.
- 425883; AL137708; Hs.161031; Homo sapiens mRNA; cDNA DKFZp4; blad, panc; mAb
- 425998; AU076629; Hs.165950; fibroblast growth factor recep; renal; mAb+s.m.
- 426028; NM_001110; Hs.172028; a disintegrin and metalloprota; blad; mAb+diag
- 426215; AW963419; Hs.155223; stannocalcin 2; breast, lung, renal, colon, ovar, uter; mAb+diag
- 426227; U67058; Hs.154299; Human proteinase activated rec; panc, lung, colon, esoph, stom; mAb+s.m.
- 426322; J05058; Hs.2012; transcobalamin I (vitamin B12 ; panc, blad, stom; diag
- 426344; H41821; Hs.322469; transcriptional activator of t; gli; CTL+s.m.
- 426427; M86699; Hs.169840; TTK protein kinase; ovar, lung, headnk, cerv, colon, uter, stom, test; CTL+s.m.
- 426451; AJ98165; Hs.169946; GATA-binding protein 3 (T-cell; blad, breast; s.m.
- 426514; BE616633; Hs.170195; bone morphogenetic protein 7 (; ovar, colon, blad, lung, cerv; mAb+diag
- 426500; NM_003378; Hs.171014; VGF nerve growth factor induc; mela, sarc; diag
- 426761; A1015709; Hs.172089; PORIMIN Pro-oncosis receptor t; lung, esoph, pros, uter, panc, colon, ovar, headnk; mAb+s.m.
- 426812; AF105365; Hs.172613; solute carrier family 12 (pot; renal; mAb+s.m.
- 426890; AA393167; Hs.41294; ESTs; renal, colon, ovar, uter, stom; CTL
- 427239; BE270447; Hs.356512; ubiquitin carrier protein; lung, blad, test, mela, sarc; CTL+s.m.
- 427335; AA448542; Hs.278444; G antigen 7B; lung, headnk, blad, mela, esoph, sarc; CTL
- 427343; AJ880044; Hs.176977; protein kinase C binding prote; gli; CTL+s.m.
- 427722; AK000123; Hs.180479; hypothetical protein FLJ20116; colon, stom, panc; CTL
- 427747; AW411425; Hs.180655; serine/threonine kinase 12; blad, lung, ovar, stom, test, esoph, sarc; s.m.
- 427923; AW274357; Hs.301408; FGENSEH predicted 11 TM protei; mela; mAb
- 427969; NM_001963; Hs.2230; epidermal growth factor (beta-; panc; mAb+diag
- 428093; AW594506; Hs.104830; ESTs; ovar, panc; CTL
- 428179; AJ127772; Hs.380877; serum/glucocorticoid regulated; breast; s.m.
- 428187; AJ687303; Hs.285529; G protein-coupled receptor 49; ovar, uter, colon, stom; mAb+s.m.
- 428242; H55709; Hs.2250; leukemia inhibitory factor (ch; ovar, panc, leuk, lung; diag

- 428296; NM_003058; Hs.183572; solute carrier family 22 (orga; renal; mAb+s.m.
 428330; U22524; Hs.2256; matrix metalloproteinase 7 (mar; uter, ovar, fibro, pros, panc, lung, blad, headnk, esoph, mela; mAb+diag+s.m.
 428358; BE440042; Hs.83326; matrix metalloproteinase 3 (st; headnk, stom, esoph, colon; diag
 428392; H10233; Hs.2265; secretory granule, neuroendocr; panc; diag
 428450; NM_014791; Hs.184339; KIAA0175 gene product; ovar, cerv, panc, lung, blad, mela; s.m.
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S; lung, blad, colon, uter, ovar; s.m.
 428484; AF104032; Hs.184601; solute carrier family 7 (catio; lung, blad, headnk, cerv, esoph, glio, uter, stom, colon, mela; mAb+s.m.
 428486; AW583497; Hs.184504; pancreatic polypeptide; panc; diag
 428505; AL035461; Hs.2281; chromogranin B (secretogranin; panc, lung; diag
 428513; BE220806; Hs.184697; plexin C1; mela, panc, breast stom, headnk; mAb
 428579; NM_005756; Hs.184942; G protein-coupled receptor 64; ovar, EWS, uter; mAb+s.m.
 428664; AK001666; Hs.189095; similar to SALL1 (sal (Drosoph; blad, ovar, pros, lung, stom, test; CTL+s.m.
 428698; AA852773; Hs.334838; KIAA1866 protein; breast, colon, lung, panc, stom, headnk, ovar, EWS; mAb
 428748; AW593206; Hs.98785; Ksp37 protein; lung, sarc; diag
 428758; AA433988; Hs.98502; CA125 antigen; mucin 16; ovar, cerv, lung, panc, stom, renal; diag
 428778; AK000530; Hs.193326; fibroblast growth factor recept; ovar; mAb+s.m.
 428953; AA306610; Hs.348183; tumor necrosis factor receptor; cerv, panc, colon, stom, headnk, renal; mAb+diag
 428969; AF120274; Hs.194689; artemin; lung, cerv; diag
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG; stom, panc, colon, ovar, fibro; mAb+s.m.
 429149; AW193360; Hs.197962; Homolog of mouse ADP-ribosylat; glio; mAb+s.m.
 429211; AF052693; Hs.198249; gap junction protein, beta 5 (t; lung, blad, headnk, cerv, esoph, stom, mela; mAb+s.m.
 429263; AA019004; Hs.198396; ATP-binding cassette, sub-fam1; lung; mAb+s.m.
 429276; AF056085; Hs.198612; G protein-coupled receptor 51; angio, blad, glio; mAb+s.m.
 429353; AL117406; Hs.335891; ATP-binding cassette transport; breast, pros; mAb+s.m.
 429547; AW009166; Hs.99376; FGENESH predicted novel secret; panc, headnk, lung, ovar; diag
 429610; AB024937; Hs.211092; LUNX protein; PLUNC (palate lu; lung, fibro; mAb+diag
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, reg; lung, mela; s.m.
 429910; NM_000867; Hs.2507; 5-hydroxytryptamine (serotonin; leio; mAb+s.m.
 430147; R60704; Hs.234434; hairy/enhancer-of-split relate; glio; s.m.
 430178; AW449612; Hs.152475; 3'UTR of achaete-scute complex; colon, stom, ovar; CTL
 430377; NM_001922; Hs.301865; dopachrome tautomerase (dopach; mela; CTL
 430413; AW842182; Hs.241392; small inducible cytokine A5 (R; fibro, esoph, mela; diag
 430486; BE062109; Hs.241551; chloride channel, calcium act; lung, blad, headnk, cerv, esoph; mAb+s.m.
 430822; AJ005371; Hs.248017; glyceraldehyde-3-phosphate dehy; mela, sarc; s.m.
 431130; NM_006103; Hs.2719; HE4; epididymis-specific, whey; ovar, uter; diag
 431462; AW583672; Hs.256311; granin-like neuroendocrine pep; panc, lung, glio, test; diag
 431515; NM_012152; Hs.258583; EDG-7 (endothelial different; ovar, pros, lung, blad; mAb+s.m.
 431620; AA126108; Hs.264981; 2'-5'-oligoadenylate synthetas; esoph, cerv; CTL+s.m.
 431629; AL077025; Hs.265827; interferon, alpha-inducible pr; panc, uter, cerv, stom, esoph, mela; mAb+diag
 431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD4; ovar, panc, blad, headnk, mela, renal; mAb+s.m.
 431745; AW972448; Hs.163425; Novel FGENESH predicted cadher; fibro, ovar, uter; mAb
 431840; AA534908; Hs.2860; POU domain, class 5, transcrip; test, renal, blad; CTL
 431846; BE019924; Hs.271580; uropalakin 1B; lung, blad, headnk, uter, cerv, stom, ovar; mAb+diag
 431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin; lung, blad, cerv, headnk, ovar, colon, pros, panc, breast, esoph, test, mela; mAb+diag
 432101; AL198950; Hs.123642; EphA3; pros, panc, EWS sarc; s.m.
 432179; X75208; Hs.2913; EphB3; ovar, colon; mAb+s.m.
 432198; AW300888; Hs.273230; hypothetical protein FLJ10830; renal; CTL
 432201; AI538613; Hs.298241; Transmembrane protease, serine; breast, colon, ovar, stom, panc, uter, cerv, lung; mAb+diag+s.m.
 432579; AF043244; Hs.278439; nucleolar protein 3 (apoptosis; renal; CTL
 432596; AJ224741; Hs.278461; matrilin 3; panc, breast, sarc; diag
 432606; NM_002104; Hs.3066; granzyme K (serine protease, g; renal, breast, lung, stom, hepC, fibro, leuk; CTL
 432829; W60377; Hs.57772; ESTs; blad; CTL+s.m.
 432874; W94322; Hs.279651; melanoma inhibitory activity; panc, stom, mela, sarc; diag
 432990; AL036071; Hs.279899; tumor necrosis factor receptor; pros, renal; mAb+s.m.
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; colon, breast, lung, blad, cerv, uter, test, mela; s.m.
 433447; U29195; Hs.3281; neuronal pentraxin II; mela, esoph, colon, renal; diag
 433848; AF095719; Hs.93764; carboxypeptidase A4; headnk, esoph, lung; s.m.
 433867; AK000596; Hs.3818; hippocalcin-like 1; renal; CTL
 434206; AW136973; Hs.362915; ESTs, Weakly similar to S69890; colon, lung, stom; CTL+s.m.
 434276; AF123659; Hs.93605; leucine zipper, putative tumor; mela; s.m.
 434293; NM_004445; Hs.3796; EphB6; blad, pros; s.m.
 435013; Hs.110024; NM_020142; Homo sapiens NADH-tub; renal, lung, sarc; CTL
 435472; AW972330; Hs.283022; triggering receptor expressed; glio; mAb
 435505; AF200492; Hs.211238; interleukin-1 homolog 1; lung, headnk; diag
 436456; AW292677; Hs.248122; melanin-concentrating hormone; mela, glio; mAb+s.m.
 436480; AJ271643; Hs.87469; putative acid-sensing ion chan; glio; mAb+s.m.
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubi; lung, blad, colon, ovar, uter, headnk, test; s.m.
 436576; AJ458213; Hs.77542; ESTs; renal, panc, headnk, lung; mAb+s.m.
 436608; AA628980; Hs.192371; down syndrome critical region; blad, lung, sarc; CTL+s.m.
 436895; AF037335; Hs.5338; carbonic anhydrase XII; breast, renal, ovar, glio; mAb+s.m.
 436961; AW375974; Hs.156704; ESTs; lung, panc, renal, uter, colon; CTL
 436982; AB018305; Hs.5378; spondin 1, (I-spondin) extrace; ovar, fibro; diag
 437016; AU076916; Hs.5398; guanine monophosphate synthetas; lung, blad, cerv, esoph, colon, headnk; s.m.
 437044; AL035864; Hs.69517; differentially expressed in Fa; headnk, cerv, lung, blad, breast, pros, ovar, stom, esoph; CTL
 437789; AI581344; Hs.127812; ESTs, Weakly similar to T17330; lung; CTL
 437852; BE001836; Hs.256897; putative GPCR; blad, lung; mAb+s.m.
 438380; T06430; Hs.6194; chondroitin sulfate proteoglyc; glio, mela; diag
 438549; BE386801; Hs.21858; trinucleotide repeat contain; mela, sarc; CTL+diag
 439018; AW300887; Hs.26638; membrane-spanning 4-domains, s; uter, stom, pros, fibro; mAb
 439223; AW238299; Hs.250618; UL16 binding protein 2; lung, headnk, cerv, esoph, leuk, blad, colon; mAb
 439477; W69813; Hs.58042; ESTs, Moderately similar to GF; lung; mAb+s.m.
 439569; AW602168; Hs.222399; CEGP1 protein; breast, pros, blad; diag
 439606; W79123; Hs.58561; G protein-coupled receptor 87; lung, blad, headnk, cerv, esoph; mAb+s.m.

- 439738; BE246502; Hs.9598; sema domain, immunoglobulin do; blad, lung, cerv, renal; mAb+s.m.
 439979; AW600291; Hs.6823; hypothetical protein FLJ10430; renal, cerv, pros, headnk, colon, test, sarc; mAb
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing; blad, ovar, lung, headnk, test; s.m.
 440065; W03476; Hs.266331; Homo sapiens Fc receptor homol; mela; diag
 440304; BE159984; Hs.125395; hepatitis A virus cellular rec; renal, colon, blad; mAb+s.m.
 440516; S42303; Hs.161; cadherin 2, type 1, N-cadherin; glio, ovar, uter, renal, hepC; mAb+diag
 440672; AF083811; Hs.7345; MAD1 (mitotic arrest deficient; mela; s.m.
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog; lung, blad, headnk, test, mela, esoph; s.m.
 442117; AW664964; Hs.128899; ESTs; hypothetical protein for; breast, lung, blad, panc, headnk, stom, ovar, pros, sarc; mAb+s.m.
 442133; AW874138; Hs.129017; ESTs; type Ia transmembrane p; ovar, uter; mAb
 442275; AW449467; Hs.54795; Homo sapiens secretoglobulin, fa; fibro; diag
 442652; AI005163; Hs.201378; Homo sapiens cDNA FLJ40427 f1; fibro, ovar, uter; CTL
 443105; X96753; Hs.9004; chondroitin sulfate proteoglyc; mela; mAb+diag
 443247; BE614387; Hs.333893; c-Myc target JPO1; colon, lung, blad, panc; CTL
 443324; R44013; Hs.164225; ESTs; fibro; mAb+diag
 443426; AF098158; Hs.9329; chromosome 20 open reading fra; colon, lung, blad, stom, test, mela, sarc; CTL
 443595; AF169312; Hs.9613; PPAR(gamma) angiopoietin relat; renal; diag
 443646; AI085198; Hs.164226; Thrombospondin 1; angio, panc, uter; diag
 443859; NM_013409; Hs.9914; follistatin; lung, cerv, headnk, blad, esoph; diag
 443887; AW163123; Hs.10071; seven transmembrane protein TM; renal; mAb+s.m.
 444006; BE395085; Hs.334762; type I transmembrane protein F; panc, colon, lung, ovar, renal, esoph, mela, blad, stom, cerv; mAb
 444090; S69115; Hs.10306; natural killer cell group 7 se; fibro, renal, mela; diag
 444371; BE540274; Hs.239; forkhead box M1; lung, headnk, blad, glio, test, mela; s.m.
 444381; BE387335; Hs.283713; hypothetical protein BC014245; breast, colon, blad, lung, panc, headnk, ovar, stom, uter, renal, angio, test, mela, esoph, sarc; CTL+diag
 444488; AW192879; Hs.355660; ancient conserved domain prote; renal; mAb+s.m.
 444527; NM_005408; Hs.11383; small inducible cytokine subfa; fibro, esoph; diag
 444781; NM_014400; Hs.11950; GPI-anchored metastasis-associ; lung, blad, headnk, cerv; mAb+diag
 444783; AK001468; Hs.62180; anillin (Drosophila Scraps hom; ovar, lung, blad, headnk, panc, cerv, stom, uter, colon, esoph; CTL+s.m.
 445417; AK001058; Hs.12680; a disintegrin-like and metallo; panc, headnk, stom, lung, esoph, sarc, colon; diag
 445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; ovar, blad, uter, breast, lung, headnk, renal, fibro, panc, cerv, sarc; mAb+diag
 445891; AW391342; Hs.199460; DPCR1 protein; stom, panc, esoph, omuc, esoph; mAb
 445895; D29954; Hs.13421; KIAA0056 protein; pros; CTL
 446051; BE048061; Hs.37054; ephrin-A3; colon, breast, mAb+diag
 446163; AA026880; Hs.25252; prolactin receptor; breast, cerv, uter; mAb+s.m.
 446341; AL040763; Hs.310735; FGENESH prediction similar to; mela; mAb+s.m.
 446619; AU076643; Hs.313; secreted phosphoprotein 1 (ost; ovar, fibro, panc, headnk, lung, colon, blad, mela, esoph, uter, sarc; diag
 446650; AB016625; Hs.15813; solute carrier family 22 (orga; renal; mAb+s.m.
 446921; AB012113; Hs.16530; small inducible cytokine subfa; breast, panc, headnk, lung, fibro, mela; diag
 447033; AJ357412; Hs.157601; Predicted gene: Eos cloned; se; colon, pros, fibro, breast, ovar, lung, panc, sarc; CTL+diag
 447072; D61594; Hs.17279; tyrosylprotein sulfotransferas; glio, panc; CTL+s.m.
 447131; NM_004585; Hs.17466; retinoid acid receptor respond; renal, breast, stom, lung, mela, ovar; mAb+s.m.
 447208; BE315291; Hs.237971; hypothetical protein MGC5627; esoph, stom, colon; CTL+diag
 447269; NM_004861; Hs.17958; carbodiimide (3'-phosphoadenyly; renal; CTL
 447342; A199268; Hs.19322; Homo sapiens, Similar to RIKEN; colon, blad, pros, lung, stom, ovar, CTL
 447400; AK000322; Hs.18457; hypothetical protein FLJ20315; colon, pros, stom, uter; mAb+diag
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; mela; s.m.
 448243; AW369771; Hs.367688; Integrin, beta 8; ovar, uter, lung, stom, headnk, glio, panc; mAb+s.m.
 448610; NM_006157; Hs.21602; nel (chicken)-like 1; mela, sarc; diag
 448733; NM_005629; Hs.187958; solute carrier family 6 (neuro; lung, renal; mAb+s.m.
 448844; AJ581519; Hs.177164; FGENESH predicted novel cell s; panc, lung, stom, omuc; mAb+s.m.
 449032; AA045573; Hs.22800; nuclear factor (erythroid-derf; colon, test, stom; CTL+s.m.
 449048; Z45051; Hs.22920; similar to S68401 (cattle) glu; panc, ovar, uter, glio, headnk, lung, sarc; mAb
 449444; AW818436; Hs.351306; solute carrier family 16 (mono; renal, panc; mAb+s.m.
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor; lung, panc, renal, stom, hepC, fibro, leuk, mela; mAb+s.m.
 449720; AA311152; Hs.288708; hypothetical protein FLJ21562; colon; CTL
 449722; BE280074; Hs.23960; cyclin B1; headnk, blad, lung, panc, angio, test, mela, esoph; s.m.
 450001; NM_001044; Hs.406; solute carrier family 6 (neuro; renal; mAb+s.m.
 450375; AA009847; Hs.352537; a disintegrin and metalloprote; breast, ovar, headnk, panc, lung, esoph, colon, sarc; mAb+diag+s.m.
 450531; AW301032; Hs.203800; (BC017500) Similar to hypothet; colon; CTL
 450701; H39960; Hs.288467; hypothetical protein XP_098151; lung, headnk, panc, breast, stom, ovar, esoph, colon, sarc; mAb+diag
 450726; AW204600; Hs.355462; HUMPSBPA Human pulmonary surfac; fibro, lung; s.m.
 450931; N25155; Hs.25648; tumor necrosis factor receptor; lung, renal; mAb+s.m.
 450983; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; blad, lung, ovar, panc; diag
 451310; AW250651; Hs.26213; Human DNA sequence from clone; colon, panc; CTL
 451527; AF022813; Hs.26518; transmembrane 4 superfamily me; renal; mAb
 451537; R56631; Hs.26550; retinoid X receptor, gamma; mela; CTL+s.m.
 451668; Z43948; Hs.326444; cartilage acidic protein 1; blad, ovar, lung; mAb+diag
 451939; U80456; Hs.27311; single-minded (Drosophila) hom; pros; CTL
 451979; F06972; Hs.27372; endothelial tyrosine kinase (E; angio; CTL+s.m.
 451988; AF263928; Hs.27410; papillomavirus regulatory fact; renal; CTL
 452017; AF109302; Hs.27495; prostate cancer associated pro; pros; s.m.
 452097; AB002364; Hs.27916; a disintegrin-like and metallo; ovar; mAb+s.m.+diag
 452190; H26735; Hs.91668; Homo sapiens clone PP1498 unk; breast, stom, panc; mAb
 452194; AI694413; Hs.373599; olfactory receptor, family 2; stom, panc, renal, colon, mela, fibro; mAb+s.m.
 452203; X57522; Hs.352018; transporter 1, ATP-binding cas; cerv, esoph, blad, stom, mela, renal; mAb+s.m.
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 f1; breast, headnk, panc, stom, lung, esoph, fibro; diag
 452401; NM_007115; Hs.29352; tumor necrosis factor, alpha-1; blad, breast, panc, headnk, stom, lung, leuk, renal, esoph; diag
 452431; U88879; Hs.29499; toll-like receptor 3; renal, hepC; mAb
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; breast, blad, lung, headnk, ovar, stom, uter, panc; mAb
 452836; U56011; Hs.30743; preferentially expressed antib; lung, ovar, breast, mela, test, esoph, renal, sarc; CTL
 452862; AW378065; Hs.8887; ADAMTS2 (a disintegrin-like α ; headnk, breast, colon, leuk, lung, blad, esoph, stom, sarc; mAb+diag
 453195; BE241876; Hs.32352; hypothetical protein DKFZp434K; renal; CTL
 453496; AA442103; Hs.33084; solute carrier family 2 (facit; renal, pros; mAb+s.m.

453837; AL138387; Hs.256126; baculoviral IAP repeat-contain; renal, mela, sarc; s.m.
 453968; AA847843; Hs.62711; High mobility group (nonhiston); lung, uter, blad, test; CTL+s.m.
 456546; AI690321; Hs.203845; KCNK15 potassium channel, subf; ovar; mAb+s.m.
 456662; NM_002448; Hs.1494; msh (Drosophila) homeo box hom; uter, ovar; CTL
 457133; M54968; Hs.351221; v-Ki-ras2 Kirsten rat sarcoma; panc; s.m.
 457489; AI693815; Hs.127179; cryptic gene; panc, pros, lung; diag
 457819; AA057484; Hs.35406; FLJ20522 Hypothetical protein; lung, cerv, headnk; mAb+diag
 458079; AI796870; Hs.381220; Homo sapiens similar to RIKEN; mela, fibro, sarc; mAb
 458627; AW088642; Hs.97984; SRY (sex determining region Y); ovar, uter, test; CTL

TABLE 2B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414991	1785136_1	D78831 C17898 D78863

TABLE 2C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
402901	8894222	Minus	175426-175667
404287	2326514	Plus	53134-53281
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404977	3738341	Minus	43081-43229
405033	7107731	Minus	142358-142546
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 3A. Disease Indications and Preferred Utilities for Selected Genes

Table 3A provides preferred disease indications and preferred utilities for about 2709 selected genes. These genes were identified using Eos/Affymetrix Genechip arrays.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number
 UnigenID: Unigene ID number
 Unigene Title: Unigene gene title
 Disease: preferred diseases indicated for selected gene as described in table 1 and abbreviated as follows: blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), glio (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrosis diseases), headnk (head & neck diseases), leio (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), ornuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), sarc (soft tissue and bone diseases), mela (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)
 Utility: preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)

Pkey; ExAccn; UnigenID; Unigene Title; Disease; Utility

100125; R02740; Hs.137555; putative chemokine receptor; G; blad; mAb+s.m.
 100131; D12485; Hs.11951; ectonucleotide pyrophosphatase; breast; mAb
 100147; D13666; Hs.136348; periostin (OSF-2os); breast, colon, blad, lung, fibro, panc; mAb+diag
 100241; BE273648; Hs.32963; cadherin 6, type 2, K-cadherin; blad; mAb
 100299; D49493; Hs.2171; growth differentiation factor; EWS; diag
 100335; AW247529; Hs.6793; platelet-activating factor ace; breast, lung, blad; s.m.
 100365; AI878927; Hs.79284; mesoderm specific transcript; colon, pros; diag
 100372; NM_014791; Hs.184339; KIAA0175 gene product; ovar, lung, cerv, panc; s.m.
 100405; AW291587; Hs.82733; nidogen 2; angio; diag
 100420; D86983; Hs.118893; Melanoma associated gene; breast, pros, lung, colon, angio, leuk; diag
 100448; AF234987; Hs.57652; cadherin, EGF LAG seven-pass G; breast; mAb+s.m.
 100452; D87742; Hs.241552; KIAA0268 protein; pros; diag
 100559; NM_000094; Hs.1640; collagen, type VII, alpha 1 (c; lung; CTL+s.m.
 100654; A03758; Hs.184411; NM_000477; Homo sapiens albumin; pros; diag
 100655; A03758; Hs.184411; Empirically selected from AFFX; pros; diag
 100668; L05424; Hs.169610; CD44 antigen (homing function; lung, breast; mAb
 100824; AI393237; Hs.193989; run-related transcription fac; ovar; CTL+s.m.
 100930; J04129; Hs.82269; progesterone-associated endomet; lung; diag
 101063; D54745; Hs.80247; cholecystokinin; pros, EWS; diag
 101097; BE245301; Hs.89414; chemokine (C-X-C motif), recep; leuk, ovar, breast, blad; mAb+s.m.
 101104; AW862258; Hs.169268; neuropeptide Y receptor Y1; breast, EWS; mAb
 101192; BE247295; Hs.78452; solute carrier family 20 (phos; angio; mAb+s.m.
 101193; L20861; Hs.152213; wingless-type MMTV integration; blad, lung; diag
 101249; L18964; Hs.1904; protein kinase C, iota; ovar; s.m.

- 101261; D30857; Hs.82353; protein C receptor, endothelial; angio; mAb+s.m.
 101389; AW951430; Hs.78888; diazepam binding inhibitor (GA); pros; mAb+s.m.
 101431; BE185289; Hs.1076; small proline-rich protein 18; lung, blad; diag
 101447; M21305; gb:Human alpha satellite and s; angio, blad; diag
 5 101461; N98569; Hs.76422; phospholipase A2, group IIA (p; pros; diag
 101485; AA296520; Hs.89546; selectin E (endothelial adhesion); pros, ovar; mAb
 101506; J02931; Hs.62192; coagulation factor III (thromb); pros; mAb
 101526; NM_002197; Hs.220529; acornitase 1, soluble; lung, colon, headnk, panc; mAb
 10 101543; M31166; Hs.2050; pentaxin-related gene, rapidly; angio, ovar; diag
 101545; BE246154; Hs.154210; endothelial differentiation, s; angio; mAb+s.m.
 101560; AW958272; Hs.347326; intercellular adhesion molecule; angio; mAb
 101626; M57399; Hs.44; pleiotrophin (heparin binding); lung; diag
 101649; AW959908; Hs.1690; heparin-binding growth factor; lung, blad; diag
 15 101714; M68874; Hs.211587; phospholipase A2, group IVA (c; angio; s.m.
 101724; L11690; Hs.198689; bullous pemphigoid antigen 1 (c; breast, pros, blad, lung; mAb+CTL
 101741; NM_003199; Hs.326198; transcription factor 4; angio; CTL+s.m.
 101748; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgar; lung, blad, headnk, cerv; mAb
 101759; M80244; Hs.184601; solute carrier family 7 (cat); lung, glio, blad, headnk; mAb+s.m.
 20 101791; M83822; Hs.62354; cell division cycle 4-like; pros; s.m.
 101804; M86699; Hs.169840; TTK protein kinase; ovar, lung, blad, cerv; CTL+s.m.
 101806; AA586894; Hs.112408; S100 calcium-binding protein A; lung, breast, blad; diag
 101809; M86849; Hs.323733; gap junction protein, beta 2; colon, blad, lung, panc, headnk; mAb
 101839; AA446644; Hs.692; GA733-2 antigen; epithelial gl; ovar, pros; mAb
 25 101845; U88957; Hs.78867; protein tyrosine phosphatase; lung, glio, headnk, cerv; mAb+s.m.
 101851; BE260964; Hs.82045; midkine (neurite growth-promot; lung, blad, ovar, breast, panc; mAb+diag
 102009; BE245149; Hs.82643; protein tyrosine kinase 9; ovar; s.m.
 102012; BE259035; Hs.118400; singed (Drosophila)-like (sea; angio; diag
 102024; AA301867; Hs.76224; EGF-containing fibulin-like ex; angio; diag
 30 102048; U07225; Hs.339; purinergic receptor P2Y, G-pro; blad; mAb
 102076; BE299197; Hs.179665; cyclin-dependent kinase inhibi; pros; CTL+s.m.
 102125; NM_006456; Hs.288215; sialyltransferase; breast, lung, ovar; s.m.
 102136; AA300576; Hs.85769; acidic 82 kDa protein mRNA; ovar; diag
 102151; T27013; Hs.3132; steroidogenic acute regulatory; ovar; diag
 35 102154; U17760; Hs.75517; laminin, beta 3 (nicotin 125kD; lung, blad, headnk; diag
 102178; AW178761; Hs.227948; serine (or cysteine) proteinase; blad; mAb+diag
 102187; U20325; Hs.1707; cocaine- and amphetamine-regul; breast; diag
 102193; AL036335; Hs.313; secreted phosphoprotein 1 (ost; ovar, lung, fibro; diag
 102200; AA232382; Hs.317432; branched chain aminotransferase; ovar; s.m.
 40 102208; U22961; Hs.184411; gb:Human mRNA clone with simi; pros; diag
 102211; BE314524; Hs.78776; putative transmembrane protein; breast, blad; mAb
 102283; AW161552; Hs.83381; guanine nucleotide binding pro; angio; CTL+s.m.
 102297; NM_001504; Hs.198252; G protein-coupled receptor 9; breast; mAb
 102304; AF015224; Hs.46452; mammaglobin 1; breast; diag
 45 102305; AL043202; Hs.90073; chromosome segregation 1 (yeas; ovar, lung, blad; diag
 102348; U37519; Hs.87539; aldehyde dehydrogenase 3 fami; lung, blad; s.m.
 102380; U40434; Hs.155981; mesothelin; ovar; diag
 102394; NM_003616; Hs.2442; a disintegrin and metalloprote; panc; s.m.
 102455; U48705; Hs.75562; discoidin domain receptor fami; breast; mAb
 102457; NM_001394; Hs.2359; dual specificity phosphatase 4; breast; s.m.
 50 102522; BE250944; Hs.183556; solute carrier family 1 (neut; pros; mAb
 102581; AU077228; Hs.77256; enhancer of zeste (Drosophila); blad, EWS, leuk; CTL+s.m.
 102610; U65011; Hs.30743; preferentially expressed antig; lung, ovar; CTL
 102623; AW249285; Hs.37110; melanoma antigen, family A, 9; lung, blad; mAb+CTL
 102669; U71207; Hs.29279; eyes absent (Drosophila) homot; lung, pros; CTL+s.m.
 55 102696; BE540274; Hs.239; forkhead box M1; lung, blad; s.m.
 102725; AB026187; Hs.374280; protocadherin 11; EWS; mAb
 102742; U79293; Hs.159264; Human clone 23948 mRNA sequenc; breast, ovar; diag
 102745; AW753865; Hs.74376; olfactomedin related ER local; EWS; diag
 102803; H48299; Hs.26126; claudin 10; ovar; mAb
 60 102829; NM_008183; Hs.80962; neurensin; lung, ovar, headnk; diag
 102836; U94320; Hs.158330; neuropeptide Y receptor Y5; EWS; mAb
 102852; V00571; Hs.75294; corticotropin releasing hormon; blad; diag
 102898; NM_002205; Hs.149609; integrin, alpha 5 (fibronectin; angio, blad, lung, pros; mAb+s.m.
 65 102915; X07820; Hs.2258; matrix metalloproteinase 10 (s; angio, blad, lung, ovar; mAb+diag+s.m.
 102917; AJ016712; Hs.287797; integrin, beta 1 (fibronectin; angio; mAb
 102927; BE512730; Hs.85114; keratin 18; ovar; diag
 102968; AU076611; Hs.154672; methylene tetrahydrofolate deh; ovar; s.m.
 102994; X51730; Hs.2905; progesterone receptor; blad; mAb+s.m.
 70 103003; AJ910275; Hs.350470; trefol factor 1 (breast cancer; breast, panc; diag
 103021; BE001596; Hs.85266; integrin, beta 4; lung blad; mAb
 103036; M13509; Hs.83169; matrix metalloproteinase 1 (tr; angio, colon, blad, lung, leuk, ovar, headnk, fibro, panc, stom; mAb+diag+s.m.
 103037; BE018302; Hs.2894; placental growth factor, vascu; angio; diag
 103060; NM_005940; Hs.155324; matrix metalloproteinase 11 (s; breast, lung, ovar, panc; mAb+diag+s.m.
 103080; AU077231; Hs.82932; cyclin D1 (PRAD1; parathyroid; breast, EWS; diag
 75 103095; NM_005424; Hs.78824; tyrosine kinase with immunoglo; angio; mAb
 103111; NM_006103; Hs.2719; epidiymis-specific, whey-acid; ovar, uter; diag
 103119; X63629; Hs.2877; cadherin 3, type 1, P-cadherin; lung, blad, ovar, colon, pros, panc, breast; mAb+diag
 103206; X72756; Hs.77397; monokine induced by gamma inte; breast, lung; diag
 103210; X72925; Hs.69752; desmocollin 1; pros; mAb
 80 103280; U84722; Hs.76206; cadherin 5, type 2, VE-cadherin; angio, fibro; mAb+s.m.
 103299; NM_005756; Hs.184942; G protein-coupled receptor 64; ovar; mAb+s.m.
 103312; Y12642; Hs.3185; lysosomal; lung, blad; mAb
 103365; X90908; Hs.74126; fatty acid binding protein 6; blad; diag

- 103408; NM_001504; Hs.198252; G protein-coupled receptor 9; breast; mAb
 103478; BE514982; Hs.38991; S100 calcium-binding protein A; lung, blad, headnk; diag
 103587; BE270266; Hs.82128; ST4 oncofetal trophoblast glyco; breast, blad, lung; mAb
 103594; AI368680; Hs.816; SRY (sex determining region Y); lung, glio; s.m.
 103692; AW137912; Hs.227583; Homo sapiens chromosome X map; angio; mAb+s.m.
 103739; AA115173; gbzn30d02s1 Stratagene neuro; pros; s.m.
 103767; BE244667; Hs.348996; CGI-100 protein; angio; diag
 103989; AA315993; Hs.105484; regenerating gene type IV; colon, omuc; mAb+diag
 104052; NM_002407; Hs.97644; mammaglobin 2; ovar; diag
 104115; AF183810; Hs.26102; opposite strand of trichorh; breast; mAb
 104252; AF002248; Hs.210863; cell adhesion molecule with ho; ovar; diag
 104301; AA768491; Hs.6783; hypothetical protein FLJ22724; ovar; diag
 104308; N25117; Hs.355957; ribosomal protein S26; pros; diag
 104394; AA129551; Hs.172129; Homo sapiens cDNA: FLJ21409 fr; colon; diag
 104542; R29657; gb:F1-1179D 22 week old human; pros; diag
 104608; AF143867; Hs.337588; ESTs, Moderately similar to S6; blad; mAb
 104659; AW969769; Hs.100343; ESTs; EWS; diag
 104660; BE298665; Hs.14846; Homo sapiens mRNA; cDNA DKFZp5; uter, colon, pros; mAb
 104667; AI239923; Hs.63931; dachshund (Drosophila) homolog; breast, pros, colon; diag
 104689; AA420450; Hs.380088; Plakophilin; lung; diag
 104691; U29590; Hs.37744; Homo sapiens beta-1 adrenergic; pros, EWS; mAb+s.m.
 104755; T49951; Hs.9029; DKFZP434G032 protein; breast, colon; diag
 104764; AI039243; Hs.278585; ESTs; angio; diag
 104786; AA027167; Hs.380438; KIAA0955 protein; angio; CTL+s.m.
 104877; AI138635; Hs.22968; Intron of VEGFR; renal; diag
 104888; AW939591; Hs.5940; mucin 13, epithelial transmembr; colon, stom, uter; mAb+s.m.
 104919; AA026880; Hs.25252; Homo sapiens cDNA FLJ13603 fis; breast, cerv, uter; mAb+s.m.
 104943; AF072873; Hs.114218; frizzled (Drosophila) homolog; ovar; mAb+s.m.
 104954; AW250651; Hs.26213; Human DNA sequence from clone; colon; diag
 104971; BE311926; Hs.15830; hypothetical protein FLJ12691; blad; CTL
 105012; AF098158; Hs.9329; chromosome 20 open reading fra; colon, lung, blad; CTL
 105038; AW503733; Hs.9414; KIAA1488 protein; breast, angio; CTL+s.m.
 105039; AA907305; Hs.36475; ESTs; breast; diag
 105093; AL137566; Hs.32405; Homo sapiens mRNA; cDNA DKFZp5; blad; diag
 105149; BE089288; Hs.8958; Homo sapiens cDNA FLJ12024 fis; pros; diag
 105175; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; colon, lung; mAb
 105263; AW388633; Hs.6682; solute carrier family 7, (cat); angio, lung, ovar, blad, panc; mAb+s.m.
 105298; BE387790; Hs.26369; hypothetical protein FLJ20287; ovar, lung; diag
 105301; AW352357; Hs.7457; MAGE1 protein; EWS; diag
 105316; AI671245; Hs.24835; hypothetical protein FLJ14594; EWS; mAb
 105329; AA234561; Hs.22862; ESTs; breast, pros; CTL+s.m.
 105330; AW338625; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio; mAb+s.m.
 105370; AF179274; Hs.22791; transmembrane protein with EGF; pros; mAb+s.m.
 105500; AW602166; Hs.222399; CEGP1 protein; breast, pros; diag
 105503; AW963624; Hs.31707; ESTs, Weakly similar to YEW4_Y; pros, breast, colon; CTL+s.m.
 105507; BE268348; Hs.380963; CCR4-NOT transcription complex; colon; diag
 105516; AK001269; Hs.30738; hypothetical protein FLJ10407; ovar; diag
 105564; BE616694; Hs.288042; hypothetical protein FLJ14299; breast; diag
 105645; AW294631; Hs.351270; ESTs; pros; diag
 105715; BE521800; Hs.29444; putative small membrane protein; colon; diag
 105743; BE246502; Hs.9598; sema domain, immunoglobulin do; breast, lung; mAb+s.m.
 105746; AW151952; Hs.46679; hypothetical protein FLJ20739; breast; CTL+s.m.
 105777; R42755; Hs.23098; ESTs; breast; diag
 105782; H09748; Hs.67987; B-cell CLL/lymphoma 11B (zinc); EWS; CTL+s.m.
 105828; AA478756; Hs.194477; E3 ubiquitin ligase SMURF2; angio; s.m.
 105990; AI690586; Hs.29403; hypothetical protein FLJ22060; breast; diag
 106000; AW194426; Hs.20726; ESTs; breast; diag
 106012; AI240665; Hs.352537; ESTs; breast, lung; diag
 106014; AF123094; Hs.180566; mucosa associated lymphoid tis; leuk; diag
 106063; BE260415; Hs.348198; hypothetical protein FLJ20262; pros; diag
 106066; AW274357; Hs.301406; hypothetical protein PP3501; mela; CTL+s.m.
 106111; AW875398; Hs.6451; PRO659 protein; EWS; CTL+s.m.
 106124; H93366; Hs.7567; branched chain aminotransferase; angio; s.m.
 106155; AA425414; Hs.33287; nuclear factor I/B; breast, pros, angio; diag
 106373; AW503807; Hs.21907; histone acetyltransferase; breast; s.m.
 106400; BE397649; Hs.279607; Homo sapiens cDNA FLJ13634 fis; colon; diag
 106414; BE568205; Hs.28827; mitogen-activated protein knaz; breast; s.m.
 106448; Z42061; Hs.27004; ESTs; pros; diag
 106533; AL134708; Hs.145998; ESTs; EWS; diag
 106574; BE044325; Hs.227280; U6 snRNA-associated Sm-like pr; colon; diag
 106579; AA456135; Hs.23023; ESTs; pros; diag
 106632; NM_014400; Hs.11950; GPI-anchored metastasis-associ; lung, blad, headnk; mAb+diag
 106738; AW149266; Hs.25130; Homo sapiens cDNA FLJ14923 fis; ovar; diag
 106793; H94997; Hs.16450; ESTs; angio; diag
 106844; AA485055; Hs.158213; sperm associated antigen 6; breast; mAb+CTL
 106906; AA861271; Hs.222024; transcription factor BMAL2; lung, blad; diag
 106990; AA280722; Hs.24758; ESTs, Weakly similar to I38022; breast; diag
 107036; AI973016; Hs.15725; hypothetical protein SBB148; pros; diag
 107102; AB037765; Hs.30652; KIAA1344 protein; pros, breast; diag
 107105; AW963419; Hs.155223; stannocalcin 2; breast; diag
 107136; AV661958; Hs.8207; GK001 protein; breast, colon; diag
 107151; AW378065; Hs.8687; ADAMTS2 (a disintegrin-like a; breast, colon, leuk, lung, blad; mAb+diag
 107216; D51059; Hs.211579; melanoma cell adhesion molecu; angio; diag

- 107248; AW263124; Hs.350547; nuclear receptor co-repressor; breast, colon, pros; mAb+s.m.
 107284; NM_005629; Hs.187958; solute carrier family 6 (neuro; lung; mAb+s.m.
 107385; NM_005397; Hs.16426; podocalyxin-like; angio; diag
 107901; L42612; Hs.335952; keratin 6B; breast, blad, lung; diag
 107922; BE153855; Hs.61460; Ig superfamily receptor LNIR; breast, blad, lung; mAb
 107932; AW392555; Hs.18878; hypothetical protein FLJ21620; lung; CTL
 108055; AJ404672; Hs.334483; hypothetical protein FLJ23571; breast, ovar; diag
 108059; S69002; Hs.234773; Homo sapiens cDNA: FLJ22281 f; ovar; CTL+s.m.
 108153; AW519204; Hs.40808; ESTs; pros; diag
 108186; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 108242; AA062746; Hs.355244; gbzm03g12.s1 Stratagene come; pros; diag
 108282; AA065142; ; gbzm50h11.r1 Stratagene fibro; pros; diag
 108505; AA083376; ; gbzm09g08.s1 Stratagene hNT n; pros; diag
 108679; AA115963; Hs.323423; ESTs, Moderately similar to B ; pros; diag
 108695; AB029000; Hs.70823; KIAA1077 protein; breast, colon, lung; diag
 108732; AA258888; Hs.107476; ATP synthase, H⁺ transporting.; pros; s.m.
 108778; AF133123; Hs.90847; general transcription factor I; ovar; diag
 108828; AK001693; Hs.273344; DKFZP56400463 protein; breast; diag
 108860; AA133334; Hs.816; ESTs; lung; s.m.
 109001; AI056548; Hs.72116; hypothetical protein FLJ20992 ; angio; CTL+diag
 109032; AI219207; Hs.72222; hypothetical protein FLJ13459; blad; CTL
 109077; AI732617; Hs.182362; ESTs; blad; diag
 109112; AW419196; Hs.257924; hypothetical protein FLJ13782; breast, pros, blad; diag
 109141; AF174600; Hs.5978; ESTs, Highly similar to AF1746; colon; CTL+s.m.
 109166; AA219691; Hs.73625; RAB6 interacting, kinesin-like; lung, blad, breast, colon, ovar, headnk, EWS; s.m.
 109220; AW958181; Hs.189998; ESTs; pros; diag
 109273; AA375752; Hs.348140; Homo sapiens mRNA; cDNA DKFZp5; breast; diag
 109282; AW975746; Hs.188662; KIAA1702 protein; breast; diag
 109454; AA232255; Hs.295232; ESTs, Moderately similar to A4; ovar; diag
 109456; AW956580; Hs.42699; ESTs; angio, panc; diag
 109514; AA234087; Hs.262346; ESTs, Weakly similar to S72482; breast ; diag
 109530; AA908645; Hs.19597; KIAA1694 protein; pros; CTL+s.m.
 109648; H17800; Hs.7154; ESTs; ovar; diag
 109680; AB037734; Hs.4993; KIAA1313 protein; ovar; diag
 110009; BE075297; Hs.6614; ESTs, Weakly similar to A43932; breast, colon; diag
 110151; H18835; Hs.31608; hypothetical protein FLJ20041; pros, EWS; diag
 110156; AA581322; Hs.4213; hypothetical protein MGC16207; lung, blad; diag
 110240; AI658594; Hs.176588; ESTs, Weakly similar to CP4Y_H; breast; diag
 110278; AF061573; Hs.19492; protocadherin 8; EWS; mAb+s.m.
 110675; H89355; Hs.249159; adrenergic, alpha-2A-, receptor; pros; mAb+s.m.
 110728; AA737105; Hs.32250; ESTs, Moderately similar to I7; EWS; s.m.
 110844; AI740792; Hs.167531; methylcrotonoyl-Coenzyme A car; pros, pros; s.m.
 110915; BE092285; Hs.29724; hypothetical protein FLJ13187; breast, pros; diag
 110971; AI760098; Hs.21411; ESTs; pros; diag
 111157; AI109729; Hs.99364; putative transmembrane protein; pros; mAb+s.m.
 111179; AK000138; Hs.10760; asporin (LRR class 1); breast, colon; CTL+s.m.
 111185; AJ245671; Hs.12844; EGF-like-domain, multiple 6; ovar, blad; mAb+diag
 111223; AA852773; Hs.334838; KIAA1866 protein; breast, colon, lung, EWS; mAb
 111299; AB033091; Hs.355925; KIAA1265 protein; ovar; diag
 111357; BE314949; Hs.87128; hypothetical protein FLJ23309; breast; diag
 111384; N94606; Hs.288969; HSCARG protein; breast; diag
 111900; AF131784; Hs.25318; Homo sapiens clone Z5194 mRNA ; breast; diag
 111929; AF027208; Hs.112360; prominin (mouse)-like 1; colon, breast, fibro; mAb
 112134; R41823; Hs.7413; ESTs; calsyntenin-2; breast, EWS; diag
 112244; AB029000; Hs.70823; KIAA1077 protein; breast, colon, blad, lung; diag
 112280; AA863360; Hs.26040; ESTs, Weakly similar to fatty ; breast; s.m.
 112283; L14561; Hs.20952; ATPase, Ca⁺⁺ transporting, plz; ovar; mAb
 112287; AB033064; Hs.236463; KIAA1238 protein; breast ; diag
 112971; Z42387; Hs.83883; transmembrane, prostate androg; colon, pros, pros; mAb+s.m.
 113003; AW292315; Hs.7215; ESTs; EWS; diag
 113021; AL122055; Hs.129836; KIAA1028 protein; pros; s.m.
 113047; AI571940; Hs.7549; ESTs; breast, colon; diag
 113073; N39342; Hs.103042; microtubule-associated protein; pros; CTL+s.m.
 113168; AW002393; Hs.337629; gbzw61d05.x1 NCL CGAP_GC6 Hom; ovar; diag
 113195; H83265; Hs.8881; ESTs, Weakly similar to S41044; angio, lung; diag
 113230; T61430; ; gbzyc06a03.s1 Stratagene lung ; blad; diag
 113361; T79589; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 113374; T79925; Hs.269165; ESTs, Weakly similar to ALU1_H; leuk; diag
 113443; AW083920; Hs.16098; claudin 2; colon, panc; mAb
 113471; AI765890; Hs.16341; MAWD binding protein; pros; diag
 113490; BE178110; Hs.173374; Homo sapiens cDNA FLJ10500 f; colon; diag
 113950; AI267652; Hs.246107; Homo sapiens mRNA; cDNA DKFZp4; breast, pros ; diag
 113970; W27249; Hs.8109; hypothetical protein FLJ21080; breast, lung, stom, uter; diag
 114124; W57654; Hs.125019; lymphoid nuclear protein (LAF-; breast; diag
 114251; H15261; Hs.21948; ESTs; breast; diag
 114292; AI815395; Hs.184641; fatty acid desaturase 2; breast; s.m.
 114334; AB037784; Hs.22941; KIAA1363 protein; ovar; diag
 114407; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp4; breast, colon, lung; diag
 114452; AI369275; Hs.243010; Homo sapiens cDNA FLJ14445 f; angio; diag
 114480; BE066778; Hs.151678; UDP-N-acetyl-alpha-D-galactose; breast; s.m.
 114531; AA053033; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 114540; AI904232; Hs.75323; prohibitin; breast; diag
 114542; AW970128; Hs.91011; anterior gradient 2 (Xenopus t; breast, pros; diag

- 114587; AF086009; Hs.296396; gb:Homo sapiens full length in; colon; diag
 114724; R64730.comp; Hs.155886; DEAD/H (Asp-Glu-Ala-Asp/His) h; ovar; CTL+s.m.
 114768; AF212848; Hs.182339; ets homologous factor; pros; breast; colon; CTL+s.m.
 114798; AA159181; Hs.54900; serologically defined colon ca; pros; CTL+s.m.
 114908; AA454985; Hs.54973; cadherin-like protein VR20; pros; diag
 114918; BE165762; Hs.23518; hypothetical protein from BCRA; pros; diag
 114965; A1733881; Hs.72472; NAME OMITTED ... receptor kinase; breast; mAb
 115060; AF052693; Hs.198249; gap junction protein, beta 5 (-); lung, blad, headnk; mAb+s.m.
 115221; AW365434; Hs.79741; hypothetical protein FLJ10116; ovar; diag
 115239; BE251328; Hs.73291; hypothetical protein FLJ10881; colon; diag
 115291; BE545072; Hs.122579; hypothetical protein FLJ10461; ovar; lung; CTL+s.m.
 115412; AW131168; Hs.372382; ESTs, Weakly similar to I38022; pros; diag
 115536; AK001468; Hs.62180; anillin (Drosophila Scraps hom; ovar, lung, blad, headnk, panc, cerv, stom, uter, colon; CTL+s.m.
 115674; AW992356; Hs.380760; Homo sapiens pyruvate dehydrog; ovar; s.m.
 115675; W87707; Hs.82065; interleukin 6 signal transduce; breast; pros; mAb+s.m.
 115683; AF255910; Hs.54650; junctional adhesion molecule 2; angio, glio; mAb
 115697; D31382; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 115719; AW992405; Hs.352406; Homo sapiens, clone IMAGE:3507; pros; breast; colon; CTL+s.m.
 115819; AA486620; Hs.41135; endomucin-2; angio; diag
 115827; AA428000; Hs.283072; actin related protein 2/3 comp; angio; diag
 115844; A1373062; Hs.332938; hypothetical protein MGC5370; pros; diag
 115881; NM_005756; Hs.184942; G protein-coupled receptor 64; ovar, EWS, uter; mAb+s.m.
 115892; AA291377; Hs.50831; ESTs; ovar, blad, lung; diag
 115909; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_H; ovar, lung; diag
 115947; R47479; Hs.94761; KIAA1691 protein; colon; diag
 115978; AL035864; Hs.69517; cDNA for differentially expres; lung, blad, breast, pros, ovar, headnk; CTL
 116003; BE275469; Hs.66493; Down syndrome critical region ; colon; mAb
 116011; AL359053; Hs.57664; Homo sapiens mRNA full length ; breast; diag
 116028; H59799; Hs.42644; thioredoxin-like; ovar, lung; diag
 116107; AL133916; Hs.47860; hypothetical protein FLJ20093; lung, breast; diag
 116202; BE159395; Hs.294092; ESTs; pros; diag
 116238; AV660717; Hs.47144; DKFZP586N0819 protein; ovar; diag
 116301; AW969706; Hs.293332; ESTs; EWS; diag
 116334; AL038450; Hs.48948; ESTs; pros; diag
 116335; AK001100; Hs.41690; desmocollin 3; lung, blad, headnk; diag
 116393; A1972402; Hs.306051; hypothetical protein MGC2648; pros; diag
 116399; AA889120; Hs.110637; homeo box A10; pros; CTL+s.m.
 116401; AW893940; Hs.59698; ESTs; ovar; diag
 116416; AW753676; Hs.39982; ESTs; ovar; diag
 116470; A1272141; Hs.351928; SRY (sex determining region Y); colon, breast, angio, blad; diag
 116483; A1346201; Hs.76118; ubiquitin carboxyl-terminal es; angio, lung; s.m.
 116610; D80449; Hs.184841; ESTs; pros; diag
 116732; AW152225; Hs.165909; ESTs, Weakly similar to I38022; colon; diag
 116787; AW362955; Hs.356547; Homo sapiens cDNA FLJ14415 fis; pros, breast, colon, pros; mAb
 116962; H79677; ; gbyu76g10.s1 Soares fetal liv; pros; diag
 117027; AW085208; Hs.130093; ESTs; breast; diag
 117280; M18217; Hs.172129; Homo sapiens cDNA: FLJ21409 fi; breast, colon, pros; diag
 117284; AK001701; Hs.183779; Homo sapiens cDNA FLJ10590 fis; pros; diag
 117320; AB024937; Hs.211092; LUNX protein; PLUNC (palate tu; lung; mAb+diag
 117367; A1041793; Hs.42502; ESTs; breast; diag
 117412; N32536; Hs.42645; solute carrier family 16 (mono; breast, ovar ; mAb+s.m.
 117425; AK000028; Hs.356100; ribosomal protein S24; pros; diag
 117563; AF055634; Hs.44553; unc5 (C.elegans homolog) c; leuk ; diag
 117602; N35020; Hs.44685; C3HC4-like zinc finger protein; EWS; CTL+s.m.
 117921; AA021459; Hs.306480; Homo sapiens mRNA; cDNA DKFZp7; pros ; diag
 117984; AF189723; Hs.106778; ATPase, Ca++ transporting, typ; pros, breast, colon; mAb
 118049; N53145; ; gbyv5509.s1 Soares fetal liv; pros; diag
 118314; N48580; Hs.46692; ESTs; blad, lung; diag
 118336; BE327311; Hs.47166; HT021; breast, ovar, blad, pros; CTL+s.m.
 118368; N64339; Hs.48956; gap junction protein, beta 6 (-); lung, blad; mAb
 118417; AF080229; ; gb:Human endogenous retrovirus; pros; s.m.
 118472; AL157545; Hs.173179; bromodomain and PHD finger con; breast; diag
 118511; N75620; Hs.43157; ESTs; angio; diag
 118901; AW292577; Hs.94445; ESTs; breast; diag
 118905; AW973708; Hs.201925; Homo sapiens cDNA FLJ13446 fis; breast; diag
 119018; AA631143; Hs.278695; Homo sapiens prostein mRNA, co; pros, pros; diag
 119036; R95872; Hs.117572; chemokine binding protein 2; breast, ovar; mAb
 119073; BE245360; Hs.45514; v-ets erythroblastosis virus E; angio, pros; CTL+s.m.
 119082; AF252297; Hs.91546; cytochrome P450 retinoid metab; EWS; diag
 119126; R45175; Hs.117183; ESTs; pros, breast, colon; diag
 119279; N57568; Hs.48028; EST; breast; diag
 119307; BE048061; Hs.37054; ephrin-A3; colon, breast; mAb+diag
 119478; A1624342; Hs.179082; ESTs; breast; diag
 119617; AA516531; Hs.55999; NK homeobox (Drosophila), fami; pros; diag
 119743; AA947552; Hs.58086; branched chain aminotransferas; ovar; s.m.
 119771; A1905687; Hs.348419; A1905687:IL-BT095-190199-019 B; breast; diag
 119780; NM_016625; Hs.191381; hypothetical protein; ovar, lung; CTL+s.m.
 119789; BE393948; Hs.50915; kallikrein 5; ovar; diag
 119845; W79123; Hs.58561; G protein-coupled receptor 87; lung, blad, headnk, cerv; mAb+s.m.
 119940; AL050097; Hs.272531; DKFZP586B0319 protein; pros; diag
 120104; AK000123; Hs.180479; hypothetical protein FLJ20116; colon, lung; diag
 120132; W57554; Hs.125019; lymphoid nuclear protein (LAF-; pros, breast; diag
 120147; A1917116; Hs.348941; hemoglobin, beta; EWS; diag

- 120206; H26735; Hs.91668; Homo sapiens clone PP1498 unk; breast; mAb
- 120242; AW969587; Hs.86366; ESTs; blad; diag
- 120328; AA923278; Hs.290905; ESTs, Weakly similar to proteax; pros; s.m.
- 120438; AW015242; Hs.99488; ESTs, Weakly similar to YK54_Y; ovar; diag
- 120471; AA251944; Hs.104058; CGL-29 protein; colon; diag
- 120486; AW368377; Hs.137569; tumor protein 63 kDa with stro; lung, blad, headnk; diag
- 120588; AA703226; Hs.16193; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
- 120624; AW407987; Hs.173518; M-phase phosphoprotein homolog; breast; s.m.
- 120830; AI568170; Hs.96886; ESTs; EWS; diag
- 120977; AA398155; Hs.97600; ESTs; breast, ovar; diag
- 121027; AI572490; Hs.99785; Homo sapiens cDNA: FLJ21245 f; blad; mAb
- 121231; AA814948; Hs.96343; ESTs, Weakly similar to ALUC_H; EWS; diag
- 121335; AA404418; ; gbzw37e02.s1 Soares_total_fet; angio; diag
- 121362; AF050147; Hs.97932; chondromodulin I precursor; EWS; mAb
- 121457; W07404; Hs.102558; hypothetical protein FLJ22055; colon; diag
- 121619; AA528339; Hs.178062; ESTs, Weakly similar to phosph; EWS; s.m.
- 121710; AF163474; Hs.96744; prostate androgen-regulated tr; pros; diag
- 121721; AL047051; Hs.199961; ESTs, Weakly similar to ALU7_H; pros; diag
- 121723; AA243499; Hs.104800; hypothetical protein FLJ10134; breast; diag
- 121748; BE536911; Hs.234545; hypothetical protein NUF2P; breast; diag
- 121779; AW513143; Hs.98367; SRY (sex determining region Y); ovar; diag
- 121791; AA815378; Hs.293317; ESTs, Weakly similar to GGC1_H; blad, headnk, lung, ovar; mAb+CTL
- 121792; AW969726; Hs.98381; ESTs, Weakly similar to serine; EWS; diag
- 121913; AI249368; Hs.98558; ESTs; protease inhibitor 15 f; breast, pros; s.m.
- 121920; AA428300; ; gbzw18b02.s1 Soares ovary tum; ovar, uter, cerv; diag
- 122041; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
- 122520; AW951324; Hs.173609; pregnancy specific beta-1-glyc; colon; diag
- 122797; AJ251027; Hs.99526; odorant-binding protein 28 (OB; breast; diag
- 122802; AI687303; Hs.285529; G protein-coupled receptor 49; ovar, uter; mAb+s.m.
- 122969; AW821252; Hs.104336; hypothetical protein; ovar; diag
- 123005; AW369771; Hs.367688; integrin, beta 8; ovar, lung, headnk, glio; mAb+s.m.
- 123044; AK001035; Hs.130881; B-cell CLL/lymphoma 11A (zinc; lung; diag
- 123137; AI073913; Hs.100686; ESTs, Weakly similar to JE0350; breast, colon, ovar, uter, lung, stom; diag
- 123158; AF161426; Hs.218329; hypothetical protein; breast; diag
- 123160; AA488687; Hs.284235; ESTs, Weakly similar to I38022; lung; diag
- 123169; AI950087; Hs.369628; gbzwq05c02.x1 NCL_CGAP_Kid12_H; ovar; diag
- 123208; AW988543; Hs.203270; ESTs, Weakly similar to ALU1_H; pros; diag
- 123308; C14187; Hs.157208; ESTs; EWS; diag
- 123339; AW188464; Hs.101515; ESTs; ovar; diag
- 123475; BE439553; Hs.12329; Homo sapiens, clone IMAGE:4098; pros; diag
- 123494; AW179019; Hs.112110; mitochondrial ribosomal prot; ovar; diag
- 123520; AA608550; ; gbzae53d12.s1 Stratagene lung; pros; s.m.
- 123533; AA608751; ; gbzae56h07.s1 Stratagene lung; colon; diag
- 123619; AA602964; Hs.366318; gb:nc97c02.s1 NCL_CGAP_Pr2 Hom; breast; CTL+s.m.
- 123689; AA399323; Hs.285130; Homo sapiens pinch-2 protein m; ovar; diag
- 123709; AA706910; Hs.112742; ESTs; breast; diag
- 123829; AF251237; Hs.112208; XAGE-1 protein; lung, blad, test; CTL
- 123972; T46848; Hs.70337; immunoglobulin superfamily, m; ovar; diag
- 124006; AI147155; Hs.279727; ESTs; homologue of PEM-3 (Cion; breast, angio, lung, ovar, EWS; diag
- 124059; BE387335; Hs.283713; ESTs, Weakly similar to S64054; breast, colon, blad, lung; CTL+diag
- 124153; AU077333; Hs.160483; erythrocyte membrane protein b; pros; mAb
- 124352; AA640891; Hs.102406; ESTs; breast, pros, ovar, lung; diag
- 124526; N62096; Hs.293185; ESTs, Weakly similar to JC7328; pros; mAb+s.m.
- 124579; AI693815; Hs.127179; cryptic gene; panc; diag
- 124777; R41933; Hs.140237; ESTs, Weakly similar to ALU1_H; pros, breast; diag
- 125103; AA570056; Hs.122730; ESTs, Moderately similar to K1; colon; mAb
- 125154; W38419; ; gbzc78a07.s1 Pancreatic Islet; ovar; diag
- 125250; W26524; Hs.356686; protein phosphatase 4 regulator; ovar; CTL+s.m.
- 125266; W90022; Hs.186809; ESTs, Highly similar to LCT2_H; angio; diag
- 125453; BE385523; Hs.18048; melanoma antigen, family A, 10; blad; mAb+CTL
- 125666; AL390172; Hs.317432; Homo sapiens cDNA: FLJ21270 f; ovar; diag
- 125770; AA143045; Hs.81665; v-kit Hardy-Zuckerman 4 feline; EWS; diag
- 125976; AA436760; Hs.35552; gbzv67d11.r1 Soares_total_fet; pros; diag
- 126399; AA088767; Hs.83883; transmembrane, prostate androg; panc; mAb+s.m.
- 126645; AA316181; Hs.61635; six transmembrane epithelial a; pros, breast, lung, panc, headnk, EWS; mAb+CTL
- 126756; AI559444; Hs.104679; ESTs; pros, breast; mAb
- 126799; AW753865; Hs.74376; olfactomedin related ER locat; EWS; diag
- 126872; AW450979; ; gb:UH-BI3-ata-a-12-0-ULs1 N; blad; diag
- 126892; AF121856; Hs.284291; sorting nexin f; ovar; diag
- 126960; AL390172; Hs.317432; branched chain aminotransferas; ovar; s.m.
- 126966; R38438; Hs.118747; solute carrier family 15 (H+); pros; mAb
- 127003; AW816515; Hs.173540; ATPase, Class V, type 10D; pros; mAb
- 127221; BE062109; Hs.241551; chloride channel, calcium act; lung, blad, headnk, cerv; mAb+s.m.
- 127240; AJ005683; Hs.86998; nuclear factor of activated T-; pros; CTL+s.m.
- 127425; AF183810; Hs.26102; trichorhinophalangeal syndrome; breast; mAb
- 127479; D31152; Hs.179729; collagen, type X, alpha 1 (Sch; breast, lung, headnk, panc; diag
- 127537; AI926047; Hs.162859; ESTs; pros; diag
- 127664; AA806164; Hs.116502; ESTs; EWS; diag
- 128046; AA873285; Hs.357313; gbzxh68h05.s1 NCL_CGAP_Kid5 Ho; pros, breast, colon; diag
- 128305; AI954968; Hs.365706; matrix Gla protein; breast; diag
- 128478; AA708205; Hs.100343; ESTs; EWS; CTL+s.m.
- 128515; BE395085; Hs.334762; type I transmembrane protein F; panc; mAb
- 128595; U31875; Hs.272499; short-chain alcohol dehydrogen; blad, breast; CTL+s.m.

- 128610; N48373; Hs.10247; activated leucocyte cell adhes; breast, pros, lung, ovar; diag
 128734; AB008390; Hs.104570; kallikrein 8 (neuropsin/ovasin; ovar; diag
 128790; AF026692; Hs.105700; secreted frizzled-related prot; breast, colon, pros, ovar, uter, panc; diag
 128797; NM_002975; Hs.105927; stem cell growth factor; lymph; EWS; leuk; diag
 128854; BE159181; Hs.168232; hypothetical protein FLJ13855; breast; diag
 128925; R67419; Hs.21851; Homo sapiens cDNA FLJ12900 fis; breast; diag
 128949; AA009647; Hs.352537; a disintegrin and metalloprote; breast, ovar, headnk, panc; mAb+diag+s.m.
 128969; Z42047; Hs.107479; Homo sapiens PRO2751 mRNA, cont; pros; diag
 129041; BE382756; Hs.169902; solute carrier family 2 (facit; lung, blad; mAb+s.m.
 129097; BE243933; Hs.108642; zinc finger protein 22 (KOX 15; ovar; CTL+s.m.
 129099; AF146074; Hs.108660; ATP-binding cassette, sub-fam; lung, blad, headnk; mAb+s.m.
 129184; AW161450; Hs.109201; CGI-86 protein; pros; mAb
 129260; AF077200; Hs.279813; hypothetical protein; colon; diag
 129284; AA318224; Hs.296141; ESTs; colon; diag
 129362; U30246; Hs.110736; solute carrier family 12 (sodi; colon, breast, pros; mAb
 129366; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA; breast; diag
 129389; NM_012445; Hs.288126; spondin 2, extracellular matr; colon, pros; diag
 129404; AJ267700; Hs.351201; ESTs; pros, ovar, lung, blad, headnk, panc; diag
 129466; L42583; Hs.334309; keratin 6A; lung, blad; diag
 129482; AA188185; Hs.289043; spindlin; breast; diag
 129534; AK002126; Hs.11260; hypothetical protein FLJ11264; pros; diag
 129571; X51630; Hs.1145; Wilms tumor 1; ovar; CTL+s.m.
 129605; AF061812; Hs.115947; keratin 16 (focal non-epidermo; lung, blad, headnk; diag
 129620; D79338; Hs.239720; CCR4-NOT transcription complex; breast, angio; diag
 129628; U38945; Hs.1174; cyclin-dependent kinase inhibi; lung, blad, ovar, headnk; s.m.
 129650; AF109298; Hs.118258; prostate cancer associated pro; pros, EWS; diag
 129689; AW748482; Hs.77873; B7 homolog 3; breast; diag
 129703; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457; EWS, leuk; diag
 129720; AA156214; Hs.12152; APMCF1 protein; breast; diag
 129750; AF056085; Hs.198612; G protein-coupled receptor 51; angio, blad; mAb+s.m.
 129869; AJ222069; Hs.13015; hypothetical protein similar t; breast; diag
 129912; AF155098; Hs.107213; hypothetical protein FLJ20585; ovar; CTL+s.m.
 129936; AJ250717; Hs.1355; cathepsin E; blad; sm+diag
 129953; AA412195; Hs.13740; ESTs; breast; diag
 129977; NM_000399; Hs.1395; early growth response 2 (Krox-; EWS; CTL+s.m.
 130010; AA301116; Hs.142838; nucleolar phosphoprotein Nopp3; ovar; diag
 130057; AF027153; Hs.324787; solute carrier family 5 (inosi; breast; mAb
 130095; AK001635; Hs.14838; hypothetical protein FLJ10773; breast; diag
 130155; AA101043; Hs.151254; kallikrein 7 (chymotryptic, st; ovar; diag
 130181; AF052119; Hs.151608; Homo sapiens clone Z3622 mRNA; pros; diag
 130184; H58306; Hs.15165; retinoic acid induced 14; angio; diag
 130262; D63216; Hs.153684; frizzled-related protein; panc, EWS, stom, renal; diag
 130343; AB040914; Hs.278628; KIAA1481 protein; breast; diag
 130376; R40873; Hs.155174; CDC5 (cell division cycle 5, S; ovar; CTL+s.m.
 130385; AW067800; Hs.155223; stanniocalcin 2; breast, lung; mAb+diag
 130455; D90041; Hs.155956; N-acetyltransferase 1 (arylam; breast; s.m.
 130511; L32137; Hs.1584; cartilage oligomeric matrix pr; breast, ovar; diag
 130558; BE564937; Hs.15984; pp21 homolog; pros; CTL+s.m.
 130577; M69241; Hs.162; insulin-like growth factor bin; ovar; diag
 130604; AA383256; Hs.1657; estrogen receptor 1; breast; mAb+s.m.
 130627; BE003054; Hs.1695; matrix metalloproteinase 12 (mc; lung, colon, blad, headnk, ovar, panc; mAb+diag+s.m.
 130637; AA356764; Hs.17109; integral membrane protein 2A; EWS; mAb+s.m.
 130648; AJ458165; Hs.17296; hypothetical protein MGC2376; colon; diag
 130667; BE246961; Hs.17639; Homo sapiens ubiquitin protein; breast; s.m.
 130690; AB006625; Hs.139033; paternally expressed 3; ovar; diag
 130714; AJ348274; Hs.18212; DNA segment on chromosome X (u; breast; diag
 130760; AW379130; Hs.18953; phosphodiesterase 9A; pros; CTL+s.m.
 130800; AJ187292; Hs.19574; hypothetical protein MGC5469; colon, lung; diag
 130839; AB011169; Hs.380875; similar to S. cerevisiae SSM4; angio; diag
 130844; U76248; Hs.20191; seven in absentia (Drosophila); breast; diag
 130892; AL120837; Hs.20993; high-glucose-regulated protein; breast; CTL+s.m.
 130941; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin; ovar; mAb
 130967; AA393071; Hs.182579; leucine aminopeptidase; ovar; s.m.
 130972; D81866; Hs.374468; Homo sapiens mRNA; cDNA DKFZp5; angio; diag
 130987; BE613269; Hs.21893; hypothetical protein DKFZp761N; colon; diag
 131046; AA321649; Hs.2248; small inducible cytokine subfa; breast, lung, blad, ovar, fibro; diag
 131080; NM_001955; Hs.2271; endothelin 1; angio; diag
 131083; Y09763; Hs.22785; gamma-aminobutyric acid (GABA); pros; mAb
 131148; AW953575; Hs.303125; p53-induced protein PIGPC1; breast, colon, angio; diag
 131216; AJ815486; Hs.243901; Homo sapiens cDNA FLJ20738 fis; colon, breast; diag
 131228; AW207469; Hs.24485; chondroitin sulfate proteoglyc; ovar; diag
 131244; AJ638429; Hs.24763; RAN binding protein 1; lung, blad, headnk; CTL+s.m.
 131288; AA278482; Hs.25328; ESTs, Moderately similar to AL; pros; diag
 131289; AA296696; Hs.333418; FXD domain-containing ion tra; colon; diag
 131307; NM_000025; Hs.2549; adrenergic, beta-3-, receptor; EWS; mAb
 131313; R96290; Hs.75874; ribosomal protein L44; EWS; diag
 131492; AJ452601; Hs.288669; nuclear receptor subfamily 2, ; pros; mAb+s.m.
 131544; AL355715; Hs.28555; programmed cell death 9 (PDCD9; breast; diag
 131559; AL076599; Hs.10784; hypothetical protein FLJ20037; breast; diag
 131564; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis; breast; diag
 131603; X81334; Hs.2936; matrix metalloproteinase 13 (c; blad; s.m.
 131643; AW410601; Hs.30026; HSPC182 protein; breast; diag
 131739; AF017988; Hs.31386; secreted frizzled-related prot; breast; mAb+s.m.

- 131817; U20636; Hs.3280; caspase 6, apoptosis-related c; fibro, breast, cerv, lung, blad, panc, gliob; s.m.
 131885; BE502341; Hs.3402; ESTs; breast; diag
 131919; T15803; Hs.272458; protein phosphatase 3 (former); pros; breast; s.m.
 131925; AF151048; Hs.183180; anaphase promoting complex sub; breast; diag
 131965; W79283; Hs.35962; ESTs; lung, ovar; diag
 131985; AA503020; Hs.36563; hypothetical protein FLJ22418; breast, ovar; diag
 132050; AI267615; Hs.38022; ESTs; angio; diag
 132173; X89426; Hs.41716; endothelial cell-specific mole; angio; diag
 132180; NM_004460; Hs.418; fibroblast activation protein; colon, panc, esoph; mAb
 132191; AA507576; Hs.288361; Homo sapiens cDNA: FLJ22696 f; ovar; diag
 132349; AW975654; Hs.181286; serine protease inhibitor, Kaz; pros; blad; s.m.
 132354; BE185289; Hs.1076; small proline-rich protein 18; lung; diag
 132358; NM_003542; Hs.46423; H4 histone family, member G; pros; CTL+s.m.
 132371; AA235448; Hs.222088; PRO2000 protein; breast; diag
 132454; BE296227; Hs.250822; serine/threonine kinase 15; blad, breast; s.m.
 132490; NM_001290; Hs.4980; LIM domain binding 2; angio; diag
 132520; AA257992; Hs.50651; Janus kinase 1 (a protein tyro; EWS; s.m.
 132528; T78736; Hs.50758; SMC4 (structural maintenance α ; ovar; CTL+s.m.
 132543; BE568452; Hs.344037; protein regulator of cytokines; colon, lung; diag
 132572; AI929659; Hs.237825; signal recognition particle 72; ovar; diag
 132592; AW803564; Hs.288850; Homo sapiens cDNA: FLJ22528 f; colon; diag
 132624; AA326108; Hs.33829; bHLH protein DEC2; ovar; diag
 132632; AU076916; Hs.5398; guanine monophosphate synthetas; ovar, lung; s.m.
 132669; W38586; Hs.380933; guanine nucleotide binding pro; colon; diag
 132710; W74001; Hs.55279; serine (or cysteine) proteinase; lung, blad, colon, headnk; diag
 132725; NM_006276; Hs.184167; splicing factor, arginine/ser; ovar; CTL+s.m.
 132767; BE182592; Hs.11261; small proline-rich protein 2A; lung; diag
 132791; AB029551; Hs.7910; RING1 and YY1 binding protein; pros; CTL+s.m.
 132837; AA370362; Hs.57958; EGF-TM7-latrophilin-related pr; angio; diag
 132856; NM_001448; Hs.58367; glypican 4; breast, colon, pros; mAb
 132888; NM_005476; Hs.5920; UDP-N-acetylglucosamine-2-epim; pros; s.m.
 132902; AI936442; Hs.59838; hypothetical protein FLJ10808; colon; diag
 132939; AB009284; Hs.61152; exostoses (multiple)-like 2; ovar; diag
 132964; AI362575; Hs.303171; ESTs; pros; diag
 132967; AA316181; Hs.61635; six transmembrane epithelial a; pros; pros; mAb+CTL
 132990; X77343; Hs.334334; transcription factor AP-2 α ; breast, lung; CTL+s.m.
 132994; AA112748; Hs.279905; clone HQ0310 PRO0310p1; colon, breast; s.m.
 133006; AW978436; Hs.62515; KIAA0494 gene product; colon; diag
 133015; AJ002744; Hs.246315; UDP-N-acetyl-alpha-D-galactose; breast, colon, pros; s.m.
 133016; AJ439688; Hs.6289; hypothetical protein FLJ20886; breast; diag
 133061; AI185431; Hs.296638; prostate differentiation factor; angio, pros, blad; diag
 133063; AI654133; Hs.356247; thyroid receptor interacting p; pros; mAb+s.m.
 133070; U92649; Hs.380136; a disintegrin and metalloprotein; leuk; diag
 133179; U81599; Hs.66731; homeo box B13; pros; CTL+s.m.
 133199; AF231981; Hs.250175; homolog of yeast long chain po; breast, angio; CTL+s.m.
 133260; AA403045; Hs.6906; Homo sapiens cDNA: FLJ23197 f; angio; diag
 133272; NM_002776; Hs.69423; kallikrein 10; colon, ovar; diag
 133314; AA102670; Hs.70725; gamma-aminobutyric acid (GABA); breast, panc; mAb
 133321; T79526; Hs.179516; integral type I protein; breast; diag
 133391; AW103364; Hs.727; inhibin, beta A (activin A, α ; breast, blad, lung; diag
 133415; X69599; Hs.73149; paired box gene 8; ovar; CTL
 133477; AW502935; Hs.740; PTK2 protein tyrosine kinase 2; breast; s.m.
 133579; X75346; Hs.75074; mitogen-activated protein kinase; pros; diag
 133626; AW836130; Hs.75277; hypothetical protein FLJ13910; pros; diag
 133736; D49958; Hs.75819; glycoprotein M6A; pros; mAb
 133829; AW630088; Hs.76550; Homo sapiens mRNA; cDNA DKFZp5; ovar; diag
 133860; S78296; Hs.76888; hypothetical protein MGC12702; blad; diag
 133944; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 133975; C18356; Hs.295944; tissue factor pathway inhibitor; angio, panc; CTL+diag
 133976; AI908165; Hs.169946; GATA-binding protein 3 (T-cell; breast, blad; mAb+s.m.
 134100; AA460085; Hs.171075; replication factor C (activator); pros; diag
 134110; U41060; Hs.79136; LIV-1 protein, estrogen regula; breast, blad, ovar, pros; mAb
 134169; AI690916; Hs.178137; transducer of ERBB2, 1; breast; CTL+s.m.
 134219; NM_000402; Hs.80206; glucose-6-phosphate dehydrogen; breast; s.m.
 134319; BE304999; Hs.285754; fumarate hydratase; colon; s.m.
 134326; AW903838; Hs.81800; chondroitin sulfate proteoglyc; ovar, breast, panc, lung; diag
 134348; AW291946; Hs.82065; interleukin 6 signal transduce; breast; mAb+s.m.
 134374; N22687; Hs.8236; ESTs; pros; diag
 134390; R35528; Hs.8258; DKFZP434D1335 protein; pros; CTL+s.m.
 134401; AI916662; Hs.211577; kinesin 1 (kinesin receptor); pros, breast; mAb+s.m.
 134405; AW067903; Hs.82772; collagen, type XI, α 1; breast, lung, ovar, headnk; CTL
 134470; X54942; Hs.83758; CDC28 protein kinase 2; lung, blad, headnk; s.m.
 134520; BE091005; Hs.349506; activated RNA polymerase II tr; ovar; s.m.
 134529; AW411479; Hs.848; FK506-binding protein 4 (59kD); breast; diag
 134570; U66615; Hs.172280; SWI/SNF related, matrix associ; EWS; CTL+s.m.
 134554; AK001741; Hs.8739; hypothetical protein FLJ10879; breast; diag
 134666; BE391929; Hs.8752; transmembrane protein 4; breast; mAb+s.m.
 134691; AW382987; Hs.88474; prostaglandin-endoperoxide synth; ovar; s.m.
 134727; X80507; Hs.84520; yes-associated protein 65 kDa; blad; diag
 134731; D89377; Hs.89404; msh (Drosophila) homeo box hom; blad; s.m.
 134786; T28618; Hs.89540; TEK tyrosine kinase, endothel; angio; s.m.
 134824; S78723; Hs.298623; 5-hydroxytryptamine (serotonin); blad; mAb
 134856; BE281128; Hs.9030; TONDU; blad; CTL+s.m.

- 134868; AB020689; Hs.90419; KIAA0882 protein; breast; diag
 134924; BE294029; Hs.279903; Ras homolog enriched in brain ; breast; mAb
 134972; AL033527; Hs.169252; v-myc avian myelocytomatosis v; ovar; CTL+s.m.
 134975; R50333; Hs.92186; Leman coiled-coil protein; breast; diag
 134989; AW968058; Hs.92381; nudix (nucleoside diphosphate ; colon; diag
 135073; W55956; Hs.94030; Homo sapiens mRNA; cDNA DKFZp5; angio; diag
 135117; W52493; Hs.94694; Homo sapiens cDNA FLJ10561 fs; breast; diag
 135166; AA135867; Hs.280858; ESTs, Highly similar to A35661; pros; diag
 135235; AW298244; Hs.266195; ESTs; angio; diag
 135242; AI583187; Hs.9700; cyclin E1; ovar; CTL+s.m.
 135243; BE463721; Hs.97101; putative G protein-coupled rec; colon; mAb+s.m.
 135255; Y13645; Hs.97234; uroplakin 2; blad; mAb
 135309; AI564123; Hs.356689; ADP-ribosylation factor-like 5; pros; diag
 135315; H81136; Hs.334604; Homo sapiens mRNA for KIAA1870; pros; diag
 135389; U05237; Hs.99872; fetal Alzheimer antigen; pros; breast, colon; CTL+s.m.
 135400; X78592; Hs.99915; androgen receptor (dihydrotest; pros; mAb+s.m.
 300254; AW183618; Hs.55610; solute carrier family 30 (zinc; pros; breast; mAb+s.m.
 300256; AW591433; Hs.298241; Transmembrane protease, serine; breast, colon, lung, ovar; mAb+diag+s.m.
 300318; AW444502; Hs.256982; ESTs, Weakly similar to NEL1_H; angio; CTL+diag
 300605; AI218847; Hs.152670; ESTs; pros; diag
 300921; AF146747; Hs.232165; polycythemia rubra vera 1; cel; pros; mAb+s.m.
 300923; AW136372; Hs.1852; acid phosphatase, prostate; pros; s.m.
 301042; AI659131; Hs.366053; hypothetical protein MGC2849; pros; mAb
 301043; AI160316; Hs.149155; voltage-dependent anion channel; pros; mAb+s.m.
 301050; AW136973; Hs.362915; ESTs, Weakly similar to S69890; colon, lung; CTL+s.m.
 301341; AA887801; Hs.208229; G protein-coupled receptor; breast, lung; mAb+s.m.
 302001; AB020711; Hs.374965; KIAA0904 protein; breast ; CTL+s.m.
 302005; BE252922; Hs.123119; MAD (mothers against decapentap; pros; diag
 302067; BE542706; Hs.222399; CEGP1 protein; breast; diag
 302167; NM_006227; Hs.283007; phospholipid transfer protein; pros; mAb
 302225; NM_007231; Hs.162211; solute carrier family 6 (neuro; panc; mAb+s.m.
 302276; AW057736; Hs.323910; HER2 receptor tyrosine kinase ; breast; mAb+s.m.
 302290; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp5; pros; breast; diag
 302372; AL117406; Hs.335891; ATP-binding cassette transport; breast; pros ; mAb+s.m.
 302384; AI678059; Hs.202676; synaptonemal complex protein 2; breast, cerv; diag
 302410; NM_004917; Hs.218366; kallikrein 4 (protease, enamel; pros; diag
 302468; AL133661; Hs.380155; DKFZP434B061 protein; pros; diag
 302562; BE149762; Hs.48958; gap junction protein, beta 6 (; lung, blad; mAb
 302881; AA508353; Hs.105314; relaxin 1 (H1); pros; diag
 303295; AA205625; Hs.208067; ESTs; blad; diag
 303380; AW962764; Hs.303171; olfactory receptor, family 51.; pros; mAb
 303506; AA340605; Hs.105887; ESTs, Weakly similar to Homolo; pros; breast, colon ; diag
 303699; BE143707; Hs.19525; hypothetical protein FLJ22794; pros; diag
 303753; AW503733; Hs.9414; KIAA1488 protein; pros; breast, colon; CTL+s.m.
 305503; AA759177; Hs.298148; ESTs, Weakly similar to KIAA05; pros; diag
 306273; AA936290; ; gbcon70a01.s1 Soares_NFL_T_GBC; pros; diag
 306676; AI005603; ; gbcon15c10.s1 NCI_CGAP_GC3 Hom; lung; diag
 306840; AI077477; Hs.307912; ESTs; angio; diag
 309177; AI951118; Hs.326736; Homo sapiens breast cancer ant; breast; pros; mAb+CTL
 309583; AW170035; Hs.326736; Homo sapiens breast cancer ant; breast; mAb+CTL
 309931; AW341683; Hs.343663; gbhd13d01.x1 Soares_NFL_T_GBC; lung; mAb
 310382; AI734009; Hs.127699; KIAA1603 protein; pros; diag
 310431; AI420227; Hs.366053; ESTs, Weakly similar to A46010; pros; diag
 310573; AW292180; Hs.156142; ESTs; pros; diag
 310636; AI814373; Hs.164175; ESTs; lung; diag
 310781; AI380797; Hs.158992; ESTs; breast; diag
 310955; AI476732; Hs.263912; ESTs; breast, angio; diag
 311034; BE567130; Hs.311389; ESTs, Highly similar to NKGD_H; lung; mAb+s.m.
 311166; AI821005; Hs.118599; Intron of BFF9 (GDNFRa); breast ; diag
 311251; AI655662; Hs.197698; ESTs; pros; diag
 311557; AF200492; Hs.211238; interleukin-1 homolog 1; lung; diag
 311596; AI682088; Hs.79375; single-minded (Drosophila) hom; pros; CTL
 311630; AI915444; Hs.372037; ESTs; colon, blad, lung, ovar, panc, headn; mAb+diag+s.m.
 311677; AA084248; Hs.372651; G protein-coupled receptor 39; ovar, angio, glior; mAb+s.m.
 311911; R19175; Hs.169793; ribosomal protein L32; pros; diag
 311928; T62216; Hs.378028; ESTs; pros; diag
 312182; T94344; Hs.326263; ESTs; pros; diag
 312252; AI128388; Hs.143655; ESTs; blad; diag
 312319; AA906997; Hs.180780; TERA protein; colon; CTL+s.m.
 312521; AI263307; Hs.356901; H2B histone family, member L; pros; breast, lung; diag
 312544; AA516420; Hs.352340; ESTs, Weakly similar to I38022; breast; diag
 312742; AI650363; Hs.116462; ESTs; colon; diag
 312795; AW975014; Hs.26; ferrochelatase (protoporphyrin; pros; s.m.
 312857; BE083868; Hs.126914; KIAA1430 protein; colon, pros; CTL+s.m.
 312922; AA329258; Hs.378739; ESTs, Moderately similar to at; pros; diag
 313328; AW449211; Hs.105445; GDNF family receptor alpha 1; breast ; mAb+s.m.
 313513; AW298600; Hs.64313; ESTs, Weakly similar to S59501; angio; mAb+s.m.
 313556; AA628517; Hs.118502; ESTs; angio; diag
 313665; AW751201; Hs.120932; ESTs; angio; diag
 313774; AI916058; Hs.144583; ESTs; colon; CTL
 313915; C18863; Hs.163443; Intron of perostin (OSF-2os); breast; diag
 313978; AI870175; Hs.13957; ESTs; angio; diag
 314078; AW129357; Hs.329700; ESTs; breast; diag

- 314097; AA648744; Hs.269493; ESTs; breast; diag
 314121; AI732083; Hs.187619; ESTs; pros; breast; diag
 314171; AI821895; Hs.193481; ESTs; pros; diag
 314506; AA833655; Hs.206868; Homo sapiens cDNA FLJ14056 fis; breast; diag
 314547; AA399272; Hs.144341; ESTs; breast; diag
 314558; AI873274; Hs.370280; ESTs; breast; pros; diag
 314589; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis; lung; blad; diag
 314691; AW207206; Hs.356962; ESTs; breast; pros; diag
 314785; AI538226; Hs.32976; guanine nucleotide binding pro; colon; pros; diag
 314907; AW971082; Hs.222888; ESTs, Weakly similar to TRHY_H; pros; diag
 315006; AI538613; Hs.298241; Transmembrane protease, serine; breast, colon, lung, ovar; mAb+diag+s.m.
 315033; AI493046; Hs.146133; ESTs; colon; diag
 315051; AW292425; Hs.163484; ESTs; breast; pros; blad; diag
 315052; AA876910; Hs.134427; ESTs; pros; breast; diag
 315196; AI367347; Hs.44898; Homo sapiens clone TCCCTA00151; breast; diag
 315368; AB037745; Hs.104696; KIAA1324 protein; pros; diag
 315408; AW273261; Hs.216292; ESTs; pros; diag
 315634; AA837085; Hs.372254; ESTs; breast; pros; diag
 315720; AA292998; Hs.163900; ESTs; blad; diag
 316177; AI904982; Hs.293102; downstream of breast cancer an; breast; mAb+CTL
 316442; AA760894; Hs.125350; ESTs; pros; diag
 316580; AA938198; Hs.146123; poly(A) polymerase gamma; breast, angio; s.m.
 316886; AA836331; Hs.170261; ESTs; breast; diag
 316943; AW014875; Hs.137007; ESTs; blad; diag
 317079; BE159984; Hs.125395; ESTs; blad; mAb+s.m.
 317140; AA885430; Hs.201925; Homo sapiens cDNA FLJ13446 fis; breast; diag
 317224; X73608; Hs.93029; sparcosteonelectin, cwcx and ka; pros, angio; diag
 317548; BE568568; Hs.159066; ESTs; pros; CTL+s.m.
 317803; AW664964; Hs.128899; ESTs; breast, lung, ovar, pros; mAb+s.m.
 317881; AI827246; Hs.224398; Homo sapiens cDNA FLJ11469 fis; breast, lung; diag
 318240; AI085377; Hs.143610; ESTs; lung; diag
 318524; AK001050; Hs.159066; hypothetical protein FLJ10188; pros, colon; CTL+s.m.
 318532; AW139377; Hs.127179; cryptic gene; panc; diag
 318744; AI793124; Hs.144479; ESTs; breast; diag
 318754; W21423; Hs.44222; CG-90 protein; pros; diag
 319080; AW967646; Hs.23023; ESTs; pros; diag
 319795; AB037821; Hs.146858; protocadherin 10; pros, glio; mAb+s.m.
 320066; BE305242; Hs.16098; claudin 2; colon, panc; diag
 320167; AA984373; Hs.90790; Homo sapiens cDNA: FLJ22930 fi; breast, pros; diag
 320203; AL049227; Hs.124776; downstream of cadherin 6 (by 3; renal, ovar; mAb+s.m.
 320211; AL039402; Hs.125783; DEME-6 protein; breast, pros; CTL
 320322; AF077374; Hs.139322; small proline-rich protein 3; lung; diag
 320324; AF071202; Hs.139336; ATP-binding cassette, sub-fam1; pros; mAb
 320561; AF085808; Hs.159330; uroplakin 3; pros, blad; diag
 320590; U67058; Hs.154299; Human proteinase activated rec; pros; mAb+s.m.
 320635; N50617; Hs.80508; small nuclear ribonucleoprotein; angio lung; diag
 320736; AA315361; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
 320796; AK001541; Hs.31218; secretory carrier membrane pro; pros, colon; diag
 320896; BE019924; Hs.271580; uroplakin 1B; lung, blad, ovar, headnk; mAb+diag
 321023; AW294316; Hs.125608; ESTs; colon; diag
 321107; AI732643; Hs.144151; downstream of breast cancer an; breast; mAb+CTL
 321412; AI674383; Hs.22891; solute carrier family 7 (catl); pros; mAb+s.m.
 321441; AF107493; Hs.201675; Homo sapiens LUCA-15 protein m; pros, breast; diag
 321644; AW975944; Hs.237396; ESTs; breast, pros; diag
 321717; AW956580; Hs.42699; ESTs; angio; diag
 321906; AW270608; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
 321911; AF026944; Hs.293797; ESTs; angio, lung, blad; diag
 322035; AL137517; Hs.306201; hypothetical protein DKFZp5640; breast, blad; mAb
 322521; AF147347; ; gb:Homo sapiens full length ln; breast; diag
 322706; AA018899; Hs.127179; cryptic gene; panc; diag
 322782; AA056060; Hs.202577; Homo sapiens cDNA FLJ12166 fis; pros; diag
 322818; AW043782; Hs.293616; ESTs; pros, breast, angio, glio; diag
 322882; AW248508; Hs.279727; Homo sapiens cDNA FLJ14035 fis; breast, lung, ovar, angio, blad; diag
 322975; C16391; ; Intron of breast cancer antige; breast; mAb+CTL
 323168; AL120862; Hs.124165; programmed cell death 9 (PDCD9; breast; diag
 323228; AF055019; Hs.355279; Homo sapiens clone 24670 mRNA; pros; diag
 323262; AL133990; Hs.190642; CEGP1 protein; breast, pros, blad; diag
 323287; AA639902; Hs.104215; ESTs, Moderately similar to SP; pros; diag
 323332; AI829520; ; gb:mf19c06.x1 NCL CGAP_U11 Hom; breast; diag
 323335; AI655499; Hs.161712; ESTs; pros, breast, mAb
 323587; AI299709; Hs.131886; Homo sapiens cDNA: FLJ22113 fi; colon; diag
 323817; AA410943; ; NAME OMITTED ... receptor kinase; breast; mAb
 324261; BE069341; ; gb:QV3-BT0381-270100-073-c08 B; breast; diag
 324295; AA434579; Hs.143691; ESTs; pros; diag
 324338; AA927668; Hs.145078; regulator of differentiation (; colon; diag
 324430; AA464018; Hs.335798; Homo sapiens cDNA: FLJ23241 fi; pros, colon; diag
 324432; AA464510; Hs.152812; ESTs; breast, lung, panc; diag
 324603; AW993522; Hs.299867; ESTs; pros, breast; diag
 324617; AA508552; Hs.222874; ESTs, Weakly similar to t38022; pros; diag
 324658; AI694767; Hs.129179; Homo sapiens cDNA FLJ13581 fis; pros; diag
 324718; AI557019; Hs.116467; small nuclear protein PRAK; colon, pros; diag
 324866; AI541214; Hs.46320; Small proline-rich protein SPR; lung, blad; diag
 324871; AI890347; Hs.271923; Homo sapiens cDNA: FLJ22785 fi; colon; diag

- 324987; AI375572; Hs.172634; ESTs; breast; diag
 325372; ; Phase 2 & 3 Exons; breast; CTL+s.m.
 325544; ; Phase 2 & 3 Exons; breast; angio; diag
 327035; ; Phase 2 & 3 Exons; lung; angio; diag
 327075; ; Phase 2 & 3 Exons; breast; lung; diag
 327414; ; Phase 2 & 3 Exons; angio; diag
 328700; ; Phase 2 & 3 Exons; breast; angio; diag
 330211; ; Phase 2 & 3 Exons; pros; CTL+s.m.
 330468; L10343; Hs.112341; protease inhibitor 3; skin-der; lung, colon, blad; diag
 330493; M27826; Hs.334372; endogenous retroviral protease; lung, colon; s.m.
 330630; NM_002902; Hs.79088; reticulocalbin 2; EF-hand calc; pros; diag
 330762; AW407332; Hs.13014; ADP-ribosylation factor GTPase; pros; CTL+s.m.
 330790; AI660243; Hs.318545; Hu01 Chip Redos; pros; blad; diag
 330814; AI955040; Hs.265398; PAR-6 beta (partitioning def; breast; diag
 330827; AI961486; Hs.249196; ESTs; lung, uter; diag
 330892; AF109298; Hs.118258; prostate cancer associated pro; pros; diag
 331014; AW770994; Hs.30340; hypothetical protein KIAA1165; colon; diag
 331151; R82331; Hs.121602; ESTs; pros; breast; diag
 331183; T40769; Hs.8469; ESTs; colon; diag
 331237; W87874; Hs.25277; Homo sapiens cDNA FLJ10717 f5; angio; diag
 331490; AF216751; Hs.26813; CDA14; pros; diag
 331578; AI246482; Hs.243010; ESTs; angio; diag
 331614; N92293; Hs.206832; EST; Moderately similar to ALU; breast; diag
 331811; AW885727; Hs.9914; Hu01 Chip Redos; lung; diag
 331889; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
 331969; AA526911; Hs.82772; collagen; type XI; alpha 1; breast; lung; CTL
 332180; AF134160; Hs.7327; claudin 1; lung; mAb
 332247; AA669097; ; ESTs; pros; breast; diag
 332396; AW579842; Hs.380730; hypothetical protein FLJ10697; pros; diag
 332453; L42583; Hs.334309; Hu01 Chip Redos; lung; diag
 332466; AB018259; Hs.118140; KIAA0716 gene product; angio; diag
 332530; M31669; Hs.1735; inhibin beta B (activin AB b; ovar; pros; diag
 332535; AF167708; Hs.19280; cysteine-rich repeat-containing; angio; diag
 332640; BE568452; Hs.344037; protein regulator of cytokines; blad; headnk; diag
 332645; AA284371; Hs.118064; ESTs; breast; colon; diag
 332686; X69699; Hs.73149; paired box gene 8; ovar; CTL+s.m.
 332697; X51405; Hs.75360; carboxypeptidase E; pros; diag
 332740; BE409869; Hs.286241; Homo sapiens cDNA: FLJ22698 f; pros; diag
 332798; ; C22000007:glj12314195[emb]CAB9; pros; breast; diag
 333769; ; NM_005940; Homo sapiens matrix; breast, colon, lung; mAb+diag+s.m.
 333904; ; Chromosome 22; pros; diag
 334223; ; NM_005080; Homo sapiens X-box; pros; breast; diag
 334447; ; NM_012429; Homo sapiens SEC14; pros; diag
 335115; ; NM_006498; Homo sapiens lectin; pros; CTL+s.m.
 335809; ; NM_014509; Homo sapiens kraken; breast; CTL+s.m.
 335824; ; ENSP00000249072; DJ222E13.1 (N; breast; pros; CTL+s.m.
 335825; ; ENSP00000249072; DJ222E13.1 (N; breast; diag
 335936; ; Chromosome 22; lung; diag
 336034; ; NM_007172; Homo sapiens nucleop; breast; angio; CTL+s.m.
 336152; ; NM_014246; Homo sapiens cadher; breast; mAb
 336336; ; C22000024:glj10645308[gb]AAG2; lung, breast; CTL+s.m.
 336008; ; NM_005940; Homo sapiens matrix; lung, breast, colon; mAb+diag+s.m.
 336033; ; Chromosome 22; lung; angio; diag
 338158; ; NM_012399; Homo sapiens phosph; lung; angio; diag
 338255; ; NM_014323; Homo sapiens zinc f; pros, breast, colon; CTL+s.m.
 400195; ; Hs.42650; NM_007057; Homo sapiens ZW10 f; lung; CTL+s.m.
 400269; ; Hs.253495; Eos Control; fibro; diag
 400285; ; Eos Control; lung; diag
 400287; S39329; Hs.181350; kallikrein 2; prostatic; pros; diag
 400288; X06256; Hs.149609; Integrin, alpha 5 (fibronectin; panc, pros, angio, blad, lung; mAb+s.m.
 400290; H18839; Hs.31608; hypothetical protein FLJ20041; pros, colon, EWS; mAb
 400294; N95796; Hs.278695; Homo sapiens protein mRNA; co; pros; pros; mAb
 400295; W72838; Hs.348419; AI905687; IL-8T095-190199-019 B; breast; diag
 400298; AA032279; Hs.61635; six transmembrane epithelial a; panc, lung, headnk, stom, EWS, ovar; mAb+CTL
 400328; X87344; ; transporter 2, ATP-binding cas; lung; mAb+s.m.
 400409; AF153341; ; Homo sapiens winged helix/ork; blad; CTL+s.m.
 400419; AF084545; ; Target; lung, sarc; diag
 400440; X83957; Hs.83870; nebulin; sarc; diag
 400494; ; ENSP00000238970; CIG30 (Fragme; angio; mAb
 400517; ; lensin; stom, cerv, uter, lung, pros, colon, hepC; diag
 400651; ; ENSP00000228031; COPPER CHAPER; sarc; s.m.
 400665; ; NM_002425; Homo sapiens matrix; lung; mAb+diag+s.m.
 400773; ; NM_003105; Homo sapiens sorf; blad; mAb
 400844; ; NM_003105; Homo sapiens sorf; blad; s.m.
 400846; ; sorf-related receptor, L(D; blad; mAb+s.m.
 400881; ; NM_025080; Homo sapiens hypothe; ovar; diag
 401093; ; C12000586:glj6330167[db]BAA8; blad, lung; CTL+s.m.
 401234; ; mitogen-activated protein kin; angio; diag
 401424; ; NM_001172; Homo sapiens arginas; pros; s.m.
 401486; ; C4000647:glj475850[ret]NP_00; headnk; mAb
 401704; ; NM_021195; Homo sapiens claud; test; mAb
 401732; ; NM_001176; Homo sapiens Rho G; panc; diag
 401747; ; Homo sapiens keratin 17 (KRT17; blad, lung, headnk, melar; diag

- 401760; ; Target Exon; blad, lung, headnk, esoph; diag
 401780; ; NM_005557*Homo sapiens kerat; lung, blad, headnk, esoph, mela; diag
 401781; ; Target Exon; lung, blad, headnk, esoph, cerv; diag
 401785; ; NM_002275*Homo sapiens kerat; lung; diag
 5 401797; ; Target Exon; sarc; diag
 401994; ; Target Exon; lung; diag
 402145; ; Target Exon; test; CTL+s.m.
 402199; ; Target Exon; test; CTL+s.m.
 10 402230; ; Fgenesh predicted: CYTOCHROME ; blad; diag
 402239; ; Target Exon; blad; diag
 402260; ; NM_001436*Homo sapiens fibril; blad; CTL+s.m.
 402265; ; Target Exon; lung; diag
 402305; ; C19000735*gi15408027[ref]NP_0; blad; CTL+s.m.
 15 402420; ; C1000823*gi10432400[emb]CAC1; lung; diag
 402424; ; NM_024901*Homo sapiens hypothe; blad; CTL+s.m.
 402447; ; C1000201*gi204416[gb]AAA02627; esoph; mAb
 402474; ; NM_004079*Homo sapiens catheps; lung, colon, stom, fibro; diag
 402550; ; Target Exon; fibro; diag
 402604; ; Target Exon; glio; diag
 20 402605; ; Target Exon; glio; diag
 402606; ; NM_024626*Homo sapiens hypothe; ovar, breast; mAb
 402680; ; Target Exon; test; mAb
 402777; ; C1002652*gi1544327[sp]Q04799; blad; diag
 25 402860; ; ENSP00000239210.DJ50024.4 (nov; mela; CTL+s.m.
 402888; ; Target Exon; sarc; diag
 402992; ; Target Exon; sarc; diag
 402994; ; NM_002463*Homo sapiens myxovi; esoph; diag
 403046; ; NM_005656*Homo sapiens transm; pros; mAb
 30 403047; ; NM_005656*Homo sapiens transm; pros, blad, colon; mAb
 403071; ; NM_003319*Homo sapiens tfin ; sarc; diag
 403088; ; NM_003319*Homo sapiens tfin ; sarc; diag
 403171; ; C2001472*gi15809678[gb]AAB418; test; diag
 403328; ; Target Exon; mela; diag
 35 403329; ; unnamed protein product [Homo ; lung; diag
 403381; ; ENSP00000231844*Ecotropic vir; blad; CTL+s.m.
 403409; ; NM_005929*Homo sapiens antigen; mela; mAb
 403433; ; NM_001622*Homo sapiens alpha-2; hepC; diag
 403478; ; NM_022342*Homo sapiens kinesin; lung; CTL+s.m.
 40 403715; ; Target Exon; lung; diag
 403740; ; NM_001076*Homo sapiens UDP gt; pros, hepC; s.m.
 403776; ; ENSP00000226542*Small inducib; panc; diag
 403903; ; C5001632*gi10645308[gb]AAG21; blad; CTL+s.m.
 404023; ; NM_018938*Homo sapiens protoc; glio; mAb
 404049; ; NM_018937*Homo sapiens protoc; glio; mAb
 45 404210; ; NM_005938*Homo sapiens myeloid; panc, uter, cerv, lung, ovar, pros, colon, stom; diag
 404240; ; NM_018950*Homo sapiens major h; fibro; mAb
 404253; ; NM_021058*Homo sapiens H2B h; lung; CTL+s.m.
 404286; ; C6001909*gi704441[db]BAA1890; panc; diag
 404298; ; C6001238*gi121715[sp]P26697; lung; s.m.
 50 404403; ; Target Exon; blad; diag
 404440; ; NM_021048*Homo sapiens melanom; lung, blad; mAb+CTL
 404866; ; ENSP00000251112*Sodium/potass; panc; s.m.
 404877; ; NM_005365*Homo sapiens melanom; lung, blad; CTL+s.m.
 55 404927; ; Target Exon; lung, headnk; diag
 404996; ; Target Exon; lung, headnk, esoph; diag
 405001; ; interleukin enhancer binding f; sarc; diag
 405025; ; Homo sapiens bone morphogenetic; angio; diag
 405121; ; mitogen-activated protein kin; angio, renat; s.m.
 60 405238; ; Target Exon; glio; diag
 405239; ; oxidative 3 alpha hydroxyster; glio; s.m.
 405451; ; Homo sapiens glutamyl-peptid; mela; s.m.
 405545; ; Target Exon; cerv; mAb
 405546; ; NM_018833*Homo sapiens transp; cerv; mAb
 65 405547; ; NM_018833*Homo sapiens transp; cerv, mela; mAb
 405646; ; C12000200*gi14557225[ref]NP_00; lung; diag
 405704; ; NM_001844*Homo sapiens collag; sarc; diag
 405770; ; NM_002362*Homo sapiens melanom; lung, esoph; mAb+CTL
 405849; ; Target Exon; panc; diag
 70 405932; ; C15000305*gi3806122[gb]AAC691; blad, lung, headnk, cerv; CTL+s.m.
 406081; ; Target Exon; blad; diag
 406137; ; NM_000179*Homo sapiens mufS (; lung; CTL+s.m.
 406173; ; ENSP00000250148*Growth hormo; panc; CTL+s.m.
 406348; ; Target Exon; breast; CTL+s.m.
 75 406360; ; Target Exon; lung, headnk; diag
 406399; ; NM_003122*Homo sapiens serine; blad; diag
 406434; ; NM_030579*Homo sapiens cytoch; blad; diag
 406467; ; Target Exon; lung, headnk, blad; diag
 406506; ; Target Exon; angio; diag
 80 406547; ; Target Exon; test; diag
 406627; T64904; Hs.163780; ESTs; angio; CTL+s.m.
 406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte; panc; mAb
 406672; M26041; Hs.198253; major histocompatibility comp; fibro; mAb
 406685; M18728; gbtHuman nonspecific crossreac; panc, colon, blad, headnk, stom, lung; mAb+CTL

- 406587; M31126; Hs.352054; matrix metalloproteinase 11 (s; breast, lung, ovar, cerv, uter, panc, esoph, mela, sarc; mAb+diag+s.m.
- 406590; M29540; Hs.220529; carcinoembryonic antigen-relat; lung, headnk, panc, stom, blad, colon, cerv; mAb+CTL
- 406706; X03740; Hs.231581; myosin, heavy polypeptide 1, s; sarc; diag
- 406850; A1624300; Hs.172928; collagen, type I, alpha 1; sarc; CTL+s.m.
- 5 406906; Z25424; ; gb:Human protein-serine/thr; blad, lung; s.m.
- 406937; U14622; ; gb:Human transketolase-like pr; test; s.m.
- 406967; M24349; ; gb:Human parathyroid hormone-r; lung; CTL+s.m.
- 406974; M57293; ; gb:Human parathyroid hormone-r; lung, blad; diag
- 10 407013; U35637; Hs.83870; gb:Human nebulin mRNA, partial; sarc; diag
- 407034; U84540; ; gb:Human dystrobrevin isoform ; glio; diag
- 407103; AA424881; Hs.256301; hypothetical protein MGC13170; pros; diag
- 407118; AA156790; Hs.262036; ESTs, Weakly similar to ZZZ3_h; pros; diag
- 407122; H20276; Hs.31742; ESTs; pros; diag
- 15 407137; T97307; ; gb:ye53h05.s1 Soares fetal liv; lung, blad, ovar, pros, panc, headnk; diag
- 407168; R45175; Hs.117183; ESTs; pros, breast, colon; diag
- 407178; AA195651; Hs.352312; AP-2 beta transcription factor; breast ; CTL+s.m.
- 407202; N58172; Hs.109370; ESTs; pros; diag
- 407216; N91773; Hs.348385; lysyl oxidase; panc; diag
- 20 407242; M18728; ; gb:Human nonspecific crossreac; panc, colon, blad, headnk, stom, lung, ovar, cerv; mAb
- 407244; M10014; ; fibrinogen, gamma polypeptide; lung; diag
- 407245; X90568; Hs.172004; tlin; sarc; diag
- 407251; U67611; Mm.29182; transaldolase 1; pros; s.m.
- 407252; AA659037; Hs.163780; ESTs; angio; CTL+s.m.
- 25 407276; A1951118; Hs.326736; Homo sapiens breast cancer ant; breast; mAb+CTL
- 407289; AA135159; Hs.203349; Homo sapiens cDNA FLJ12149 fis; lung; diag
- 407356; AF026942; Hs.17518; gb:Homo sapiens cig33 mRNA, pa; ovar, hepC, stom, mela, esoph; diag
- 407581; R48402; Hs.173508; P3ECSL; blad; CTL+s.m.
- 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gat; blad; mAb
- 30 407619; AL050341; Hs.37165; collagen, type IX, alpha 2; sarc; diag
- 407634; AW016559; Hs.136414; UDP-GlcNAc:betaGal beta-1,3-N-; lung, headnk; s.m.
- 407710; AW022727; Hs.23616; ESTs; test; diag
- 407720; AB037776; Hs.38002; KIAA1355 protein; lung; mAb
- 407746; AK001962; Hs.38114; hypothetical protein FLJ11100; lung; diag
- 35 407756; AA116021; Hs.38260; ubiquitin specific protease 18; panc, lung, esoph, fibro, mela; CTL+s.m.
- 407758; D50915; Hs.38365; KIAA0125 gene product; lung; diag
- 407777; AA161071; Hs.71465; squalene epoxidase; panc, esoph; s.m.
- 407782; AA608958; Hs.112619; ESTs, Moderately similar to PU; lung; diag
- 407786; AA687538; Hs.38972; tetraspan 1; pros, colon, uter, stom, ovar, cerv; mAb
- 40 407788; BE514982; Hs.38991; S100 calcium-binding protein A; headnk, panc, blad, lung, fibro; diag
- 407818; AL021938; Hs.40154; jumonji (mouse) homolog; test; CTL+s.m.
- 407824; AA147884; Hs.9812; Homo sapiens cDNA FLJ14388 fis; sarc; diag
- 407839; AA045144; Hs.161566; ESTs; blad, headnk; mAb
- 407846; AA426202; Hs.40403; Cbp/p300-interacting transacti; mela; diag
- 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homo; colon; stom, renal, breast, ovar, uter, cerv; diag
- 45 407856; AA045281; Hs.266175; phosphoprotein associated with; mela; diag
- 407872; AB039723; Hs.40735; frizzled (Drosophila) homolog ; ovar; mAb
- 407881; AW072003; Hs.40968; heparan sulfate (glucosamine) ; panc; s.m.
- 407910; AA650274; Hs.41296; fibronectin leucine rich trans; fibro; mAb
- 407944; R34008; Hs.239727; desmocollin 2; lung, headnk, esoph; mAb
- 50 407949; W21874; Hs.247057; ESTs, Weakly similar to 210926; fibro, blad; diag
- 407962; A1133530; Hs.62930; ESTs, Weakly similar to S59501; angio; mAb+s.m.
- 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (; breast, pros, blad, lung, headnk, cerv, esoph; mAb+CTL
- 408015; AW136771; Hs.244349; epidermal differentiation comp; mela, sarc; diag
- 408045; AW138959; Hs.245123; ESTs; breast ; diag
- 55 408056; AA312329; Hs.42331; ephrin-A4; ovar; diag
- 408063; BE086548; Hs.381047; calcineurin-binding protein ca; pros, lung; diag
- 408081; AW451597; Hs.167409; Intron of basic-helix-loop-hel; ovar, glio; diag
- 408101; AW968504; Hs.278346; CDC2-related protein kinase 7; breast, lung, stom; s.m.
- 408122; A1432652; Hs.42824; hypothetical protein FLJ10718; lung; diag
- 60 408209; NM_004454; Hs.43697; ets variant gene 5 (ets-relate; mela; CTL+s.m.
- 408296; AL117452; Hs.44155; DKFZP586G1517 protein; angio; diag
- 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D; panc, renal, colon; mAb
- 408353; BE439838; Hs.44298; mitochondrial ribosomal protei; lung; diag
- 408430; S79876; Hs.44926; dipeptidylpeptidase IV (CD26, ; pros; mAb
- 65 408522; AJ541214; Hs.46320; Small proline-rich protein SPR; lung, blad, headnk, eosph, cerv; diag
- 408561; A1308037; Hs.84120; hypothetical protein MGC13016; mela; CTL+s.m.
- 408570; AL048406; Hs.103483; KIAA1798 protein; angio; CTL+s.m.
- 408572; AA055611; Hs.226568; ESTs, Moderately similar to AL; lung; diag
- 70 408591; AF015224; Hs.46452; mammaglobin 1; breast, cerv; diag
- 408611; NM_004367; Hs.46468; chemokine (C-C motif) receptor; mela; mAb
- 408633; AW963372; Hs.222088; PRO2000 protein; blad, lung, headnk, pros; diag
- 408660; AA525775; Hs.89040; ESTs, Moderately similar to PC; ovar, panc, pros, esoph, sarc; diag
- 408728; AL137379; Hs.47125; hypothetical protein FLJ13912; test; diag
- 408758; NM_003686; Hs.47504; exonuclease 1; mela; CTL+s.m.
- 75 408770; AW270608; Hs.170195; bone morphogenetic protein 7 (; ovar; mAb+diag
- 408771; AW732573; Hs.47584; potassium voltage-gated channel; lung; mAb
- 408780; D31797; Hs.652; tumor necrosis factor (ligand); leuk; diag
- 408795; AW749126; Hs.170345; hypothetical protein FLJ13710; ovar; diag
- 408826; AF216077; Hs.48376; Homo sapiens clone HB-2 mRNA s; panc, pros; diag
- 80 408833; AW612232; Hs.254835; ESTs; pros; diag
- 408877; AA479033; Hs.130315; ESTs, Weakly similar to A47582; breast; diag
- 408915; NM_016651; Hs.48950; hepatocellular carcinoma novel ; panc, sarc; diag
- 408930; AA146721; Hs.334686; hypothetical protein FLJ21588; blad; CTL+s.m.

- 408952; BE386436; Hs.44317; SRY (sex determining region Y); mela; diag
 408992; AA059325; Hs.30114; guanine nucleotide binding pro; lung; diag
 408998; AJ979168; Hs.82226; glycoprotein (transmembrane) n; mela; mAb+s.m.
 409012; AL117435; Hs.49725; DKFZP434I216 protein; sarc; CTL+s.m.
 409038; T97490; Hs.50002; small inducible cytokine subfa; mela; diag
 409051; AA080912; ; gbzn04d03.r1 Stratagene hNT n; pros; s.m.
 409077; AA063037; Hs.66803; ESTs; lung; diag
 409093; BE243834; Hs.50441; CGI-04 protein; lung; diag
 409123; AA063403; ; gbzn04d12.s1 Stratagene come; pros; s.m.
 409142; AL136877; Hs.50758; SMC4 (structural maintenance o; ovar, lung, mela; diag
 409153; W03754; Hs.50813; hypothetical protein FLJ20022; fibro; diag
 409200; AL042914; Hs.51039; KIAA0076 gene product; sarc; CTL+s.m.
 409203; AA780473; Hs.687; cytochrome P450, subfamily IVB; fibro, blad, ovar; diag
 409228; R16811; Hs.22010; ESTs, Weakly similar to 210926; lung; mAb
 409231; AA446644; Hs.692; GA733-2 antigen; epithelial gt; pros, ovar, breast, uter, panc, colon, stom; mAb
 409243; AB037761; Hs.51743; KIAA1340 protein; test; diag
 409262; AK000631; Hs.52256; hypothetical protein FLJ20624; pros; CTL+s.m.
 409264; NM_014937; Hs.52453; KIAA0966 protein; mela; CTL+s.m.
 409269; AA576953; Hs.22972; steroid 5 alpha-reductase 2-4; breast, ovar, lung, panc, uter; mAb
 409327; L11162; Hs.53563; collagen, type IX, alpha 3; colon, panc, sarc; CTL+s.m.
 409340; BE174629; Hs.32130; hypothetical protein MGC2771; mela; CTL+s.m.
 409342; AU077058; Hs.54089; BRCA1 associated RING domain 1; test; CTL+s.m.
 409348; AL401535; Hs.146090; ESTs; renal, glo; diag
 409361; NM_005982; Hs.54416; sine oculis homeobox (Drosophi; blad, lung, pros; CTL+s.m.
 409389; AB007979; Hs.301281; Homo sapiens mRNA, chromosome ; glo; diag
 409395; U46745; Hs.336678; dystrobrevin, alpha; glo; diag
 409402; AF208234; Hs.695; cystatin B (steifin B); blad; diag
 409415; AA579258; Hs.6083; Homo sapiens cDNA: FLJ21028 f; mela; diag
 409421; AA199883; Hs.67624; ESTs; test; diag
 409430; R21945; Hs.346735; splicing factor, arginine/seri; mela; diag
 409432; D49372; Hs.54460; small inducible cytokine subfa; stom, esoph; diag
 409433; AA074382; Hs.135255; ESTs; glo, sarc; diag
 409509; AL036923; Hs.322710; ESTs; angio; diag
 409512; AW979187; Hs.293591; melanoma differentiation assoc; mela, esoph; CTL+s.m.
 409542; AA503020; Hs.36563; hypothetical protein FLJ22418; breast, ovar; diag
 409582; R27430; Hs.271565; ESTs; lung; diag
 409601; AF237621; Hs.80828; keratin 1 (epidermolytic hyper; headnk, mela, sarc; CTL+s.m.
 409633; AW449822; Hs.55200; ESTs; sarc; diag
 409637; AA323948; Hs.55407; Homo sapiens mRNA; cDNA DKFZp4; renal; diag
 409638; AW450420; Hs.21335; ESTs; glo; diag
 409670; AJ368109; Hs.381163; KIAA1856 protein; test; CTL+s.m.
 409703; NM_006187; Hs.56009; 2'-5'-oligoadenylate synthetas; panc, esoph, mela; s.m.
 409705; M37762; Hs.56023; brain-derived neurotrophic fac; lung; diag
 409719; AJ769160; Hs.108681; Homo sapiens brain tumor assoc; lung; diag
 409731; AA125985; Hs.56145; thymosin, beta, identified in ; pros, sarc; CTL+s.m.
 409745; AA077391; ; gb7B14E12 Chromosome 7 Fetal ; ovar, renal; CTL+s.m.
 409935; AW511413; Hs.187393; ESTs; lung; diag
 409958; NM_001523; Hs.57697; hyaluronan synthase 1; panc, ovar; mAb
 409988; N27687; Hs.334334; transcription factor AP-2 alph; mela; diag
 410008; AW732308; Hs.57783; eukaryotic translation initiat; test; diag
 410037; AB020725; Hs.58009; KIAA0918 protein; pros; diag
 410044; BE566742; Hs.58165; highly expressed in cancer, rt; blad; diag
 410048; W76467; Hs.343874; proline oxidase homolog; test s.m.
 410076; T05387; Hs.7991; ESTs; lung, pros; diag
 410079; U94362; Hs.380757; glycogenin 2; mela; diag
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; pros; diag
 410102; AW248508; Hs.279727; ESTs; homologue of PEM-3 (Cion; ovar, breast, blad, lung, angio, sarc; diag
 410174; AA306007; Hs.59461; DKFZP434C245 protein; mela; diag
 410240; AL157424; Hs.61289; synaptotagmin 2; angio; diag
 410247; AF181721; Hs.61345; RU2S; ovar; CTL+s.m.
 410268; AA316181; Hs.61635; six transmembrane epithelial a; panc, pros, EWS; mAb+CTL
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A; mela; diag
 410310; J02931; Hs.62192; coagulation factor III (thromb; pros, panc; mAb
 410361; BE391804; Hs.62661; guanylate binding protein 1, I; mela, esoph, hepC, fibro, uter; diag
 410438; AW748012; Hs.45207; hypothetical protein KIAA1335; lung; CTL+s.m.
 410467; AF102546; Hs.63931; dachshund (Drosophila) homolog; breast, colon, uter, stom; diag
 410480; R97457; Hs.63984; cadherin 13, H-cadherin (heart; angio; mAb
 410491; AA465131; Hs.64001; Homo sapiens clone 25218 mRNA ; mela, esoph; diag
 410530; M25809; Hs.64173; ATPase, H transporting, lysoso; ovar; mAb
 410553; AW016824; Hs.272068; hypothetical protein MGC14128; blad, lung; diag
 410555; U92649; Hs.380136; a disintegrin and metalloprote; leuk, lung; mAb
 410561; BE540255; Hs.6994; Homo sapiens cDNA: FLJ22044 f; lung; diag
 410566; AA373210; Hs.43047; Homo sapiens cDNA FLJ13585 f; panc; diag
 410600; AW575742; Hs.351676; ESTs, Moderately similar to S6; mela; mAb+s.m.
 410621; AA194329; Hs.172004; filin; sarc; diag
 410681; AW246890; Hs.65425; calbindin 1, (28kD); lung; diag
 410687; U24389; Hs.65436; lysyl oxidase-like 1; panc; diag
 410733; D84284; Hs.66052; CD38 antigen (p45); pros; mAb+CTL
 410763; AF279145; Hs.8966; hypothetical protein FLJ21776; panc; mAb
 410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; test; CTL+s.m.
 410867; X63556; Hs.750; fibrillin 1 (Marfan syndrome); panc; diag
 410870; U81599; Hs.66731; homeo box B13; pros; CTL+s.m.
 410883; D43767; Hs.66742; CCL17 chemokine (TARC) (SCYA1; leuk; diag

- 410889; X91662; Hs.66744; twist (Drosophila) homolog (ac; sarc; CTL+s.m.
 410929; H47233; Hs.30643; ESTs; ovar; test; diag
 411078; AJ222020; Hs.182364; CoccoaCrisp; pros; glio; breast; diag
 411089; AA456454; Hs.214291; cell division cycle 2-like 1 l; lung; fibro; CTL+s.m.
 411243; AB039886; Hs.69319; CA11; esoph; diag
 411248; AA551538; Hs.69321; Homo sapiens cDNA FLJ14408 fis; blad; diag
 411257; AA628967; Hs.115274; Indian hedgehog protein (IhH); ovar; diag
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centro; lung; blad; headnk; CTL+s.m.
 411296; BE207307; Hs.10114; growth suppressor 1; sarc; diag
 411358; R47479; Hs.94761; KIAA1691 protein; mela; renal; sarc; mAb
 411388; X72925; Hs.69752; desmocollin 1; headnk; mela; mAb
 411393; AW797437; Hs.69771; B-factor, properdin (COMPLEMEN; ovar; diag
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA); panc; pros; stom; breast; uter; cerv; ovar; mAb
 411573; AB029000; Hs.70823; KIAA1077 protein; panc; headnk; lung; stom; diag
 411579; AC005258; Hs.70830; U6 snRNA-associated Sm-like pr; lung; diag
 411732; U47924; Hs.71642; guanine nucleotide binding pro; lung; diag
 411768; NM_013371; Hs.71979; interleukin 19; ovar; uter; cerv; diag
 411789; AF245505; Hs.72157; Adfican; breast; panc; lung; stom; headnk; ovar; uter; esoph; sarc; diag
 411825; AK000334; Hs.352415; solute carrier family 39 (zinc; colon; ovar; mAb
 411828; AW161449; Hs.72290; wingless-type MMTV integration; ovar; diag
 411869; W20027; Hs.23439; ESTs; angio; diag
 411874; AA096106; Hs.20403; ESTs; blad; diag
 411880; AW872477; ; gbchm30f03.x1 NCL CGAP_Thy4 Ho; blad; diag
 411945; AL033527; Hs.92137; L-myc-2 protein (MYCL2); blad; ovar; CTL+s.m.
 412006; AW451618; Hs.380683; ESTs; sarc; diag
 412026; AA383618; Hs.73073; testis-specific ankyrin motif; test; diag
 412045; AA099802; Hs.83883; transmembrana, prostate androg; pros; mAb+s.m.
 412099; U64198; Hs.73165; interleukin 12 receptor, beta; leuk; mela; mAb
 412104; AW205197; Hs.240951; Homo sapiens, Similar to RIKEN; panc; fibro; diag
 412115; AK001763; Hs.73239; hypothetical protein FLJ10901; lung; blad; CTL+s.m.
 412116; AW402166; Hs.784; Epstein-Barr virus induced gen; panc; mAb
 412133; U83460; Hs.380728; solute carrier family 31 (copp; pros; mAb
 412228; AW503785; Hs.73792; complement component (3d/Epste; mela; mAb
 412247; AF022375; Hs.73793; vascular endothelial growth fa; renal; glio; blad; colon; diag
 412265; AA101325; Hs.86154; hypothetical protein FLJ12457; test; CTL+s.m.
 412326; R07566; Hs.73817; small inducible cytokine A3 (h; pros; leuk; diag
 412351; AL135960; Hs.73828; T-cell acute lymphocytic leuke; angio; CTL+s.m.
 412420; AL035668; Hs.73853; bone morphogenetic protein 2; blad; glio; lung; stom; angio; diag
 412448; L12964; Hs.73895; tumor necrosis factor receptor; leuk; mAb
 412471; M63193; Hs.73946; endothelial cell growth factor; cerv; mela; esoph; diag
 412490; AW803564; Hs.288850; Homo sapiens cDNA: FLJ2528 fi; mela; diag
 412519; AA196241; Hs.73980; troponin T1, skeletal, slow; sarc; diag
 412530; AA766268; Hs.266273; hypothetical protein FLJ13345; blad; lung; diag
 412564; X83703; Hs.355934; cardiac ankyrin repeat protein; angio; diag
 412580; AA113262; Hs.17901; similar to CABLES [Homo saplen; mela; diag
 412610; X90908; Hs.74126; fatty acid binding protein 6; ; blad; diag
 412661; N32860; Hs.24611; ESTs, Weakly similar to I54374; blad; CTL+s.m.
 412715; NM_000947; Hs.74519; primase, polypeptide 2A (58kD); pros; s.m.
 412723; AA648459; Hs.335951; hypothetical protein AF301222; lung; blad; headnk; colon; stom; uter; diag
 412755; BE144306; Hs.179891; ESTs, Weakly similar to P4HA_H; angio; s.m.
 412811; H06382; Hs.349705; ESTs; lung; diag
 412817; AL037159; Hs.74619; proteasome (prosome, macropain; lung; s.m.
 412843; AF007555; Hs.74624; protein tyrosine phosphatase; ; pros; mAb
 412856; BE386745; Hs.74631; basigin (OK blood group); mela; mAb
 412926; A1879076; Hs.75061; macrophage myristoylated atan; mela; CTL+s.m.
 412939; AW411491; Hs.75069; eukaryotic translation elongat; mela; renal; diag
 412970; AB026436; Hs.177534; dual specificity phosphatase 1; breast; mela; s.m.
 412986; X81120; Hs.75110; cannabinoid receptor 1 (brain); glio; mAb
 413004; T35901; Hs.75117; interleukin enhancer binding f; lung; diag
 413011; AW068115; Hs.821; biglycan; lung; CTL+s.m.
 413049; NM_002151; Hs.823; hepsin (transmembrane protease; pros; mAb
 413095; AA494359; Hs.30715; potassium voltage-gated channel; panc; stom; renal; colon; mAb+s.m.
 413125; BE244589; Hs.75207; glyoxalase I; pros; s.m.
 413126; AW419203; Hs.174174; ESTs; angio; diag
 413129; AF292100; Hs.104613; RP42 homolog; lung; diag
 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent; angio; CTL+s.m.
 413142; M81740; Hs.75212; ornithine decarboxylase 1; lung; s.m.
 413163; Y00815; Hs.75216; protein tyrosine phosphatase; ; pros; mAb
 413171; AA318325; Hs.75219; tyrosinase-related protein 1; mela; mAb
 413190; AA151802; Hs.40358; adaptor-related protein comple; mela; diag
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis; esoph; cerv; diag
 413223; A1732182; Hs.191866; ESTs; lung; diag
 413268; AL039079; Hs.75256; regulator of G-protein signal; headnk; CTL+s.m.
 413281; AA861271; Hs.222024; transcription factor BMAL2; lung; blad; headnk; panc; angio; diag
 413313; NM_002047; Hs.293885; glycyl-tRNA synthetase; test; s.m.
 413328; Y15723; Hs.75295; guanylate cyclase 1, soluble; ; pros; s.m.
 413335; A1613318; Hs.48442; ESTs; ovar; diag
 413364; BE536218; Hs.137516; fiddelin-like 1; lung; diag
 413372; H55532; Hs.349695; tubulin, alpha 2; test; diag
 413435; X51405; Hs.75360; carboxypeptidase E; pros; glio; panc; sarc; diag
 413436; AF238083; Hs.68061; sphingosine kinase 1; sarc; s.m.
 413472; BE242870; Hs.75379; solute carrier family 1 (glut; glio; mAb
 413566; AW604451; Hs.381153; sprouty (Drosophila) homolog 4; sarc; CTL+s.m.

- 413573; A1733859; Hs.149089; ESTs; lung; diag
 413582; AW295647; Hs.71331; hypothetical protein MGC5350; lung; diag
 413597; AW302885; Hs.117183; ESTs; pros; diag
 413623; AA825721; Hs.246973; Intron of Bicaudal D homolog 1; ovar, pros; diag
 413691; AB023173; Hs.75478; ATPase, Class VI, type 11B; lung; mAb
 413711; AW291765; Hs.75486; heat shock transcription factor; renal; diag
 413753; U17760; Hs.75517; laminin, beta 3 (nicein (125kD); lung, blad, headnk, panc, cerv, esoph, colon; diag
 413762; AW411479; Hs.848; FK506-binding protein 4 (59kD); test; diag
 413778; AA090235; Hs.75535; myosin, light polypeptide 2, r; sarc; diag
 413794; AF234532; Hs.61638; myosin X; melar; diag
 413804; T64682; ; gb:yc48b02.r1 Stratagene liver; blad; diag
 413808; J00287; Hs.350038; Homo sapiens mRNA for caldesmo; esoph; diag
 413813; M96958; Hs.75561; teratocarcinoma-derived growth; colon; diag
 413833; Z15005; Hs.75573; centromere protein E (312kD); lung; CTL+s.m.
 413842; M29383; Hs.856; interferon, gamma; leuk; diag
 413869; NM_000876; Hs.75598; interleukin 2 receptor, beta; fibro, renal; mAb
 413880; A1660842; Hs.110915; Interleukin 22 receptor; panc, colon; mAb+s.m.
 413924; AL119564; Hs.75616; seladin-1; pros, breast, ovar; diag
 413943; AW294416; Hs.144687; Homo sapiens cDNA FLJ12981 fis; blad, lung; CTL+s.m.
 413985; A1018666; Hs.75667; synaptophysin; glio, sarc; mAb
 414004; AA737033; Hs.7155; ESTs, Moderately similar to 21; panc, melar; diag
 414020; NM_002984; Hs.75703; CCL4 Chemokine (C-C motif) lig; pros; diag
 414034; U89277; Hs.305985; early development regulator 1; test; CTL+s.m.
 414035; Y00630; Hs.75716; serine (or cysteine) proteinase; lung, cerv, headnk, blad; s.m.
 414053; BE391635; Hs.75725; transgelin 2; blad; diag
 414061; NM_000699; Hs.300280; amylase, alpha 2A; pancreatic; ovar; diag
 414065; AW515373; Hs.271249; Homo sapiens cDNA FLJ13580 fis; pros; diag
 414085; AA114016; Hs.75746; aldehyde dehydrogenase 1 family; pros, panc, sarc; s.m.
 414142; AW368397; Hs.334485; hemiscentin (fibulin 6); fibro, panc, sarc; diag
 414161; AA136106; Hs.184852; KIAA1553 protein; test; diag
 414166; AW888941; Hs.75789; N-myc downstream regulated; pros, renal; diag
 414217; A1309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fi; glio; diag
 414219; W20010; Hs.75823; ALL1-fused gene from chromosome; sarc; diag
 414221; AW450979; ; gb:U1-H-B13-ala-a-12-D-U1.s1 N; blad; diag
 414251; AL042306; Hs.97689; VASA protein; test; CTL+s.m.
 414259; W44633; Hs.301296; Integrin, beta-like 1 (with EG; panc; diag
 414334; AA824298; Hs.21331; hypothetical protein FLJ10036; test; diag
 414359; M62194; Hs.75929; cadherin 11, type 2, OB-cadher; breast, ovar, uter, pros, colon, panc, sarc; mAb
 414368; W70171; Hs.75939; uridine monophosphate kinase; lung; s.m.
 414386; X00442; Hs.75990; haploglobin; ovar; diag
 414416; AW409985; Hs.76084; hypothetical protein MGC2721; blad, lung; CTL+s.m.
 414420; AA043424; Hs.76095; immediate early response 3; panc, colon; diag
 414430; A1346201; Hs.76118; ubiquitin carboxyl-terminal ex; lung; s.m.
 414443; AU077268; Hs.76144; platelet-derived growth factor; sarc, panc, headnk; mAb
 414476; AA301867; Hs.76224; EGF-containing fibulin-like ex; angio; diag
 414477; U41635; Hs.76228; amplified in osteosarcoma; sarc; diag
 414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antig; melar; mAb
 414521; D28124; Hs.76307; neuroblastoma, suppression of; breast, ovar, uter, pros, blad, panc, colon, stom, fibr; diag
 414565; AA502972; Hs.183390; hypothetical protein FLJ13590; pros; diag
 414569; AF109298; Hs.118258; prostate cancer associated pro; pros, EWS; diag
 414575; H11257; Hs.375743; Homo sapiens clone IMAGE:45183; renal; diag
 414595; AA641726; Hs.289015; hypothetical protein MGC4171; blad; diag
 414602; AW630088; Hs.76550; Homo sapiens mRNA; cDNA DKFZp5; pros; mAb
 414683; S78296; Hs.76888; hypothetical protein MGC12702; blad, lung, test; diag
 414732; AW410976; Hs.77152; minichromosome maintenance def; test, blad; diag
 414761; AU077228; Hs.77256; enhancer of zeste (Drosophila); lung, blad, test; CTL+s.m.
 414776; AA155598; Hs.212839; hypothetical protein FLJ14195; angio; diag
 414786; A1246482; Hs.243010; Homo sapiens cDNA FLJ14372 fis; angio; diag
 414799; A1752416; Hs.77326; insulin-like growth factor bin; renal; diag
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; lung; mAb
 414807; A1738616; Hs.77348; hydroxyprostaglandin dehydroge; blad; s.m.
 414809; A1434699; Hs.77356; transferrin receptor (p90, CD7; lung; mAb+s.m.
 414825; X06370; Hs.77432; epidermal growth factor recept; glio, lung, renal, esoph, panc, headnk, leuk; mAb+s.m.
 414915; NM_002462; Hs.76391; myxovirus (influenza) resistant; esoph; diag
 414918; A1219207; Hs.72222; hypothetical protein FLJ13459; blad; CTL
 414921; BE390551; Hs.77628; steroidogenic acute regulatory; breast; diag
 414945; BE076358; Hs.77667; lymphocyte antigen 6 complex; ; melar; mAb
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; blad, panc, esoph; diag
 414998; NM_002543; Hs.77729; oxidised low density lipoprote; fibro, ovar, panc, colon; mAb
 415003; M11437; Hs.77741; kininogen; panc; diag
 415025; AW207091; Hs.72307; ESTs; blad; diag
 415091; AL044872; Hs.77910; 3-hydroxy-3-methylglutaryl-CoA; lung, headnk; s.m.
 415178; D80503; Hs.46692; ESTs; blad; diag
 415214; A1445236; Hs.125124; EphB2; colon, stom; mAb
 415314; N88802; Hs.5422; glycoprotein M6B; melar; mAb
 415457; AW081710; Hs.7369; Homo sapiens testes specific A; fibro, ovar, uter; CTL+s.m.
 415511; A1732617; Hs.182362; ESTs; blad, ovar, renal; diag
 415542; R13474; Hs.290263; ESTs, Weakly similar to I38022; blad; diag
 415724; NM_003580; Hs.78687; neutral sphingomyelinase (N-SM; test; CTL+s.m.
 415752; BE314524; Hs.78776; putative transmembrane protein; endo, uter, breast, stom, blad, melar; mAb
 415785; AW419196; Hs.257924; hypothetical protein FLJ13782; breast, pros, blad; diag
 415787; H01463; Hs.93534; ESTs; pros; diag
 415819; AU077330; Hs.360791; transcription elongation factor; test; CTL+s.m.

- 415829; AW450198; Hs.163742; ESTs; test; diag
 415857; AA866115; Hs.127797; Homo sapiens cDNA FLJ11381 f1; lung; test; diag
 415910; U20350; Hs.78913; chemokine (C-X3-C) receptor 1; glio; mAb
 415947; U04045; Hs.78934; mutS (E. coli) homolog 2 (colo); test; diag
 5 415989; AJ267700; Hs.351201; ESTs; pros; ovar; blad; lung; headnk; panc; colon; sarc; diag
 415992; C05837; Hs.145807; hypothetical protein FLJ13593; pros; fibro; mAb
 415999; AA172179; Hs.294029; ESTs; pros; uter; diag
 416018; AW138239; Hs.78977; proprotein convertase subtilisin; colon; panc; lung; diag
 10 416030; H15261; Hs.21948; ESTs; breast; fibro; diag
 416065; BE267931; Hs.78996; proliferating cell nuclear ant; blad; lung; headnk; mela; CTL+s.m.
 416111; AA033813; Hs.79018; chromatin assembly factor 1, s; lung; stom; CTL+s.m.
 416188; BE157260; Hs.79070; v-myc avian myelocytomatosis v; pros; diag
 416201; AA467752; Hs.195161; ESTs; test; diag
 15 416208; AW291168; Hs.41295; ESTs, Weakly similar to MUC2_H; lung; diag
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand cat; ovar; diag
 416225; AA577730; Hs.188684; ESTs, Weakly similar to PC4259; pros; blad; diag
 416350; AF188625; Hs.189507; phospholipase A2, group IID; test; mela; fibro; diag
 416370; N90470; Hs.203697; CD38 antigen (p45); pros; glio; mAb+CTL
 20 416373; AA195845; Hs.73680; ESTs, Weakly similar to S12658; sarc; diag
 416402; NM_000715; Hs.1012; complement component 4-binding; fibro; diag
 416448; L13210; Hs.79339; lectin, galactoside-binding, s; ovar; colon; stom; diag
 416498; U33632; Hs.79351; potassium channel, subfamily K; panc; stom; breast; ovar; colon; mAb
 416539; Y07909; Hs.79368; epithelial membrane protein 1; pros; headnk; diag
 25 416602; NM_006159; Hs.367895; Protein kinase C-binding protei; breast; diag
 416640; BE262476; Hs.13406; neuron-specific protein; mela; diag
 416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; blad; lung; headnk; cerv; panc; angio; diag
 416773; AK000340; Hs.79828; hypothetical protein FLJ20333; test; CTL+s.m.
 416815; U41514; Hs.80120; UDP-N-acetyl-alpha-D-galactosa; angio; s.m.
 30 416819; U77735; Hs.80205; pim-2 oncogene; lung; test; diag
 416881; N32520; Hs.141358; ESTs; mela; diag
 416929; N20535; Hs.43265; melanotin 1; mela; diag
 416975; NM_004131; Hs.1051; granzyme B (granzyme 2, cytol; mela; s.m.
 35 417003; AL038170; Hs.80756; betaine-homocysteine methyltra; blad; s.m.
 417070; Z19077; Hs.172004; tlin; sarc; diag
 417105; X60992; Hs.81226; CD6 antigen; fibro; mAb
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotei; test; CTL+s.m.
 417124; BE122762; Hs.25338; ESTs; angio; diag
 417148; AA359896; Hs.374554; hypothetical protein FLJ14902; panc; diag
 417151; AA194055; Hs.293858; ESTs; blad; diag
 40 417153; X57010; Hs.81343; collagen, type II, alpha 1 (pr; pros; sarc; diag
 417218; AA005247; Hs.285754; met proto-oncogene (hepatocyte; lung; mAb+s.m.
 417237; H86385; Hs.81737; palmitoyl-protein thioesterase; mela; s.m.
 417259; AW903638; Hs.81800; chondroitin sulfate proteoglyc; panc; breast; diag
 417275; X63578; Hs.295449; parvalbumin; blad; diag
 45 417295; AW993524; Hs.43148; epithelial membrane protein 1; pros; diag
 417308; H06720; Hs.81892; KIAA0101 gene product; lung; headnk; blad; cerv; angio; mela; sarc; diag
 417312; AW888411; Hs.250811; leukemia-associated phosphopro; blad; CTL+s.m.
 417333; AL157545; Hs.173179; bromodomain and PHD finger con; breast; diag
 50 417355; D13168; Hs.82002; endothelin receptor type B; glio; mela; mAb
 417365; D50683; Hs.82028; transforming growth factor, bet; fibro; angio; mAb
 417366; BE185289; Hs.1076; small proline-rich protein 1B; lung; blad; headnk; panc; esoph; mela; diag
 417370; T28651; Hs.374466; tryptophanyl-tRNA synthetase; fibro; mela; diag
 417391; AW291946; Hs.82065; interleukin 6 signal transduce; breast; mAb+s.m.
 55 417400; AA663486; Hs.123072; RAB3B, member RAS oncogene fam; pros; diag
 417407; AA923278; Hs.290905; ESTs, Weakly similar to protea; test; pros; s.m.
 417409; BE272508; Hs.82109; syndecan 1; blad; diag
 417412; X16896; Hs.82112; interleukin 1 receptor, type I; fibro; pros; panc; mAb
 417426; NM_002291; Hs.82124; laminin, beta 1; angio; diag
 60 417437; U52682; Hs.82132; interferon regulatory factor 4; mela; CTL+s.m.
 417512; X76534; Hs.82226; glycoprotein (transmembrane) n; lung; mela; headnk; panc; breast; mAb
 417515; L24203; Hs.82237; ataxia-telangiectasia group D; lung; headnk; blad; diag
 417542; J04129; Hs.82269; progestagen-associated endomet; lung; mela; diag
 417592; AA204664; Hs.182437; ESTs, Weakly similar to I54383; test; diag
 65 417599; AA204688; Hs.62954; ESTs; blad; esoph; diag
 417621; AV654694; Hs.82316; interferon-induced, hepatitis; esoph; diag
 417698; BE241624; Hs.82401; CD69 antigen (p60, early T-cell; pros; mAb
 417705; AW134952; Hs.175220; hypothetical protein FLJ14541; test; mAb
 417715; AW969587; Hs.86366; ESTs; blad; lung; headnk; diag
 70 417720; AA205625; Hs.208067; ESTs; blad; lung; esoph; headnk; diag
 417750; AJ267720; Hs.260523; synovial sarcoma, translocated; sarc; diag
 417777; AJ823763; Hs.7055; ESTs, Weakly similar to I78885; test; s.m.
 417791; AW966339; Hs.44269; ESTs; ovar; blad; lung; headnk; CTL+s.m.
 417801; AA417383; Hs.82582; integrin, beta-like 1 (with EG; panc; fibro; diag
 75 417805; U38545; Hs.82587; phospholipase D1, phosphatidyl; angio; s.m.
 417831; H16423; Hs.82685; CD47 antigen (Rb-related antig; ovar; mAb
 417843; W07361; Hs.22545; Homo sapiens cDNA FLJ12935 f1; pros; diag
 417847; A1521558; Hs.7331; hypothetical protein FLJ22316; ovar; diag
 417849; AW291587; Hs.82733; nidogen 2; angio; headnk; diag
 80 417874; BE616160; Hs.82829; protein tyrosine phosphatase; panc; mAb+s.m.
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesio; mela; mAb
 417886; AA214584; ESTs; test; ovar; diag
 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20; lung; stom; test; blad; headnk; cerv; esoph; CTL+s.m.
 417911; AA333387; Hs.82916; chaperonin containing TCP1, su; test; diag

- 417944; AU077196; Hs.82985; collagen, type V, alpha 2; sarc; diag
 417975; AA641836; Hs.30085; hypothetical protein FLJ23186; colon, stom, lung; mAb
 417976; BE565892; Hs.83077; interleukin 18 (interferon-gam; colon, stom, fibros; diag
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 famit; lung, headnk, esoph; s.m.
 418036; Z37976; Hs.83337; latent transforming growth fac; angio; diag
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; lung, angio, test, sarc; diag
 418067; AU127958; Hs.83393; cystatin E/M; headnk, panc, blad; diag
 418068; AW971155; Hs.293902; ESTs, Weakly similar to ISHUS; blad; s.m.
 418113; AU272141; Hs.83484; SRY (sex determining region Y); blad, breast, uter, colon, lung, ovar, glio, test, sarc; CTL+s.m.
 418134; AA397769; Hs.86617; ESTs; test; diag
 418140; BE613836; Hs.83551; microfibrillar-associated prot; lung, headnk, esoph, ovar, sarc; diag
 418156; W17056; Hs.83623; nuclear receptor subfamily 1, ; fibro; mAb+s.m.
 418203; X54942; Hs.83758; CDC28 protein kinase 2; lung, blad, test, mela, stom; s.m.
 418216; AA652240; Hs.283099; AF15q14 protein; headnk, lung, blad; diag
 418245; AA088767; Hs.83883; transmembrane, prostate androg; panc; mAb+s.m.
 418283; S79895; Hs.83942; cathepsin K (pseudodysostosis); breast, cerv, ovar, uter, pros, headnk, lung, panc, colon, stom; diag
 418318; U47732; Hs.84072; transmembrane 4 superfamily me; panc, pros, colon, stom, omuc; mAb
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibi; headnk, lung, blad; s.m.
 418338; NM_002522; Hs.84154; neuronal pentraxin I; sarc; diag
 418339; AA639902; Hs.104215; ESTs, Moderately similar to SF; pros; diag
 418345; AJ001696; Hs.241407; serine (or cysteine) proteinase; cerv, lung; s.m.
 418371; M13560; Hs.84298; CD74 antigen (invariant polype; renal; mAb
 418379; AA218940; Hs.137516; fidgetin-like 1; lung; diag
 418394; AF132818; Hs.84728; Kruppel-like factor 5 (intest; panc; CTL+s.m.
 418396; AJ765805; Hs.26691; SLC2A12 Solute carrier family; pros; mAb
 418397; NM_001269; Hs.84746; chromosome condensation 1; lung; diag
 418399; AF131781; Hs.84753; hypothetical protein FLJ12442; test, blad, sarc; diag
 418406; X73501; Hs.84905; cytokeratin 20; blad, colon; diag
 418432; M14156; Hs.85112; insulin-like growth factor 1 (; pros, fibro; diag
 418460; M26315; Hs.85258; CD8 antigen, alpha polypeptide; fibro; mAb
 418462; BE001596; Hs.85266; integrin, beta 4; lung, blad, cerv, headnk, ovar; mAb
 418543; NM_005329; Hs.85962; hyaluronan synthase 3; blad, lung; mAb
 418576; AW968159; Hs.302740; Epithelial calcium channel 2, ; pros; mAb+s.m.
 418610; AW245993; Hs.32417; hypothetical protein MGC2742; pros; diag
 418641; BE243136; Hs.86947; a disintegrin and metalloprote; cerv, lung, panc, blad, headnk, stom; mAb
 418655; AA226354; Hs.111240; ESTs; pros; diag
 418661; NM_001949; Hs.1189; E2F transcription factor 3; ovar, lung, mela; CTL+s.m.
 418663; AK001100; Hs.41690; desmocollin 3; lung, blad, headnk, cerv, esoph; mAb
 418683; U90908; Hs.87241; hypothetical protein from clon; angio; CTL+s.m.
 418686; Z36830; Hs.87268; annexin A8; blad, lung; diag
 418693; AF150878; Hs.87409; thrombospondin 1; angio, panc; diag
 418698; AW959433; Hs.326290; hypothetical protein FLJ12581; test; diag
 418739; AA310964; Hs.88012; SHP2 Interacting transmembrane; mela; diag
 418756; AA252254; Hs.226949; ESTs; test; diag
 418825; AA228861; Hs.22394; hypothetical protein FLJ10893; angio; diag
 418829; AA516531; Hs.55599; NK homeobox (Drosophila), famit; pros; diag
 418882; NM_004996; Hs.89433; ATP-binding cassette, sub-famit; ovar, pros, breast, lung; diag
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate r; fibro; s.m.
 418888; AU076801; Hs.89436; cadherin 17, LI cadherin (live; colon, stom, ovar, uter, panc; mAb+s.m.
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red b; mela, fibro; mAb
 418932; L34059; Hs.89484; cadherin 4, type 1, R-cadherin; glio; mAb
 418941; AA452970; Hs.239527; E1B-55kDa-associated protein 5; angio, blad; diag
 418968; NM_000078; Hs.89538; cholesteryl ester transfer pro; mela; diag
 418994; AA296520; Hs.89548; selectin E (endothelial adhes; pros, angio; mAb
 419038; AW134924; Hs.88290; ESTs; pros; diag
 419073; AW372170; Hs.183918; transmembrane receptor Unc5H2; ovar, renal, blad, lung; mAb
 419078; M93119; Hs.89584; insulinoma-associated 1; blad, lung, panc, sarc; diag
 419079; AW014836; Hs.18844; ESTs; esoph, lung, stom, colon; diag
 419086; NM_000216; Hs.89591; Kallmann syndrome 1 sequence; fibro; diag
 419092; J05581; Hs.89603; mucin 1, transmembrane; breast, panc, lung, blad, fibro; mAb
 419222; AD001528; Hs.89718; spermine synthase; pros; s.m.
 419223; X60111; Hs.1244; CD9 antigen (p24); breast, pros, ovar; mAb
 419231; AL046294; Hs.136245; ESTs, Weakly similar to T17227; fibro; diag
 419261; X07876; Hs.89791; wingless-type MMTV Integration; panc; diag
 419264; AA877104; Hs.293672; ESTs, Weakly similar to ALUB_H; pros; diag
 419290; AI128114; Hs.112885; spinal cord-derived growth fac; panc; diag
 419356; AI656166; Hs.7331; hypothetical protein FLJ22316; uter, ovar; diag
 419359; AL043202; Hs.90073; chromosome segregation 1 (yeas; lung, blad, test; diag
 419440; AB020689; Hs.90419; KIAA0882 protein; breast; diag
 419485; AA489023; Hs.99807; ESTs, Weakly similar to unname; mela; diag
 419490; NM_006144; Hs.90708; granzyme A (granzyme 1, cytotox; fibro; s.m.
 419519; AI198719; Hs.176376; ESTs; mela; diag
 419551; AW582256; Hs.91011; anterior gradient 2 (Xenopus t; panc, pros, breast; diag
 419559; Y07828; Hs.91096; ring finger protein; blad, colon, stom; CTL+s.m.
 419568; AB026116; Hs.283078; hOAT4; renal; mAb
 419569; AI971651; Hs.91143; jagged 1 (Alagille syndrome); headnk, lung; diag
 419628; H67546; Hs.49768; ESTs; mela, sarc; diag
 419667; AU077005; Hs.92208; a disintegrin and metalloprote; breast, cerv, angio; mAb
 419693; AA133749; Hs.301350; FXD domain-containing ion tra; pros, breast, ovar, panc, lung; mAb
 419721; NM_001650; Hs.315369; aquaporin 4; glio, lung, fibro; mAb
 419743; AW408762; Hs.5957; Homo sapiens clone 24416 mRNA; blad, headnk; diag
 419749; X73608; Hs.93029; sparcolectonectin, cwcv and ka; pros, panc, lung; diag
 419752; AA249573; Hs.152618; ESTs, Moderately similar to ZN; lung; diag

- 419839; U24577; Hs.93304; phospholipase A2, group VII (p; pros, lung; diag
419870; AW403911; Hs.266175; phosphoprotein associated with; mela; diag
419875; AA853410; Hs.93557; proenkephalin; sarc; diag
419948; AB041035; Hs.93847; NM_016931: Homo sapiens NADPH c; angio; mAb
419956; AL137939; Hs.40096; cadherin 19, type 2; mela; mAb
419958; X04430; Hs.93913; interleukin 6 (interferon, bet; lung, panc, esoph; diag
419981; AA897581; Hs.128773; ESTs; angio; diag
420005; AW271106; Hs.133294; ESTs; lung, test, blad, colon; diag
420062; AW411096; Hs.94785; TGF(beta)-induced transcript; test; CTL+s.m.
420067; T52431; Hs.94795; Homo sapiens mRNA; cDNA DKFZp5; sarc; diag
420137; AA306478; Hs.95327; CD3D antigen, delta polypeptide; fibro; mAb
420154; AI093155; Hs.95420; G antigen family C 1 protein (i; pros, lelo; CTL+s.m.
420174; AI824144; Hs.199749; ESTs; angio; CTL+s.m.
420208; BE276055; Hs.95972; silver (mouse homolog) like; mela; sarc; mAb
420209; AA256444; Hs.126485; hypothetical protein FLJ12604; angio; diag
420218; AW958037; Hs.381105; ribosomal protein L4; mela; pros; diag
420255; NM_007289; Hs.1298; membrane metallo-endopeptidase; pros; mAb
420256; U84722; Hs.76206; cadherin 5, type 2, VE-cadher; angio, fibro; mAb
420267; N37030; Hs.173337; ESTs; mela; sarc; diag
420281; AI523693; Hs.323494; Predicted cation efflux pump; lung, blad, ovar, panc; mAb
420301; AA767526; Hs.22030; paired box gene 5 (B-cell line; mela; diag
420338; AA825595; Hs.88269; Homo sapiens, clone MGC:17339; mela; mAb
420340; NM_000734; Hs.97087; CD3Z antigen, zeta polypeptide; fibro; mAb
420344; BE463721; Hs.97101; putative G protein-coupled rec; colon, pros, blad, headnk, panc, stom, ovar; mAb
420347; AL033539; Hs.97124; Human DNA sequence from clone; test; diag
420360; U83171; Hs.97203; small inducible cytokine subfa; leuk; diag
420367; AA259090; Hs.257028; ESTs; test; diag
420376; AL137471; Hs.97266; protocadherin 18; sarc; mAb+s.m.
420378; NM_014143; Hs.97269; B7-H1 protein; leuk; mAb
420380; AA640891; Hs.102406; ESTs; lung; diag
420424; AB033036; Hs.97594; KIAA1210 protein; pros; diag
420462; AF050147; Hs.97932; chondromodulin I precursor; lung, EWS, sarc; mAb
420474; L09753; Hs.1313; tumor necrosis factor (ligand); leuk; mAb
420544; AA677577; Hs.380213; Homo sapiens Chromosome 16 BAC; pros; diag
420576; AA297634; Hs.54925; KIAA1858 protein; sarc; diag
420596; NM_002692; Hs.99185; polymerase (DNA directed), eps; test; CTL+s.m.
420633; NM_014581; Hs.274480; odorant-binding protein 2B (OB; breast, endor; diag
420656; AA279098; Hs.187638; ESTs; fibro; diag
420710; NM_007009; Hs.99875; zona pellucida binding protein; test; diag
420728; AW964897; Hs.290825; ESTs; pros; diag
420757; X78592; Hs.99915; androgen receptor (dihydrotest; pros; mAb+s.m.
420759; T11832; Hs.127797; Homo sapiens cDNA FLJ11381 f1; test; diag
420783; AI659838; Hs.99823; lectin, galactoside-binding, s; lung, blad, headnk; diag
420789; AI670057; Hs.198882; ESTs; renal; diag
420859; AW468397; Hs.100000; S100 calcium-binding protein A; sarc; diag
420908; AL049974; Hs.100261; Homo sapiens mRNA; cDNA DKFZp5; panc; diag
420923; AF097021; Hs.273321; differentially expressed in he; blad, colon; diag
420931; AF044197; Hs.100431; small inducible cytokine B sub; breast, lung, mela; diag
420981; L40904; Hs.100724; peroxisome proliferative activ; colon; mAb+s.m.
421016; AA504583; Hs.101047; transcription factor 3 (E2A lmy; test; CTL+s.m.
421044; AF061871; Hs.101302; Human DNA sequence from clone; panc; diag
421059; AI654133; Hs.356247; thyroid receptor interacting p; pros; mAb+s.m.
421064; AI245432; Hs.101382; tumor necrosis factor, alpha-t; blad, uter; diag
421070; AA283185; Hs.19327; ESTs; blad; diag
421100; AW351839; Hs.124660; Homo sapiens cDNA: FLJ21763 f1; blad; diag
421133; AA814971; Hs.26410; ESTs; lung; diag
421154; AA284333; Hs.287631; Homo sapiens cDNA FLJ14269 f1; BPH; diag
421155; H87879; Hs.102267; lysyl oxidase; headnk, panc, renal, sarc; diag
421218; NM_000499; Hs.72912; cytochrome P450, subfamily I (i; blad, angio; diag
421233; AA209534; Hs.284243; tetraspan NET-6 protein; pros, breast, ovar; mAb
421241; X91817; Hs.102866; transketolase-like 1; test; s.m.
421302; T34462; Hs.103291; neuritin; uter, endo; diag
421305; BE397354; Hs.324830; diphtheria toxin resistance pro; ovar; diag
421307; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp4; breast, lung, angio, test, sarc; diag
421341; AJ243212; Hs.279611; deleted in malignant brain tum; panc, lung; diag
421350; AW301608; Hs.278188; ESTs, Moderately similar to I5; test; diag
421373; AA808229; Hs.222088; ESTs; blad; diag
421433; AI829192; Hs.22380; ESTs; pros; diag
421451; AA291377; Hs.50931; ESTs; ovar, blad, lung; diag
421458; NM_003654; Hs.104576; carbohydrate (keratan sulfate; sarc; s.m.
421478; AI583243; Hs.97258; ESTs, Moderately similar to S2; ovar, blad, renal, uter; diag
421481; AW391972; Hs.104696; KIAA1324 protein; pros; diag
421502; AF111856; Hs.105039; solute carrier family 34 (sodi; ovar, fibro; mAb
421506; BE302796; Hs.105097; thymidine kinase 1, soluble; lung, headnk, esoph; s.m.
421508; NM_004833; Hs.105115; absent in melanoma 2; blad, esoph, lung, mela; CTL+s.m.
421535; AB002359; Hs.105478; phosphoribosylmethylglycinamid; test; s.m.
421537; BE383488; Hs.105547; neural proliferation, differen; pros; diag
421566; NM_000399; Hs.1395; early growth response 2 (Krox-; pros; CTL+s.m.
421579; NM_002975; Hs.105927; stem cell growth factor; lymph; sarc; mAb
421633; AF121860; Hs.106260; sorting nexin 10; mela; diag
421650; AA781795; Hs.343800; ESTs; mela; diag
421666; AL035250; Hs.1408; endothelin 3; mela; diag
421727; Y13153; Hs.107318; kynurenine 3-monooxygenase (ky; breast; s.m.

- 421773; W69233; Hs.112457; ESTs; mela, esoph, sarc; diag
 421777; BE562088; Hs.108196; HSPC037 protein; esoph, cerv, lung; diag
 421779; AJ879159; Hs.108219; wingless-type MMTV integration; colon, ovar; diag
 421798; N74880; Hs.355462; N-acylsphingosine amidohydrolase; fibro; s.m.
 421814; L12350; Hs.108623; thrombospondin 2; panc; diag
 421831; AA298836; Hs.22026; ESTs; similar to TRANSMEMBRAN; angio; mAb+s.m.
 421887; AW161450; Hs.109201; CGI-86 protein; pros; mAb
 421896; N52293; Hs.45107; ESTs; pros; diag
 421917; AB028943; Hs.109445; KIAA1020 protein; test; diag
 421920; BE551245; Hs.1438; gamma-aminobutyric acid (GABA); sarc; mAb
 421924; BE514514; Hs.109606; coronin, actin-binding protein; fibro; diag
 421948; L42583; Hs.334309; keralin 6A; lung, headnk, blad, esoph, cerv, mela; diag
 421952; AA300900; Hs.98849; dynein light chain 2B (DNLC2B); fibro; diag
 421991; NM_014918; Hs.110488; KIAA0990 protein; panc; diag
 421996; AW583807; Hs.1460; glucagon; panc; diag
 422002; X70070; Hs.110642; neurotensin receptor 1 (high a; colon; mAb
 422027; AL043100; Hs.288828; fatty acid amide hydrolase; pros; s.m.
 422033; AW245805; Hs.110903; claudin 5 (transmembrane prote; glior; mAb
 422087; X58968; Hs.111301; matrix metalloproteinase 2 (ge; sarc; diag
 422089; AA523172; Hs.103135; ESTs, Weakly similar to SFR4_H; pros; diag
 422094; AF129535; Hs.272027; F-box only protein 5; blad, lung; CTL+s.m.
 422095; AB868872; Hs.282804; hypothetical protein FLJ22704; lung, panc, ovar, breast; CTL+s.m.
 422099; AA156022; Hs.111518; hypothetical protein; angio; CTL+s.m.
 422100; AI096988; Hs.111554; ADP-ribosylation factor-like 7; lung, esoph; CTL+s.m.
 422110; AJ376736; Hs.121555; secreted protein, acidic, cyst; panc; diag
 422119; AJ277829; Hs.111862; KIAA0590 gene product; blad; diag
 422134; AW179019; Hs.112110; mitochondrial ribosomal protei; lung; diag
 422152; AA909249; Hs.112282; solute carrier family 30 (zinc; blad; mAb+s.m.
 422163; AF027208; Hs.112360; promilin (mouse)-like 1; colon, breast, fibro; mAb
 422164; NM_014312; Hs.112377; coric al thymocyte receptor (-; blad; mAb+s.m.
 422168; AA586894; Hs.112408; S100 calcium-binding protein A; lung, blad, headnk, breast, mela, esoph, sarc, cerv; CTL+s.m.
 422170; AJ791949; Hs.112432; anti-Mullerian hormone; uter, blad; diag
 422173; BE385828; Hs.250619; phorbol-like protein MDS019; mela; diag
 422247; U18244; Hs.113602; solute carrier family 1 (high; blad; mAb
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog; ovar, headnk, blad, cerv, lung, panc, stom; mAb
 422309; U79745; Hs.114924; solute carrier family 16 (mono; mela; mAb+s.m.
 422311; AF073515; Hs.114948; cytokine receptor-like factor; lung, fibro; diag
 422355; AW403724; Hs.300697; coagulation factor VII (serum; fibro; diag
 422363; T55979; Hs.115474; replication factor C (activator; mela, colon; diag
 422398; AI476149; Hs.334489; hypothetical protein FLJ21992; fibro; CTL+s.m.
 422406; AF025441; Hs.116206; Opa-interacting protein 5; blad, lung; diag
 422420; U03398; Hs.1524; tumor necrosis factor (ligand); colon, panc, stom, leuk; mAb
 422423; AF283777; Hs.116481; CD72 antigen; spleen, leuk; mAb
 422440; NM_004812; Hs.116724; aldo-keto reductase family 1,; lung, headnk; s.m.
 422487; AJ010901; Hs.198267; mucin 4, tracheobronchial; lung, headnk, panc, sarc; diag
 422532; AL008726; Hs.118126; protective protein for beta-ga; renal, mela; s.m.
 422565; BE259035; Hs.118400; singed (Drosophila)-like (sea; panc, test, mela; diag
 422573; AW297985; Hs.295726; integrin, alpha V (vitronectin; panc; mAb+s.m.
 422596; AF063611; Hs.118533; 2'-5'-oligoadenylate synthetase; esoph, mela; s.m.
 422603; BE242587; Hs.118651; hematopoietically expressed hor; angio; CTL+s.m.
 422633; X56832; Hs.118804; enolase 3, (beta, muscle); sarc; s.m.
 422658; AF231981; Hs.250175; homolog of yeast long chain po; pros; diag
 422689; AW856665; Hs.299797; gbr:RC3-CT0297-290100-013-d03 C; test; diag
 422726; U11690; Hs.1572; faclogenic dysplasia (Aarskog; test; diag
 422728; AW937826; Hs.103262; MAD (mothers against decapenta; pros; diag
 422789; AK001113; Hs.120842; hypothetical protein FLJ10251; test; CTL+s.m.
 422835; BE218705; Hs.121378; metallothionein-like 5, testis; breast; diag
 422871; AL031228; Hs.121509; collagen, type XI, alpha 2; sarc; diag
 422887; AI751848; Hs.49215; ESTs; sarc; CTL+s.m.
 422938; NM_001809; Hs.1594; centromere protein A (17kD); lung, test; CTL+s.m.
 422963; M79141; Hs.13234; ESTs; lung, panc; diag
 422997; BE018212; Hs.122908; DNA replication factor; test; CTL+s.m.
 423017; AW178761; Hs.227948; serine (or cysteine) proteinase; blad, headnk, mela; mAb+diag
 423052; M28214; Hs.123072; RAB3B, member RAS oncogene fam; pros; diag
 423189; M59371; Hs.171596; EphA2; colon, ovar; mAb
 423196; AK001866; Hs.125139; hypothetical protein FLJ11004; fibro; CTL+s.m.
 423198; M81933; Hs.1634; cell division cycle 25A; test; CTL+s.m.
 423201; NM_000163; Hs.125180; growth hormone receptor; pros; mAb
 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (a; lung, esoph; diag
 423271; W47225; Hs.126256; interleukin 1, beta; blad, stom, esoph; diag
 423309; BE006775; Hs.126782; sushi-repeat protein; lung, colon; diag
 423354; AB011130; Hs.127436; calcium channel, voltage-depend; test, fibro; mAb
 423387; AJ012074; Hs.348500; vasoactive intestinal peptide; pros; mAb
 423397; NM_001838; Hs.1652; chemokine (C-C motif) receptor; blad, mela; mAb
 423412; AF109300; Hs.351615; prostate cancer associated pro; pros; diag
 423422; AC005175; Hs.128425; NY-REN-24 antigen; glior; mAb+CTL
 423445; NM_014324; Hs.128749; alpha-methylacyl-CoA racemase; pros; s.m.
 423453; AW450737; Hs.128791; CGI-09 protein; lung; CTL+s.m.
 423458; AJ204212; Hs.351113; ESTs; test; CTL+s.m.
 423511; AF036329; Hs.129715; gonadotrophin-releasing hormone; lung; diag
 423515; AA327017; Hs.176594; ESTs; ovar; diag
 423541; AA296922; Hs.129778; serine protease inhibitor, Kaz; colon, panc; diag
 423575; C18863; Hs.163443; intron of perostin (OSF-2os); headnk, breast, panc, lung, fibro, esoph; diag

- 423605; AF047826; Hs.129887; cadherin 19, type 2; meta; mAb
 423642; AW452650; Hs.157148; hypothetical protein MGC13204; lung; diag
 423662; AK001035; Hs.130881; B-cell CLL/lymphoma 11A (zinc); lung; diag
 423685; BE350494; Hs.49753; uveal autoantigen with coiled; panc, uter, colon; CTL+s.m.
 423725; AJ403108; Hs.132127; hypothetical protein LOC57822; lung, headnk, blad; diag
 423739; AA398155; Hs.97600; ESTs; breast, ovar, panc; diag
 423761; NM_005194; Hs.132576; paired box gene 9; headnk; CTL+s.m.
 423765; R23858; Hs.143375; Homo sapiens, clone IMAGE:3840; test; diag
 423778; Y09267; Hs.132821; flavin containing monooxygenase; fibro; s.m.
 423779; AW071837; Hs.57971; TRANSCRIPTION FACTOR HES-5; glio; diag
 423787; AJ295745; Hs.236204; nuclear pore complex protein; test, esoph; diag
 423798; AF047033; Hs.132904; solute carrier family 4, sodiu; angio; mAb
 423799; AW026300; Hs.132906; 19A24 protein; meta; mAb
 423849; AL157425; Hs.133315; Homo sapiens mRNA; cDNA DKFZp7; lung; diag
 423887; AL080207; Hs.134585; DKFZP434G232 protein; headnk, lung; diag
 423899; NM_001427; Hs.134989; engrailed homolog 2; meta; CTL+s.m.
 423905; AW579960; Hs.135150; lung type-I cell membrane-asso; test; mAb
 423909; AJ223183; Hs.135194; immunoglobulin superfamily, mer; test; diag
 423934; U89995; Hs.159234; forkhead box E1 (thyroid trans; lung; CTL+s.m.
 424001; W67883; Hs.137476; paternally expressed 10; breast, ovar; diag
 424012; AW368377; Hs.137569; tumor protein 63 kDa with stro; lung, blad, headnk, esoph; diag
 424036; AA770688; Hs.348495; H2A histone family, member L; panc, ovar, CTL+s.m.
 424054; AA334511; Hs.26638; membrane-spanning 4-domains, s; pros, fibro; mAb
 424078; AB006625; Hs.139033; paternally expressed 3; ovar, uter; CTL+s.m.
 424081; NM_006413; Hs.139120; ribonuclease P (30kD); test; s.m.
 424098; AF077374; Hs.139322; small proline-rich protein 3; lung, blad, headnk, esoph, cerv; diag
 424125; M31669; Hs.1735; inhibin, beta B (activin AB be; ovar, pros; diag
 424144; AA454033; Hs.41644; AKAP-associated sperm protein; fibro; diag
 424153; AA451737; Hs.141496; MAGE-like 2; meta; CTL+s.m.
 424165; AW582904; Hs.142255; islet amyloid polypeptide; panc; mAb
 424212; NM_005814; Hs.143131; glycoprotein A33 (transmembran; colon, stom, ovar; mAb
 424218; AF031824; Hs.143212; crystallin F (leukocystatin); meta, fibro; diag
 424244; AV647184; Hs.143801; hypothetical protein hCLA-Iso; blad; diag
 424252; AK000520; Hs.143811; hypothetical protein FLJ20513; colon, stom; diag
 424264; D80400; Hs.239388; Human DNA sequence from clone; blad; mAb
 424308; AW975531; Hs.154443; minichromosome maintenance def; blad, lung, test; diag
 424310; AA338648; Hs.50334; testes development-related NYD; fibro; diag
 424332; AA338919; Hs.101615; ESTs; pros; diag
 424339; BE257148; Hs.145416; endoglycan; pros, lung; diag
 424343; AW956360; Hs.4748; adenylate cyclase activating p; glio, ovar, uter; mAb
 424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763; lung, blad, headnk, cerv; diag
 424399; AI905687; Hs.348419; AI905687:IL-BT095-190199-019 B; breast, uter, headnk; diag
 424420; BE614743; Hs.146688; prostaglandin E synthase; lung, blad; s.m.
 424440; AA340743; Hs.133208; ESTs; sarc; diag
 424441; X14850; Hs.147097; H2A histone family, member X; lung; diag
 424450; AL137526; Hs.147472; dynein intermediate chain 2; fibro; diag
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 9; breast, cerv, ovar, uter, blad, colon, stom; s.m.
 424527; AW138558; Hs.334873; ESTs, Weakly similar to I54374; fibro; diag
 424578; AK001973; Hs.150890; hypothetical protein; test; CTL+s.m.
 424581; M52062; Hs.150917; catenin (cadherin-associated p; glio, ovar, uter; mAb+s.m.
 424586; NM_003401; Hs.150930; X-ray repair complementing def; panc; CTL+s.m.
 424629; M90656; Hs.151393; glutamate-cysteine ligase, cat; lung; CTL+s.m.
 424635; AA420687; Hs.115455; Homo sapiens cDNA FLJ14259 fis; glio; diag
 424676; Y08565; Hs.151678; UDP-N-acetyl-alpha-D-galactose; breast; s.m.
 424704; AI263293; Hs.152095; cytochrome P450, subfamily 1J; renal; s.m.
 424711; NM_005795; Hs.152175; calcitonin receptor-like; angio; mAb
 424717; H03754; Hs.152213; wingless-type MMTV Integration; blad, lung, headnk; diag
 424800; AL035588; Hs.153203; MyoD family inhibitor; test, pros; diag
 424806; AA382523; Hs.105689; MSTP031 protein; angio; mAb
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis; lung, blad, ovar, headnk, esoph, cerv, uter; diag
 424846; AU077324; Hs.1832; neuropeptide Y; pros; diag
 424897; D63216; Hs.153684; fizzled-related protein; panc, EWS, stom, renal; diag
 424902; NM_003866; Hs.153687; inositol polyphosphate-4-phosp; panc, leuk, meta; CTL+s.m.
 424954; NM_000546; Hs.1846; tumor protein p53 (Li-Fraumeni; meta, colon; CTL+s.m.
 424971; AA479005; Hs.154036; tumor suppressing subtransfera; panc, meta; CTL+s.m.
 424998; U58515; Hs.154138; chitinase 3-like 2; glio; diag
 425023; AW956889; Hs.154210; EDG-1 (endothelial differenti; angio; mAb
 425048; H05468; Hs.164502; ESTs; lung, blad; diag
 425057; AA826434; Hs.1619; achaeta-scute complex (Drosoph; glio, lung; CTL+s.m.
 425088; AA663372; Hs.169395; hypothetical protein FLJ12015; glio, meta; diag
 425154; NM_001851; Hs.154850; collagen, type IX, alpha 1; sarc; diag
 425159; NM_004341; Hs.154868; carbamoyl-phosphate synthetase; lung, test; s.m.
 425200; BE255203.comp; Hs.155101; ATP synthase, H transporting; panc; s.m.
 425206; NM_002153; Hs.155109; hydroxysteroid (17-beta) dehyd; blad; mAb
 425211; M18667; Hs.1867; progastricin (pepsinogen C); fibro, esoph, pros; diag
 425234; AW152225; Hs.165909; ESTs, Weakly similar to I38022; lung, angio, blad, meta; diag
 425235; AA363113; Hs.105468; Homo sapiens cDNA: FLJ22743 f; angio; diag
 425237; U07695; Hs.155227; EphB4; test; mAb
 425245; A1751768; Hs.155314; KIAA0095 gene product; lung; diag
 425259; AL049280; Hs.145010; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 425262; D87119; Hs.155418; GS3955 protein; meta, renal; CTL+s.m.
 425268; J00077; Hs.155421; alpha-fetoprotein; lung; diag
 425274; BE281191; Hs.155462; minichromosome maintenance def; test; diag

- 425289; AW139342; Hs.155530; Interferon, gamma-inducible p1; mel; CTL+s.m.
 425308; M97639; Hs.155585; receptor tyrosine kinase-like; pros; sarc; mAb
 425367; BE271188; Hs.155975; protein tyrosine phosphatase; fibro; diag
 425371; D49441; Hs.155981; mesothelin; ovar; lung; fibro; mAb
 5 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (1); lung, blad, panc, angio, test, mel; CTL+s.m.
 425427; A1652662; Hs.317432; branched chain aminotransferase; test; s.m.
 425428; AL110261; Hs.157211; DKFZP586B0621 protein; panc; diag
 425465; L18964; Hs.1904; protein kinase C, α ; ovar; pros; colon; s.m.
 425525; AA358883; Hs.23871; ESTs; sarc; diag
 10 425545; N98529; Hs.158295; Homo sapiens, clone MGC12401; sarc; diag
 425555; AA359291; Hs.130767; Homo sapiens cDNA: FLJ23553 f1; fibro; CTL+s.m.
 425572; AB011076; Hs.158307; undifferentiated embryonic cell; test; CTL+s.m.
 425601; AW629485; Hs.140720; GSK-3 binding protein FRAT2; test; CTL+s.m.
 425606; U52112; Hs.158331; renin-binding protein; mel; diag
 15 425628; NM_004476; Hs.1915; folate hydrolase (prostate-spe; pros; s.m.
 425638; NM_012337; Hs.158450; nasopharyngeal epithelium spec; fibro; CTL+s.m.
 425679; X05997; Hs.159177; lipase, gastric; esoph; s.m.
 425692; D90041; Hs.155956; N-acetyltransferase 1 (arylami; breast; s.m.
 425695; NM_005401; Hs.159238; protein tyrosine phosphatase; lung; mAb+s.m.
 20 425709; AA383076; Hs.159274; outer dense fibre of sperm tail; test; diag
 425710; AF030880; Hs.159275; solute carrier family, member 1; pros; mAb
 425722; A1659076; Hs.97031; hypothetical protein MGC13047; mel; diag
 425726; AF085808; Hs.159330; uroplakin 3; pros; blad; diag
 25 425769; U72513; Hs.159486; Human RPL13-2 pseudogene mRNA; test; diag
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort; test; diag
 425849; AJ000512; Hs.296323; serum/glucocorticoid regulated; lung, headnk; s.m.
 425921; NM_007231; Hs.162211; solute carrier family 6 (neuro; stom; panc; mAb
 425976; C75094; Hs.334514; NG22 protein; pros; ovar; mAb
 30 426027; NM_002608; Hs.1976; platelet-derived growth factor; sarc; diag
 426050; AF017307; Hs.166096; E74-like factor 3 (ets domain; ovar; blad, stom; CTL+s.m.
 426059; BE292842; Hs.166120; interferon regulatory factor 7; esoph; cerv; CTL+s.m.
 426067; AW664691; Hs.97053; ESTs; lung; diag
 426088; AF038007; Hs.166196; ATPase, Class I, type B9, memb; blad, lung; mAb
 35 426094; AF034611; Hs.166206; cubilin (intrinsic factor-cofactor; renal; diag
 426116; AA868729; Hs.144694; ESTs; fibro; diag
 426125; X87241; Hs.166994; FAT tumor suppressor (Drosophila; colon, stom, panc, pros, renal, fibro, cerv; mAb
 426156; BE244537; Hs.167382; natriuretic peptide receptor A; ovar; mAb
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic; breast, ovar, uter, pros, blad, panc, colon, fibro, mel; diag
 40 426172; AA371307; Hs.125056; ESTs; pros; diag
 426174; AA547959; Hs.115838; Homo sapiens similar to Echino; breast, pros, fibro; diag
 426212; S71824; Hs.167988; neural cell adhesion molecule 1; glio; mAb
 426271; AF026547; Hs.169047; chondroitin sulfate proteoglycan; glio; diag
 426274; D38122; Hs.2007; tumor necrosis factor (ligand); fibro, mel; mAb
 45 426300; U15979; Hs.169228; delta-like homolog (Drosophila; ovar, sarc; mAb
 426310; NM_000909; Hs.169266; neuropeptide Y receptor Y1; breast; mAb
 426312; AF026939; Hs.181874; Interferon-induced protein wit; esoph, mel; diag
 426320; W47595; Hs.169300; transforming growth factor, β ; ovar, pros, blad, panc; diag
 426350; NM_003245; Hs.2022; transglutaminase 3 (E polypept; cerv; s.m.
 426363; M58524; Hs.2025; transforming growth factor, β ; pros; diag
 50 426370; R98288; Hs.281706; sorbitin 1; sarc; diag
 426416; AW612744; Hs.169824; killer cell lectin-like recept; fibro; mAb
 426440; BE382756; Hs.169902; solute carrier family 2 (facit; lung, panc, ovar, blad, headnk, esoph; mAb
 426462; U59111; Hs.169993; dermatan sulphate proteoglycan; sarc; diag
 55 426470; AA528794; Hs.128644; ESTs; mel; diag
 426471; M22440; Hs.170009; transforming growth factor, α ; headnk, renal, panc; diag
 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; panc; mAb+s.m.
 426501; AW043782; Hs.293616; ESTs; pros, breast, glio, lung, mel; mAb
 426502; Y07759; Hs.170157; myosin VA (heavy polypeptide 1); mel; diag
 60 426534; U58096; Hs.2051; testis specific protein, Y-link; test; CTL+s.m.
 426535; AU077012; Hs.170279; ESTs, Weakly similar to ubiquitin; angio; diag
 426555; NM_000372; Hs.2053; tyrosinase (oculocutaneous alb; mel; sarc; mAb
 426559; AB001914; Hs.170414; paired basic amino acid cleav; hepC, breast, ovar, renal; diag
 426575; M74826; Hs.170808; glutamate decarboxylase 2 (pan; panc; s.m.
 65 426627; AF012359; Hs.195685; ESTs; test; diag
 426635; BE395109; Hs.129327; hypothetical protein MGC13057; ovar; CTL+s.m.
 426682; AV660038; Hs.2056; UDP glycosyltransferase 1 famit; blad, lung; s.m.
 426691; NM_006201; Hs.171834; PCTAIRE protein kinase 1; ovar; CTL+s.m.
 426696; AW363332; Hs.171844; Homo sapiens cDNA: FLJ22296 f1; angio; mAb
 70 426721; AA383588; Hs.288545; ESTs, Weakly similar to T29012; fibro; diag
 426726; AA488915; Hs.171955; trophinin associated protein (1; test; diag
 426747; AA535210; Hs.171995; kallikrein 3, (prostate specif; pros; diag
 426752; X69490; Hs.172004; titin; sarc; diag
 426759; A1590401; Hs.21213; ESTs; mel; diag
 75 426793; X89887; Hs.172350; HIR (histone cell cycle regula; pros; CTL+s.m.
 426828; NM_000020; Hs.172670; activin A receptor type II-B; angio; mAb
 426866; U02330; Hs.172816; neuregulin 1; esoph; CTL+s.m.
 426897; AW976570; Hs.97387; ESTs; lung; diag
 426900; AW163564; Hs.142375; ESTs; blad, pros; mAb
 80 426935; NM_000088; Hs.172928; collagen, type I, alpha 1; test, sarc; CTL+s.m.
 426966; AJ493134; Hs.349204; sclerostin; lung; diag
 426968; U07616; Hs.173034; amphiphysin (Stiff-Mann syndro; blad; mAb+CTL
 426991; AK001536; Hs.214410; Homo sapiens cDNA FLJ10674 f5; ovar, sarc; diag
 427080; AW068287; Hs.301175; ras-related C3 botulinum toxin; mel; diag

- 427099; AB032953; Hs.173560; odd Oz/ten-m homolog 2 (Drosop; headnk, esoph; diag
427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase; breast; mAb
427244; AA402400; Hs.178045; ESTs; esoph; diag
5 427260; AA663848; gbrae70b06.s1 Stratagene schiz; lung; diag
427274; NM_005211; Hs.174142; colony stimulating factor 1 re; pros, sarc; mAb
427298; AA400495; ESTs; test; diag
427318; AF186081; Hs.175783; zinc transporter; pros; mAb
427333; AF067797; Hs.176658; aquaporin 8; panc, colon; mAb
10 427344; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin; ovar; mAb
427356; AW023482; Hs.97849; ESTs; ovar, breast, pros, blad, lung; diag
427398; AW390020; Hs.20415; chromosome 21 open reading fra; pros; diag
427427; AF077345; Hs.177936; lectin, superfamily member 1 (; breast; diag
427441; AA412605; Hs.293266; SPANX family, member C; lung, esoph; CTL+s.m.
15 427461; AA531527; Hs.332040; hypothetical protein MGC13010; pros; mAb
427474; U13192; Hs.2159; aggrecan 1 (chondroitin sulfat; sarc; diag
427486; AA974433; Hs.362432; fibroblast growth factor 4 (he; test; diag
427510; Z47542; Hs.179312; small nuclear RNA activating c; lung; CTL+s.m.
427515; T79526; Hs.179516; integral type I protein; pros; diag
20 427521; AW973352; ESTs; test; diag
427528; AU077143; Hs.179565; minichromosome maintenance def; mela; CTL+s.m.
427535; R29543; Hs.2164; pro-platelet basic protein (in; fibro; diag
427546; AA405280; Hs.36793; hypothetical protein FLJ23188; lung; diag
427550; BE242818; Hs.311609; nuclear RNA helicase, DECD var; mela; CTL+s.m.
25 427557; NM_002659; Hs.179657; plasminogen activator, urokin; panc, colon, ovar, cerv, blad, lung, headnk, esoph; mAb
427578; A1591305; Hs.169084; ESTs, Highly similar to TUL3_H; test; diag
427583; M82962; Hs.179704; meprin A, alpha (PABA peptide; colon; mAb
427584; BE410293; Hs.179718; v-myb avian myeloblastosis vir; test; CTL+s.m.
427585; D31152; Hs.179729; collagen, type X, alpha 1 (Sch; breast, lung, headnk, panc, stom, colon, ovar, cerv, sarc; diag
30 427615; BE410107; Hs.179817; CG-82 protein, PSDR1; pros; diag
427634; A1399745; Hs.18449; hypothetical protein MGC10820; mela, sarc; diag
427647; W19744; Hs.180059; Homo sapiens cDNA FLJ20653 fis; sarc; diag
427666; A1791495; Hs.180142; calmodulin-like skin protein (; breast, cerv, blad, lung, headnk, esoph; diag
427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 fis; test; diag
35 427668; AA298760; Hs.180191; hypothetical protein FLJ14904; lung, test; diag
427681; AB018263; Hs.284232; tumor necrosis factor receptor; ovar; mAb+s.m.
427698; AW972594; Hs.335499; ESTs; fibro; CTL+s.m.
427701; AA411101; Hs.243886; nuclear autoantigenic sperm pr; lung; mAb+CTL
427715; BE245274; Hs.180428; KIAA1181 protein; pros; diag
427719; A1393122; Hs.134726; ESTs; test; blad; diag
40 427730; AW250549; Hs.180577; granulin; mela; diag
427786; BE407863; Hs.256871; ESTs; esoph, blad; diag
427809; M26380; Hs.180878; lipoprotein lipase; ovar; mAb
427811; M81057; Hs.180884; carboxypeptidase B1 (tissue); breast; s.m.
427897; NM_017413; Hs.303084; epetin; peptide ligand for APJ; angio, renal, pros; diag
45 427912; AL022310; Hs.181097; tumor necrosis factor (ligand); angio; mAb
427958; AA418000; Hs.376771; potassium intermediate/small c; pros, glio; mAb
427961; AW293165; Hs.143134; ESTs; lung, sarc; diag
428001; H97428; Hs.219907; ESTs, Moderately similar to Tr; mela; diag
50 428004; AA449563; Hs.151393; glutamate-cysteine ligase, cat; lung; s.m.
428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 f; lung; diag
428046; AW812785; Hs.337534; ESTs, Moderately similar to I3; lung, colon; diag
428062; AA420683; Hs.98321; hypothetical protein FLJ14103; angio; diag
428087; AA100573; Hs.182421; troponin C2, fast; sarc; CTL+s.m.
55 428141; D50402; Hs.182611; solute carrier family 11 (prot; glio; mAb
428153; AW513143; Hs.98357; SRY (sex determining region Y); ovar; diag
428169; A1928984; Hs.182793; golgi phosphoprotein 2; pros; diag
428182; BE386042; Hs.293317; ESTs, Weakly similar to GGC1_H; blad, headnk, lung, ovar, sarc; CTL+s.m.
428183; AW969726; Hs.98381; ESTs, Weakly similar to serine; EWS; diag
60 428206; AB020643; Hs.183006; KIAA0836 protein; angio; mAb
428221; U96781; Hs.183075; ATPase, Ca transporting, card; sarc; s.m.
428227; AA321649; Hs.2248; small inducible cytokine subfa; breast, lung, blad, ovar, headnk, fibro, colon, stom, cerv, leuk, renal, test, mela, esoph, hepC; diag
428248; A1126772; Hs.40479; ESTs; sarc; diag
428293; BE250944; Hs.183556; solute carrier family 1 (neutr; pros; mAb
65 428305; AA446528; Hs.2799; cartilage linking protein 1; sarc; diag
428329; AA426091; Hs.98453; ESTs, Moderately similar to R2; test; diag
428336; AA503115; Hs.183752; microseminoprotein, beta-; pros; diag
428355; BE256452; Hs.2257; vitronectin (serum spreading f; colon; diag
428398; A1249368; Hs.98558; ESTs; pros, breast; diag
70 428405; Y00762; Hs.2266; cholinergic receptor, nicotin; esoph, sarc; mAb
428423; AU076517; Hs.184276; solute carrier family 9 (sodiu; ovar; CTL+s.m.
428434; AW363590; Hs.65551; Homo sapiens, Similar to DNA s; lung, fibro; diag
428467; AK002121; Hs.184465; hypothetical protein FLJ11259; fibro; mAb
428471; X57348; Hs.184510; stratifin; lung, headnk, colon, panc; diag
75 428645; AA431400; Hs.98729; ESTs, Weakly similar to 201720; lung; s.m.
428651; AF196478; Hs.188401; annexin A10; blad, stom, panc; diag
428667; A1375550; Hs.346868; nuclear protein p40; homolog; fibro, uter; diag
428722; U76456; Hs.190787; tissue inhibitor of metallopro; glio; diag
428728; NM_016625; Hs.191381; hypothetical protein; ovar, lung, BPH; CTL+s.m.
80 428771; AB028992; Hs.193143; KIAA1069 protein; lung; CTL+s.m.
428784; Y12851; Hs.193470; purinergic receptor P2X, ligand; glio, mela; mAb
428800; M57627; Hs.193717; interleukin 10; fibro; diag
428801; AW277121; Hs.254881; ESTs; pros; diag
428804; AK000713; Hs.193736; hypothetical protein FLJ20706; mela; diag

- 428810; AF068236; Hs.193788; nitric oxide synthase 2A (indu; lung; s.m.
 428819; AL135623; Hs.193914; KIAA0575 gene product; pros; CTL+s.m.
 428824; W23624; Hs.173059; ESTs; panc; diag
 428832; AA578229; Hs.324239; ESTs, Moderately similar to ZN; panc, uter; diag
 5 428841; AJ418430; Hs.104935; ESTs; renal; diag
 428848; NM_000230; Hs.194236; leptin (murine obesity homolog; sarc; diag
 428862; NM_000346; Hs.2316; SRY (sex determining region Y); pros, sarc; CTL+s.m.
 428927; AA441837; Hs.90250; Homo sapiens hypothetical prot; fibro; mAb+diag
 428928; BE409838; Hs.194657; cadherin 1, type 1, E-cadherin; pros, breast, stom, blad; mAb
 10 428949; AA442153; Hs.104744; hypothetical protein DKFZp434J; sarc; diag
 428957; NM_003881; Hs.194679; WNT1 inducible signaling pathw; cerv; diag
 428959; AF100779; Hs.194680; WNT1 inducible signaling pathw; sarc; diag
 428977; AK001404; Hs.194698; cyclin B2; test; CTL+s.m.
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2_H; sarc; diag
 15 429002; AW248439; Hs.2340; junction plakoglobin; blad; CTL+s.m.
 429010; Y18198; Hs.194725; one cut domain, family member 1; panc; diag
 429038; AL023513; Hs.194766; seizure related gene 6 (mouse); lung; mAb
 429058; AF138863; Hs.35254; hypothetical protein FLB6421; esoph; diag
 429065; AI753247; Hs.29543; Homo sapiens cDNA FLJ13101 f1; lung; diag
 20 429083; Y09397; Hs.227817; BCL2-related protein A1; mel; diag
 429113; D28235; Hs.196384; prostaglandin-endoperoxide synt; angio, blad, stom; s.m.
 429120; AK001673; Hs.196530; hypothetical protein FLJ10811; test; diag
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; ovar; mAb
 429163; AA884766; g; gram20a10.s1 Soares_NFL_T_GBC; pros; diag
 25 429170; NM_0011394; Hs.2359; dual specificity phosphatase 4; breast, panc, stom, lung, mel; s.m.
 429201; X03178; Hs.198246; group-specific component (vita; panc; diag
 429220; AW207206; Hs.356962; ESTs; breast, pros, BPH; diag
 429228; AI553633; Hs.356828; ESTs; lung, fibro, headnk, esoph; diag
 30 429259; AA420450; Hs.380088; Plakophilin; lung, headnk; diag
 429290; AF203032; Hs.198760; neurofilament, heavy polypept; pros; CTL+s.m.
 429299; AI620463; Hs.347408; hypothetical protein MGC13102; pros, cerv; diag
 429329; AA456140; Hs.99235; Homo sapiens pannexin 3 (PANX3; sarc; mAb
 429345; R11141; Hs.199695; hypothetical protein; blad; diag
 35 429359; W00482; Hs.2399; matrix metalloproteinase 14 (m; headnk, breast, cerv, ovar, blad, lung, esoph, mel, sarc; mAb
 429413; NM_014058; Hs.201877; DESC1 protein; lung, blad; diag
 429415; NM_002593; Hs.202097; procollagen C-endopeptidase en; sarc; diag
 429423; AI016712; Hs.380983; integrin, beta 1 (fibronectin; angio; mAb
 429432; AI678059; Hs.202676; synaptonemal complex protein 2; breast, cerv; diag
 40 429441; AJ224172; Hs.204096; lipophilin B (uteroglobin fam; breast, pros, ovar; diag
 429466; M85835; Hs.12827; ESTs; glio, uter; CTL+s.m.
 429469; M64590; Hs.380791; glycine dehydrogenase (decarbo; test; s.m.
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; blad, lung, headnk, test; diag
 429500; X78565; Hs.289114; hexabrachion (tenascin C, cyto; lung, glio, headnk, mel, sarc; diag
 45 429504; X99133; Hs.204238; lipocalin 2 (oncogene 24p3) (N; ovar, lung, blad; diag
 429505; AW820035; Hs.278679; a disintegrin and metalloprote; colon, leuk; mAb
 429538; BE182592; Hs.139322; small proline-rich protein 2A; lung, esoph; diag
 429563; BE619413; Hs.2437; eukaryotic translation Initiat; lung; diag
 429586; T73510; Hs.209153; angiotensin-like 3; hepC; CTL+s.m.
 429597; NM_003816; Hs.2442; a disintegrin and metalloprote; panc, colon, stom, lung; mAb
 50 429609; AF002246; Hs.210863; cell adhesion molecule with hor; ovar, mel; diag
 429612; AF062649; Hs.252587; pituitary tumor-transforming 1; lung, blad, headnk; diag
 429655; U48959; Hs.211582; myosin, light polypeptide kin; pros; s.m.
 429653; M88874; Hs.211587; phospholipase A2, group IVA (c; angio, lung; s.m.
 55 429664; L20433; Hs.211588; POU domain, class 4, transcrip; sarc; CTL+s.m.
 429736; AF125304; Hs.212680; tumor necrosis factor receptor; lung; mAb
 429747; M87507; Hs.2490; caspase 1, apoptosis-related c; colon, stom, fibro; s.m.
 429764; BE245076; Hs.216958; KIAA0194 protein; pros; mAb
 429769; NM_004917; Hs.218366; kallikrein 4 (protease, enamel; pros; s.m.
 60 429784; M89796; Hs.30; membrane-spanning 4-domains, s; fibro; mAb
 429823; AA459443; Hs.181400; ESTs; sarc; diag
 429859; NM_007050; Hs.225952; protein tyrosine phosphatase; breast; mAb+s.m.
 429918; AW873986; Hs.119383; ESTs; pros, glio; diag
 429921; AA526911; Hs.82772; collagen, type XI, alpha 1; headnk, panc, sarc; CTL
 65 429983; W92620; Hs.260855; ESTs; blad; diag
 429986; AF092047; Hs.227277; sine oculis homeobox (Drosophila; lung; CTL+s.m.
 430014; H59354; Hs.374303; actinin, alpha 4; renal; diag
 430016; NM_004736; Hs.227655; xenotropic and polytropic retr; ovar; mAb
 430044; AA464510; Hs.152812; ESTs; breast, lung, panc, headnk, ovar, stom, esoph; diag
 70 430056; X97548; Hs.228059; KRAB-associated protein 1; test; CTL+s.m.
 430129; BE301708; Hs.233955; hypothetical protein FLJ20401; angio; diag
 430130; AL137311; Hs.234074; Homo sapiens mRNA; cDNA DKFZp7; pros; mAb
 430144; AJ732722; Hs.98927; ERGL protein; ERGIC-53-like pr; pros; diag
 430152; AB001325; Hs.234642; aquaporin 3; blad, fibro; mAb
 75 430154; AW583058; Hs.234726; serine (or cysteine) proteinase; pros; diag
 430157; BE348706; Hs.278543; ESTs; blad; diag
 430168; AW968343; Hs.145582; DKFZP434I1735 protein; blad; diag
 430223; NM_002514; Hs.235935; nephroblastoma overexpressed g; mel; diag
 430226; BE245562; Hs.2551; adrenergic, beta-2-, receptor; pros; mAb
 80 430228; AW950939; Hs.6382; ESTs, Highly similar to T00391; glio; diag
 430252; AI638774; Hs.105328; testes development-related NYD; test; CTL+s.m.
 430253; AK001514; Hs.236844; hypothetical protein FLJ10652; test; CTL+s.m.
 430255; AK000703; Hs.323822; Homo sapiens mRNA for KIAA1551; test; CTL+s.m.
 430259; BE550182; Hs.375142; Raf-GEF-like protein 3, mouse h; ovar; CTL+s.m.

- 430280; AA361258; Hs.237858; interleukin 7 receptor; mela, lung, panc, stom, esoph, headnk, fibro; mAb+s.m.
 430287; AW182459; Hs.125759; ESTs, Weakly similar to LEUS_H; test; diag
 430294; AI538226; Hs.32976; guanine nucleotide binding pro; pros; diag
 430337; M36707; Hs.239600; calmodulin-like 3; lung; diag
 430354; AA954810; Hs.239784; human homolog of Drosophila Sc; ovar; diag
 430378; Z29572; Hs.2556; tumor necrosis factor receptor; lung, fibro, breast headnk, blad, breast, colon, stom; diag
 430393; BE185030; Hs.241305; estrogen-responsive B box prot; lung; diag
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; panc; diag
 430407; H23551; Hs.30974; ESTs; panc; diag
 430439; AL133561; Hs.380155; DKFZP434B061 protein; lung, test; diag
 430451; AA836472; Hs.297939; cathepsin B; ovar, lung, headnk, panc, stom; diag
 430454; AW469011; Hs.105635; ESTs; lung; diag
 430476; AA447465; Hs.2563; tachykinin, precursor 1 (subst; sarc; diag
 430487; D87742; Hs.241552; KIAA0268 protein; pros; diag
 430491; AL109791; Hs.241559; Homo sapiens mRNA full length ; ovar; diag
 430498; X02910; Hs.241570; tumor necrosis factor (TNF sup; leuk; diag
 430508; AJ015435; Hs.104637; ESTs; lung; mAb+s.m.
 430521; NM_016383; Hs.242183; HOM-TES-85 tumor antigen; test; CTL+s.m.
 430540; AW245422; Hs.106357; Homo sapiens cDNA: FLJ22105 f; mela; mAb
 430563; AA481269; Hs.348628; ATP-binding cassette, sub-fam; lung; diag
 430594; AK000790; Hs.246885; hypothetical protein FLJ20783; mela; diag
 430634; AI860651; Hs.26685; calyphosine; ovar; diag
 430637; BE160081; Hs.256290; S100 calcium-binding protein A; mela; diag
 430647; AC003682; Hs.127988; ESTs, Weakly similar to Z211_H; test; diag
 430676; AF084866; Hs.372585; gb:Homo sapiens envelope prote; test; diag
 430677; Z26317; Hs.359784; desmoglein 2; lung, colon; mAb
 430678; AI458174; Hs.192855; ESTs; lung; diag
 430686; NM_001942; Hs.2633; desmoglein 1; lung, headnk, mela; mAb
 430691; C14187; Hs.157208; aristaleless-related homeobox pr; EWS, ovar, panc; diag
 430704; AW813091; Hs.335799; ESTs; stom; diag
 430770; AA765694; Hs.123296; ESTs; mela; diag
 430832; AJ073913; Hs.100686; ESTs, Weakly similar to JE0350; breast, colon, ovar, uter, lung, stom, fibro; diag
 430838; N46664; Hs.169395; hypothetical protein FLJ12015; mela; CTL+s.m.
 430890; X54232; Hs.2699; glypican 1; glio, lung, cerv, blad, esoph; mAb
 430985; AA490232; Hs.27323; ESTs, Weakly similar to I78885; lung; mAb
 431009; BE149762; Hs.48956; gap junction protein, beta 6 (; lung, blad, headnk, esoph; mAb
 431053; S40369; Hs.249141; Glutamate receptor subunit; glio; mAb
 431070; AW408164; Hs.249184; transcription factor 19 (SC1); blad; diag
 431089; BE041395; Hs.374629; ESTs, Weakly similar to unknown; blad, lung, pros, angio, fibro; diag
 431099; Y13367; Hs.249235; phosphoinositide-3-kinase, cla; pros; CTL+s.m.
 431103; M57399; Hs.44; pleiotrophin (heparin binding ; sarc, mela; diag
 431124; AF284221; Hs.59506; doublesex and mab-3 related tr; lung; CTL+s.m.
 431151; BE207083; Hs.366053; gb:ba10d10.y1 NIH_MGC_7 Homo s; pros; mAb
 431164; AA493650; Hs.94367; thyroid transcription factor 1; fibro; CTL+s.m.
 431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasm; mela, pros, panc, colon, stom; mAb
 431211; M86849; Hs.323733; gap junction protein, beta 2 ; colon, blad, lung, panc, headnk, esoph; mAb
 431217; NM_013427; Hs.250830; Rho GTPase activating protein ; pros; CTL+s.m.
 431221; AA449015; Hs.286145; SRB7 (suppressor of RNA polyme; lung; CTL+s.m.
 431222; X56777; Hs.273790; zona pellucida glycoprotein 3A; pros; diag
 431250; BE264649; Hs.251377; taxol resistance associated ga; esoph; diag
 431322; AW970622; Hs.376626; gb:EST382704 MAGE resequences.; blad, ovar, uter; diag
 431347; AI133461; Hs.251684; insulin-like growth factor 2 (; blad; mAb+diag
 431354; BE046958; Hs.251673; DNA (cytosine-5)-methyltransf; test; CTL+s.m.
 431360; NM_000427; Hs.251680; lorcinin; mela, sarc; diag
 431362; AI874223; Hs.293560; ESTs; angio; diag
 431369; BE184455; Hs.251754; secretory leukocyte protease I; ovar, blad; diag
 431384; BE158000; Hs.334372; gb:MR2-HT0377-150200-202-e03 H; lung; diag
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, s; panc; diag
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gat; ovar, pros, blad; mAb
 431448; AL137517; Hs.306201; hypothetical protein DKFZp564O; blad; mAb
 431457; NM_012211; Hs.256297; Integrin, alpha 11; headnk; mAb
 431474; AL133990; Hs.190642; CEGP1 protein; breast, pros, blad; diag
 431494; AA991355; Hs.298312; hypothetical protein DKFZp434A; lung; diag
 431512; BE270734; Hs.2795; lactate dehydrogenase A; panc; s.m.
 431548; AI834273; Hs.9711; novel protein; lung, angio, pros; diag
 431553; X78075; Hs.2799; cartilage linking protein 1; sarc; diag
 431579; AW971082; Hs.222886; ESTs, Weakly similar to TRHY_H; pros; diag
 431616; AA508552; Hs.222874; ESTs, Weakly similar to I38022; pros, panc, colon ; mAb
 431674; AA098901; Hs.301642; G-protein coupled receptor; ovar; mAb+s.m.
 431723; AW058350; Hs.278956; Homo sapiens mRNA; cDNA DKFZp5; fibro; diag
 431728; NM_007351; Hs.268107; multimerin; angio; diag
 431808; M30703; Hs.270833; amphiregulin (schwannoma-deriv; breast, headnk, panc, colon; diag
 431836; AF178532; Hs.271411; beta-site APP-cleaving enzyme ; mela; mAb
 431870; AW449902; Hs.105500; ESTs; renal; diag
 431890; X17033; Hs.271988; integrin, alpha 2 (CD49B, alph; blad, headnk, lung, panc, cerv, stom; mAb
 431938; AA938471; Hs.54431; specific granule protein (28 k; panc; diag
 431939; AW008061; Hs.231994; ESTs; renal, colon; diag
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 f; cerv, glio; diag
 431989; AW972870; Hs.291059; ESTs; ovar; diag
 431992; NM_002742; Hs.2891; protein kinase C, mu; pros, glio; s.m.
 432004; BE018302; Hs.2894; placental growth factor, vascul; renal; diag
 432015; AL157504; Hs.159115; Homo sapiens mRNA; cDNA DKFZp5; blad; diag
 432023; AW273128; Hs.300268; EST; lung; diag

- 432097; X51730; Hs.2905; progesterone receptor; blad; mAb+s.m.
 432117; AL036195; Hs.2909; protamine 1; test; CTL+s.m.
 432128; AA127221; Hs.66; ESTs; angio; diag
 432141; BE410964; Hs.272736; nuclear receptor binding prote; test; mAb+s.m.
 432189; AA527941; ; gb:nh30c04.s1 NCI_CGAP_Pr3 Hom; pros; diag
 432199; AI693815; Hs.127179; cryptic gene; panc; diag
 432210; AI6947421; Hs.273330; Homo sapiens, clone IMAGE:3544; ovar, lung, blad; diag
 432222; AI204995; ; gb:an03c03.x1 Stratagene schiz; angio, blad, fibro; diag
 432231; AA339977; Hs.274127; CLST 11240 protein; fibro; diag
 432239; X81334; Hs.2936; matrix metalloproteinase 13 (c; blad, lung, headnk, esoph, sarc; s.m.
 432240; AI694767; Hs.129179; Homo sapiens cDNA FLJ13581 f1; pros; diag
 432305; M52402; Hs.274313; insulin-like growth factor bin; cerv; diag
 432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 f1; cerv, lung, fibro, pros; diag
 432407; AA221036; ; gb:zr03f12.r1 Stratagene NT2 n; lung, test, colon; diag
 432415; T16971; ; ESTs, Weakly similar to A43932; ovar, pros; diag
 432432; AA541323; Hs.115831; ESTs; uter, pros; diag
 432435; BE218886; Hs.282070; ESTs; pros, uter, colon, stom, fibro; diag
 432441; AW292425; Hs.163484; intron of hepatocyte nuclear f; blad, fibro, pros; diag
 432473; AI202703; Hs.152414; ESTs; pros; diag
 432481; AW451645; Hs.151504; intron of collagen, type XI, α ; sarc; diag
 432512; NM_003284; Hs.3017; transition protein 1 (during h; test; CTL+s.m.
 432519; AI221311; Hs.130704; ESTs, Weakly similar to BCHUA; fibro, ovar, uter; CTL+s.m.
 432527; AW975028; Hs.102754; ESTs; pros, uter, ovar, cerv; diag
 432542; AW083920; Hs.16098; claudin 2; colon, panc; diag
 432583; AW023624; Hs.162282; potassium channel TASK-4; pota; lung; mAb
 432615; AA557191; Hs.55028; ESTs, Weakly similar to I54374; pros; diag
 432621; AJ298501; Hs.21192; ESTs, Weakly similar to T46428; pros; mAb
 432629; AW860548; Hs.280658; ESTs; ovar; diag
 432653; N62096; Hs.293185; ESTs, Weakly similar to JC7328; pros, lung; mAb+s.m.
 432666; AW024069; Hs.351118; ESTs, Weakly similar to unname; test; diag
 432706; NM_013230; Hs.286124; CD24 antigen (small cell lung; colon, ovar, pros; mAb+CTL
 432730; AI066520; Hs.131358; ESTs; test; diag
 432731; R31178; Hs.287820; fibronectin 1; panc, fibro; diag
 432788; AA521091; Hs.178499; Homo sapiens cDNA: FLJ23117 f1; lung, ovar; CTL+s.m.
 432800; BE391046; Hs.278962; AIM-1 protein; mela, pros; mAb
 432842; AW674093; Hs.334822; hypothetical protein MGC4485; blad, lung, headnk; CTL+s.m.
 432850; X87723; Hs.3110; angiotensin receptor 2 (AT2); test; mAb
 432855; AF017988; Hs.279565; secreted frizzled-related prot; panc; diag
 432867; AW016936; Hs.233364; ESTs; stom, colon; diag
 432878; BE388490; Hs.279663; Pirin; mela; CTL+s.m.
 432887; AI926047; Hs.162859; AK056805; Homo sapiens cDNA FL; pros; diag
 432938; T27013; Hs.3132; steroidogenic acute regulatory; ovar; diag
 432966; AA650114; Hs.325198; ESTs; pros; diag
 433012; NM_004045; Hs.279910; ATX1 (antioxidant protein 1, γ ; mela; diag
 433013; AI697890; Hs.127337; axin 2 (conductin, axl); colon; CTL+s.m.
 433043; W57554; Hs.125019; lymphoid nuclear protein (LAF; pros, breast; diag
 433068; NM_008456; Hs.288215; sialyltransferase; breast, ovar, mela; s.m.
 433078; AW015188; Hs.121575; Homo sapiens cDNA FLJ12231 f1; blad; diag
 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex; blad, lung, headnk, cerv; mAb
 433147; AF091434; Hs.43080; platelet derived growth factor; ovar, panc, fibro; diag
 433158; AB035898; Hs.150587; kinesin-like protein 2; ovar, uter, colon, blad; diag
 433170; AB037816; Hs.8982; KIAA1395; angio; diag
 433183; AF231338; Hs.222024; transcription factor BMAL2; lung; diag
 433228; F28212; Hs.14953; KIAA1491 protein; test; CTL+s.m.
 433258; AI806626; Hs.207300; ESTs, Weakly similar to ALUB_H; lung; diag
 433285; AW975944; Hs.237396; ESTs; breast, pros; diag
 433293; AF007835; Hs.32417; hypothetical protein MGC2742; fibro, pros, stom, panc; CTL+s.m.
 433323; AA805132; Hs.159142; ESTs; pros; diag
 433334; AI927208; Hs.231958; matrix metalloproteinase 28; panc; s.m.
 433336; AF017988; Hs.31386; secreted frizzled-related prot; ovar, fibro, headnk, lung, panc, blad; diag
 433364; AI075407; Hs.296083; ESTs, Moderately similar to IS; mela; diag
 433365; AF026944; Hs.293797; ESTs; blad; diag
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related c; angio; s.m.
 433388; AI432672; Hs.288539; hypothetical protein FLJ22191; ovar; CTL+s.m.
 433404; T32982; Hs.352670; Homo sapiens cDNA FLJ32064 f1; pros; diag
 433437; U20536; Hs.3280; caspase 6, apoptosis-related c; fibro, breast, cerv, lung, blad, panc, glio, colon; s.m.
 433444; AW975324; Hs.129816; ESTs; pros; diag
 433468; AA508353; Hs.105314; relaxin 1 (H1); pros; diag
 433485; AI493076; Hs.306098; aldo-keto reductase family 1, ; lung; s.m.
 433495; AW373784; Hs.71; α -2-glycoprotein 1, zinc; breast, pros; diag
 433576; BE080715; Hs.161091; ESTs; mela; diag
 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene; colon; diag
 433671; AW138797; Hs.132906; 19A24 protein; fibro; mAb
 433701; AW445023; Hs.15155; ESTs; test; diag
 433724; AI827749; Hs.144924; serine/threonine protein kinase; test; CTL+s.m.
 433764; AW753676; Hs.39982; zinc finger protein RINZF (NM; pros, ovar; diag
 433800; AI034361; Hs.135150; lung type-I cell membrane-assoc; glio, lung, test; mAb
 433914; AF108138; Hs.112160; Homo sapiens DNA helicase homo; test; s.m.
 434011; AW953437; Hs.5486; clone FLB5214; pros; diag
 434105; AW952124; Hs.13094; presenilins associated rhombol; lung; diag
 434217; AW014795; Hs.23349; ESTs; angio; diag
 434262; AF121858; Hs.12169; sorting nexin 8; mela; CTL+s.m.
 434274; AA628539; Hs.57783; ESTs, Moderately similar to AL; test; diag

- 434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 f1; test; diag
 434340; AI193043; Hs.353146; ESTs, Weakly similar to T17226; lung; diag
 434360; AW015415; Hs.127780; ESTs; lung; diag
 434370; AF130988; Hs.58346; ectodysplasin 1, anhidrotic re; colon, stom; diag
 434377; AW137148; Hs.306593; intron of periostin (OSF-2os); headnk; diag
 434398; AA121098; Hs.3838; serum-inducible kinase (SNK); angio, breast; CTL+s.m.
 434411; AA632649; Hs.201372; ESTs; stom, leuk; diag
 434414; AI798376; gb:tr34b07.x1 NCL_CGAP_Ov23 Ho; lung, test, colon; diag
 434423; NM_006769; Hs.3844; LIM domain only 4; panc; diag
 434449; AW953484; Hs.3849; hypothetical protein FLJ22041; sarc; diag
 434487; AF143867; Hs.337588; ESTs, Moderately similar to S6; blad; mAb+s.m.
 434596; T59638; gb:cyb55g12.s1 Stratagene ovary; angio; s.m.
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; test; CTL+s.m.
 434609; R76593; gb:yi60c11.r1 Soares placenta; pros; diag
 434636; AA083764; Hs.349208; hypothetical protein MGC3178; angio; diag
 434649; AA738254; Hs.165390; ESTs, Highly similar to A40350; test; diag
 434665; AA642125; Hs.74502; gb:nr60c01.s1 NCL_CGAP_Lym3 Ho; panc; diag
 434666; AF151103; Hs.112259; T cell receptor gamma locus; pros; mAb+s.m.
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 f1; panc; diag
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphat; melar; s.m.
 434846; AW295389; Hs.119768; ESTs; angio; diag
 434876; AF160477; Hs.61460; Ig superfamily receptor LNIR; lung, blad; mAb
 434927; H46612; Hs.293815; Homo sapiens HSPC285 mRNA, par; angio; diag
 434973; AW449285; Hs.313636; EST; pros; diag
 435045; BE297155; Hs.143698; ESTs; test; diag
 435047; AA454985; Hs.54973; cadherin-like protein VR20; pros; mAb
 435066; BE261750; Hs.4747; dyskeratosis congenita 1, dysk; colon; CTL+s.m.
 435080; AI831760; Hs.155111; hypothetical protein FLJ14428; renal; mAb
 435094; AI560129; Hs.289008; EST; ovar, cerv; diag
 435099; AC004770; Hs.4756; flap structure-specific endonu; blad, test, melar; CTL+s.m.
 435140; AA668123; Hs.134170; ESTs; fibro; diag
 435159; AA668879; Hs.116649; ESTs; lung; diag
 435206; AI432364; Hs.160594; ESTs; test; diag
 435243; AW292886; Hs.348932; hypothetical protein dJ434014; cerv, headnk; diag
 435282; N20514; Hs.172965; ESTs; melar; diag
 435299; AI745458; Hs.343026; ESTs, Weakly similar to T20593; fibro; diag
 435479; AF197137; Hs.155101; ATP synthase, H transporting; pros; s.m.
 435496; AW840171; Hs.265398; PAR-6 beta; breast, panc, ovar; diag
 435563; AF210317; Hs.95497; solute carrier family 2 (facil; blad; mAb+s.m.
 435575; AF213457; Hs.44234; triggering receptor expressed; fibro; mAb+s.m.
 435602; AF217515; Hs.283532; uncharacterized bone marrow pr; test; diag
 435615; Y15065; Hs.4975; potassium voltage-gated channel; glio; mAb
 435652; N32388; Hs.334370; uncharacterized hypothalamus p; panc; diag
 435793; AB037734; Hs.4993; KIAA1313 protein; ovar, lung, uter; diag
 435849; BE305242; Hs.16098; claudin 2; colon, panc; diag
 435876; AW812586; Hs.160271; G protein-coupled receptor 48; pros; mAb
 435897; AF269223; Hs.128322; l-complex 11 (a murine top hom; test; diag
 435904; AF261655; Hs.8910; 1,2-alpha-mannosidase IC; blad; s.m.
 435918; AF263538; Hs.86232; growth differentiation factor; test; diag
 435974; U29690; Hs.37744; Homo sapiens beta-1 adrenergic; pros, EWS; mAb+s.m.
 436032; AA150797; Hs.109276; latexin protein; panc, angio; diag
 436063; AK000028; Hs.356100; ribosomal protein S24; pros; diag
 436120; AI248193; Hs.119860; ESTs; fibro; diag
 436199; R38946; Hs.127951; hypothetical protein FLJ14503; renal; diag
 436246; AW450963; Hs.119991; ESTs; blad; diag
 436251; BE151065; Hs.296585; nucleolar protein (PKE/D repeat; colon, test, blad; CTL+s.m.
 436278; BE396290; Hs.5097; synaptogyrin 2; pros; mAb
 436291; BE568452; Hs.344037; protein regulator of cytokines; lung, blad, headnk; diag
 436293; AI601188; Hs.306201; ESTs; blad; diag
 436302; AL355841; Hs.99330; hypothetical protein FLJ23588; lung; diag
 436315; BE390513; Hs.27935; hypothetical protein MGC4837; melar; diag
 436396; AI683487; Hs.152213; wingless-type MMTV integration; lung, headnk, pros, panc; diag
 436420; AA443966; Hs.31595; ESTs; angio; mAb
 436476; AA326108; Hs.33829; bHLH protein DEC2; panc; diag
 436511; AA721252; Hs.291502; ESTs; lung; diag
 436553; AW407157; Hs.181125; immunoglobulin lambda locus; lung; diag
 436569; BE439539; Hs.301961; glutathione S-transferase M2 (l; blad; s.m.
 436614; AW104388; Hs.149091; ESTs; melar; CTL+s.m.
 436700; AI693690; Hs.301406; hypothetical protein PP3501; melar; mAb
 436729; BE621807; Hs.351316; transmembrane 4 superfamily me; panc, colon, stom, ovar, lung, blad; mAb
 436772; AW975688; Hs.348918; metallothionein 1E (functional; angio; diag
 436775; AA731111; Hs.372225; ESTs; uter, ovar; diag
 436839; AA767346; Hs.372277; ESTs; lung; diag
 436856; AI469355; Hs.127310; ESTs; melar; diag
 436954; AA740151; Hs.130425; ESTs; fibro, uter, ovar; diag
 436972; AA284679; Hs.25640; claudin 3; ovar, lung, pros; mAb
 437052; AA861697; Hs.120591; ESTs; pros; diag
 437099; N77793; Hs.48659; ESTs, Highly similar to S14458; test; diag
 437100; AI761073; Hs.14535; Homo sapiens cDNA: FLJ22314 f1; panc, renal; diag
 437119; AI379921; Hs.177043; XP_171387 similar to rhotekin; fibro; diag
 437145; AF007216; Hs.5462; solute carrier family 4, sodiu; panc, pros, stom; mAb
 437155; AI916600; Hs.121194; Homo sapiens cDNA: FLJ21569 f1; stom, renal, colon; diag
 437181; AI306615; Hs.125343; ESTs, Weakly similar to KIAA07; blad; mAb+s.m.

- 437204; AL110216; Hs.355961; ESTs, Weakly similar to I55214; lung; CTL+s.m.
 437212; AI785021; Hs.210775; ESTs; renal, uter, ovar; diag
 437224; AL117628; Hs.97808; ESTs; test; diag
 437259; AI377755; Hs.120695; ESTs; lung; diag
 437267; AW511443; Hs.258110; ESTs; BPH; diag
 437269; AA334384; Hs.149420; ESTs; angio; diag
 437330; AL353944; Hs.50115; Homo sapiens mRNA; cDNA DKFZp7; sarc; diag
 437381; NM_003684; Hs.5591; MAP kinase-interacting serine; glio; CTL+s.m.
 437390; AI125859; Hs.112607; ESTs; lung; diag
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp5; lung; diag
 437435; AA249439; Hs.27027; hypothetical protein DKFZp762H; lung; diag
 437437; AA226869; Hs.351623; hypothetical protein DKFZp762L; test; CTL+s.m.
 437478; AL390172; Hs.317432; branched chain aminotransferase; angio; s.m.
 437553; AI829535; Hs.130497; ESTs, Weakly similar to MAT8_H; blad; mAb
 437571; AA760894; Hs.125350; ESTs; pros; diag
 437623; D63880; Hs.5719; chromosome condensation-relate; test; diag
 437740; AA810265; Hs.122915; ESTs; mela; diag
 437802; AI475995; Hs.122910; ESTs; panc; diag
 437862; AW978107; Hs.5884; Homo sapiens mRNA; cDNA DKFZp5; mela; CTL+s.m.
 437908; AI082424; Hs.351043; ESTs; test; diag
 437915; AI637993; Hs.202312; Homo sapiens clone N11 Ntera2D; lung, headnk, ovar, blad, uter; diag
 437931; AI249458; Hs.124434; ESTs; blad; diag
 437935; AW939591; Hs.5940; mucin 13, epithelial transmembr; colon, stom, uter, panc; mAb+s.m.
 437938; AI950087; Hs.369628; gbawq05c02.x1 NCI_CGAP_KGd12 H; renal, ovar, uter, cerv, blad; diag
 437939; AW298600; Hs.64313; ESTs, Weakly similar to S59501; angio; mAb+s.m.
 437960; AI669586; Hs.369312; ESTs; uter, ovar; diag
 438167; R28363; Hs.24286; chemokine binding protein 2 (C; ovar, breast, uter; mAb
 438199; AW016531; Hs.122147; hypothetical protein FLJ13189; breast; diag
 438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nucl; mela; mAb+s.m.
 438233; W52448; Hs.56147; ESTs; pros, cerv; diag
 438274; AI918906; Hs.55080; ESTs; headnk; diag
 438403; AA806607; Hs.292206; ESTs; lung; mAb
 438438; AA257992; Hs.50651; Janus kinase 1 (a protein tyro; EWS; s.m.
 438450; AI050856; Hs.65853; nodal, mouse, homolog; test; diag
 438456; AA913381; Hs.279763; ESTs; test; diag
 438552; AJ245820; Hs.6314; type I transmembrane receptor; pros, ovar; diag
 438670; AI275803; Hs.123428; ESTs; fibro; CTL+s.m.
 438702; AI879064; Hs.7164; ESTs; lung; diag
 438707; L08239; Hs.5326; amino acid system N transport; ovar; mAb
 438746; AI885815; Hs.184727; Human melanoma-associated anti; panc, blad, mela, ovar; mAb+CTL
 438817; AI023799; Hs.163242; ESTs; ovar, uter, blad, renal; diag
 438859; AI559626; Hs.93522; Homo sapiens mRNA for KIAA1647; renal; diag
 438866; U44385; Hs.6441; tissue inhibitor of metallopro; mela; diag
 438873; AI302471; Hs.124292; Homo sapiens cDNA: FLJ23123 f1; fibro; diag
 438898; AI819863; Hs.106243; ESTs; lung; diag
 438915; AA280174; Hs.355711; Williams-Beuren syndrome chrom; lung, test, mela; diag
 438929; AW195515; Hs.253177; ESTs; renal; diag
 438956; W00847; Hs.135056; Human DNA sequence from clone; lung; diag
 438966; AW979074; ; gb-EST391184 MAGE resequences; renal; diag
 438983; AF085884; Hs.20029; proacrosin binding protein sp3; test; CTL+s.m.
 438993; AA828995; ; gb-rod77b08.s1 NCI_CGAP_Ov2 Hom; ovar; mAb+s.m.
 439053; BE244588; Hs.6456; chaperonin containing TCP1, su; test; diag
 439092; AA830149; ; gb-oc44f08.s1 NCI_CGAP_GCB1 Ho; pros; diag
 439176; AI446444; Hs.190394; ESTs, Weakly similar to B28096; pros; diag
 439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic; breast, ovar, uter, pros, blad, panc, colon, fibro, mela; mAb
 439221; AA737108; Hs.32250; ESTs, Moderately similar to I7; EWS; s.m.
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582; mela, fibro; diag
 439239; AI031540; Hs.235331; ESTs; blad; diag
 439285; AL133916; Hs.47860; hypothetical protein FLJ20093; lung, breast; diag
 439310; AF086120; Hs.102793; ESTs; mela; diag
 439318; AW837046; Hs.6527; G protein-coupled receptor 56; colon, breast, ovar, uter, cerv, pros, lung, headnk, blad, mela; mAb+s.m.
 439335; AA742697; Hs.62492; NM_052863; Homo sapiens secretor; fibro, uter; diag
 439366; AF100143; Hs.6540; fibroblast growth factor 13; pros; CTL+s.m.
 439382; BE247684; Hs.103070; ESTs; angio; diag
 439394; AA149250; Hs.56105; ESTs; lung; diag
 439410; AA632012; Hs.188748; ESTs; angio; diag
 439453; BE264974; Hs.6566; thyroid hormone receptor inter; lung, esoph, ovar; mAb+s.m.
 439496; BE616501; Hs.32343; Homo sapiens, Similar to RIKEN; mela, esoph; diag
 439559; AW970780; Hs.59483; leucine-rich repeat-containing; ovar, stom, mela, colon; mAb
 439568; AI091277; Hs.302634; frizzled (Drosophila) homolog; ovar, uter; mAb
 439570; AF088076; Hs.59507; ESTs, Weakly similar to AC0048; lung, headnk, cerv; diag
 439702; AW085525; Hs.55964; ESTs; mela; diag
 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_H; ovar, lung, headnk; diag
 439735; AI635386; Hs.142846; hypothetical protein; pros; diag
 439737; AI751438; Hs.41271; Homo sapiens mRNA full length; panc; diag
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length; panc, fibro, breast; diag
 439755; AW748482; Hs.77873; B7 homolog 3; sarc; mAb
 439759; AL359055; Hs.67709; Homo sapiens mRNA full length; colon, stom, panc, leuk, lung; diag
 439778; AI109729; Hs.99364; putative transmembrane protein; pros; mAb+s.m.
 439780; AI109688; ; gb-Homo sapiens mRNA full leng; blad, esoph; diag
 439820; AL360204; Hs.283853; Homo sapiens mRNA full length; ovar, uter, cerv, breast, pros; diag
 439864; AI720078; Hs.291997; ESTs, Weakly similar to A47582; test; diag
 439867; AA847510; Hs.161292; ESTs; panc; diag

- 439920; H05430; Hs.288433; neurotrophin; panc; mAb+diag
 439926; AW014875; Hs.137007; ESTs; blad, esoph, lung, cerv; diag
 439963; AW247529; Hs.6793; platelet-activating factor ace; breast, lung, blad; s.m.
 440042; A1073387; Hs.133898; ESTs; ovar; CTL+s.m.
 440066; NM_005402; Hs.6906; v-rat simian leukemia viral on; angio; diag
 440099; AL080058; Hs.6909; DKFZP584G202 protein; panc; diag
 440119; AA865455; Hs.125331; ESTs, Moderately similar to un; test; diag
 440138; AB033023; Hs.318127; hypothetical protein FLJ10201; lung; CTL+s.m.
 440151; AA868167; gb:ak38e07.s1 Soares_testis_NH; sarc; diag
 440207; A1371978; Hs.128326; ESTs; test; diag
 440209; H05049; Hs.247837; neurexin 3; fibro; diag
 440210; AW674562; Hs.122128; ESTs; glio; diag
 440225; BE295782; Hs.159; tumor necrosis factor receptor; glio; mAb
 440238; AW451970; Hs.155644; paired box gene 2; ovar; diag
 440260; A1972867; Hs.7130; copine IV; pros; diag
 440273; A1805392; Hs.325335; Homo sapiens cDNA: FLJ23523 f; lung, fibro; diag
 440274; R24595; Hs.7122; scrapie responsive protein 1; sarc; diag
 440311; A1733079; Hs.125407; ESTs, Moderately similar to AL; renal; diag
 440325; NM_003812; Hs.7164; a disintegrin and metalloprote; lung; mAb
 440333; A1378424; Hs.288761; hypothetical protein FLJ121749; pros; CTL+s.m.
 440449; AA885430; Hs.201925; Homo sapiens cDNA FLJ13446 f; breast; diag
 440452; A1925136; Hs.55150; ESTs, Weakly similar to CAYP_H; fibro; diag
 440457; BE387593; Hs.21321; Homo sapiens clone FLB9213 PRO; mel; diag
 440484; BE328156; Hs.150356; ESTs; panc; diag
 440529; AW207640; Hs.16478; Homo sapiens cDNA: FLJ21718 f; pros; diag
 440659; AF134160; Hs.7327; claudin 1; lung; mAb
 440704; M69241; Hs.162; insulin-like growth factor bin; lung, glio, ovar; diag
 440773; AA352702; Hs.37747; Homo sapiens, Similar to RIKEN; test; diag
 440801; AA906366; Hs.370038; ESTs; pros; diag
 440819; A1809444; Hs.202108; ESTs; pros; diag
 440901; AA909358; Hs.128812; ESTs; ovar, pros; diag
 440943; AW082298; Hs.146161; hypothetical protein MGC2408; lung; diag
 440983; M20581; Hs.7594; sokuie carrier family 2 (facil; test; mAb
 441020; W79283; Hs.35962; ESTs; lung, panc; diag
 441031; A110684; Hs.7645; fibrinogen, B beta polypeptide; lung, panc, colon; CTL+s.m.
 441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 f; panc, ovar, stom, uter, lung; diag
 441134; W29092; Hs.346950; cellular retinoic acid-binding; sarc; diag
 441247; AW118681; Hs.128051; Homo sapiens thymic stromal ly; pros; diag
 441321; H17182; Hs.7771; B-cell associated protein; test; diag
 441345; AW068579; Hs.7780; Homo sapiens mRNA; cDNA DKFZp5; pros; diag
 441350; AB020690; Hs.7782; paraneoplastic antigen MA2; panc; mAb+CTL
 441377; BE218239; Hs.202656; ESTs; uter, endo, lung; diag
 441384; AA447849; Hs.288660; retinoic acid induced 3; ovar; mAb+s.m.
 441392; AW451831; Hs.222119; ESTs, Weakly similar to S30433; renal; diag
 441457; AW996651; Hs.43838; ESTs; angio; diag
 441495; AW294603; Hs.127039; ESTs; blad; diag
 441525; AW241867; Hs.127728; ESTs; lung; diag
 441553; AA281219; Hs.121296; ESTs; lung, test, ovar; CTL+s.m.
 441633; AW958544; Hs.112242; normal mucosa of esophagus spe; blad, lung, cerv, headnk, colon, panc; diag
 441790; AW294909; Hs.132208; ESTs; lung; diag
 441801; AW242799; Hs.86356; ESTs; blad; diag
 441835; AB036432; Hs.184; advanced glycosylation end pro; fibro; mAb
 441859; AW194364; Hs.380444; Interleukin-4 induced gene-1 p; ovar, mel, fibro; mAb
 441878; A1801869; Hs.127982; ESTs; test; diag
 442006; AW975183; Hs.372210; ESTs, Weakly similar to S72482; fibro, angio; CTL+s.m.
 442082; R41823; Hs.7413; calyntenin-2; breast, pros, ovar; diag
 442104; L20971; Hs.188; phospholipase 4B, cAMP-spe; angio; CTL+s.m.
 442108; AW452649; Hs.343259; ESTs; lung; diag
 442242; AV647908; Hs.90424; Homo sapiens cDNA: FLJ23285 f; BPH; diag
 442323; AW016669; Hs.29190; ESTs; breast; diag
 442333; A1650877; Hs.129302; ESTs; test; diag
 442432; BE093589; Hs.38178; hypothetical protein FLJ23468; blad, lung, panc, esoph, mel; CTL+s.m.
 442438; AA995998; Hs.370007; gb:os26b03.s1 NCL_CGAP_Kds H; uter, ovar, renal; diag
 442441; A1820662; Hs.129598; ESTs; breast; diag
 442503; AF147078; Hs.375031; p53-responsive gene 5; mel; diag
 442506; BE566411; Hs.41726; ESTs; angio; diag
 442573; H93366; Hs.7567; branched chain aminotransferas; ovar, panc, angio, test; s.m.
 442577; AA282998; Hs.163900; ESTs; blad, panc, colon, stom, ovar; diag
 442580; A1733682; Hs.130239; ESTs; breast; diag
 442609; AL020996; Hs.8518; selenoprotein N; mel; diag
 442613; A1004002; Hs.130522; Kv channel-interacting protein; glio; diag
 442622; NM_000435; Hs.8546; Notch (Drosophila) homolog 3; ovar; mAb
 442711; AF151073; Hs.8645; hypothetical protein; angio, mel, sarc; diag
 442739; NM_007274; Hs.8679; cytosolic acyl coenzyme A thio; mel; s.m.
 442757; A1739528; Hs.28345; ESTs; mel; diag
 442818; AK001741; Hs.8739; hypothetical protein FLJ10879; breast; diag
 442821; BE391929; Hs.8752; transmembrane protein 4; ovar; diag
 442832; AW206560; Hs.253569; ESTs; pros, fibro; diag
 442896; R37725; Hs.283093; ESTs; panc; diag
 442994; A1026718; Hs.16954; ESTs; blad, fibro; diag
 443054; A1745185; Hs.84520; yes-associated protein 65 kDa; blad; diag
 443162; T49951; Hs.9029; DKFZP434G032 protein; blad, lung; CTL+s.m.
 443171; BE281128; Hs.9030; TONDU; blad, ovar; diag

- 443184; AI638728; Hs.135159; ESTs; sarc; diag
 443211; AI128388; Hs.143655; ESTs; blad, ovar, lung, headnk, stom, colon; diag
 443216; W80487; Hs.324521; hypothetical protein DC50; test; diag
 443257; AI334040; Hs.11614; HSPC065 protein; fibro; CTL+s.m.
 443400; R28424; Hs.250648; ESTs; lung; diag
 443523; AK001575; Hs.9536; hypothetical protein FLJ10713; test; CTL+s.m.
 443537; D13305; Hs.203; cholecystokinin B receptor; test; mAb
 443648; AI085377; Hs.143610; ESTs; lung, headnk; diag
 443709; AI082692; Hs.134662; ESTs; fibro; diag
 443715; AI583187; Hs.9700; cyclin E1; lung, stom, ovar, colon; CTL+s.m.
 443785; AW449552; Hs.190125; basic-helix-loop-helix-PAS pro; glio, uter, ovar; CTL+s.m.
 443802; AW504924; Hs.9805; KIAA1291 protein; sarc; diag
 443883; AA114212; Hs.9930; serine (or cysteine) proteinase; sarc; s.m.
 443885; H91806; Hs.15284; ESTs; melar; diag
 443892; AI889572; Hs.246875; ESTs; lung; diag
 443950; NM_001425; Hs.9999; epithelial membrane protein 3; melar; mAb
 443968; AA287702; Hs.10031; KIAA0955 protein; angio; diag
 443983; H04482; Hs.163724; ESTs; melar; mAb
 443991; NM_002250; Hs.10082; potassium intermediate/small c; pros, colon, uter; mAb
 444009; AI380792; Hs.135104; ESTs; angio; diag
 444151; AW972917; Hs.128749; alpha-methylacyl-CoA racemase; pros; mAb
 444159; AF116846; Hs.10431; dead ringer (Drosophila)-like; test; CTL+s.m.
 444163; AI126098; ; FGENESH predicted RNaseH domain; blad; s.m.
 444301; AK000136; Hs.10760; asporin (LRR class 1); panc; diag
 444325; AW152618; Hs.16757; ESTs; esoph; diag
 444330; AI597655; Hs.49265; ESTs; angio; diag
 444342; NM_014398; Hs.10887; similar to lysosome-associated; hepC, lung, fibro, blad, esoph; diag
 444378; R41339; Hs.47860; neurotrophic tyrosine kinase, ; lung, glio; mAb+s.m.
 444409; AI792140; Hs.49265; ESTs; angio; diag
 444444; AI149332; Hs.14855; ESTs; blad; diag
 444471; AB020684; Hs.11217; KIAA0877 protein; glio, lung, colon; mAb
 444476; AF020038; Hs.11223; isocitrate dehydrogenase 1 (NA; blad; s.m.
 444484; AK002126; Hs.11260; hypothetical protein FLJ11264; pros; diag
 444633; AF111713; Hs.12284; junctional adhesion molecule 1; ovar, uter, breast, cerv, blad, headnk; mAb
 444649; AW207523; Hs.371001; ESTs; blad; diag
 444670; H58373; Hs.332938; hypothetical protein MGC5370; sarc; diag
 444754; TB3911; Hs.11881; transmembrane 4 superfamily me; panc, omuc, stom, lung, colon; mAb+s.m.
 444809; BE207568; Hs.208219; oculostatin; melar; mAb
 444823; BE262989; Hs.12045; putative protein; test; diag
 444863; AW384082; Hs.104679; serine (or cysteine) proteinase; melar; s.m.
 444895; AI674383; Hs.22891; solute carrier family 7 (catio; ovar; mAb+s.m.
 444995; AJ272265; Hs.12230; secreted phosphoprotein 2, 24k; hepC, panc; diag
 445019; AI205540; Hs.281295; ESTs; headnk, lung, colon; diag
 445070; NM_000677; Hs.258; adenosine A3 receptor; glio, renal; mAb
 445076; AI206888; Hs.154131; ESTs; test; diag
 445084; H38914; Hs.250848; hypothetical protein FLJ14761; sarc; mAb
 445093; AI207197; Hs.156905; ESTs; test; diag
 445109; AF039916; Hs.12330; ecdonucleoside triphosphate di; pros; s.m.
 445119; AF035121; Hs.12337; kinase insert domain receptor; angio; mAb
 445160; AI299144; Hs.101937; sine oculis homeobox (Drosophila); sarc; CTL+s.m.
 445182; AW189787; Hs.361778; ESTs; blad; diag
 445247; AW274290; Hs.153997; ESTs; melar; diag
 445279; R41900; Hs.22245; ESTs; angio; diag
 445363; NM_005993; Hs.12570; tubulin-specific chaperone d; test; diag
 445413; AA151342; Hs.12677; CGI-147 protein; pros, colon, uter, ovar, lung, panc; diag
 445418; AW139377; Hs.127179; cryptic gene; panc; diag
 445424; AB028945; Hs.12696; cortactin SH3 domain-binding p; pros; diag
 445443; AV653838; Hs.295131; ESTs; lung; diag
 445654; X91247; Hs.13046; thioredoxin reductase 1; lung; s.m.
 445684; AK001696; Hs.13109; Ran binding protein 11; angio; diag
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; angio; CTL+s.m.
 445784; AI253155; Hs.146065; ESTs; melar; CTL+s.m.
 445885; AI734009; Hs.127699; KIAA1603 protein; pros, fibro; diag
 445900; AF070526; Hs.125036; Homo sapiens clone 24787 mRNA; renal, leuk; mAb
 445911; AI985987; Hs.145645; ESTs, Moderately similar to AL; blad; diag
 445982; BE410233; Hs.13501; pescadillo (zebrafish) homolog; melar; diag
 446057; AI420227; Hs.366053; Trp-p8 transient receptor pote; pros; mAb
 446082; AI274139; Hs.156452; ESTs; blad; diag
 446098; AW072215; Hs.208470; ESTs; angio; diag
 446100; AW957109; Hs.13804; hypothetical protein dJ462023; pros; diag
 446102; AW168067; Hs.317694; ESTs; lung; diag
 446113; AW957553; Hs.323518; Homo sapiens mRNA for FLJ00083; test; mAb
 446269; AW263155; Hs.14559; hypothetical protein FLJ10540; lung, headnk; CTL+s.m.
 446291; BE397753; Hs.14623; interferon, gamma-inducible p; melar; diag
 446292; AF081497; Hs.279682; Rh type C glycoprotein; lung, cerv; mAb
 446293; AI420213; Hs.149722; LIM domain transcription factor; ovar, test; diag
 446320; AF126245; Hs.14791; acyl-Coenzyme A dehydrogenase; pros; s.m.
 446332; AK001635; Hs.14838; hypothetical protein FLJ10773; breast; diag
 446342; BE298665; Hs.14846; solute carrier family 7 (catio; uter, colon, pros, melar; mAb
 446428; AW082270; Hs.12496; ESTs, Weakly similar to ALL4_H; fibro; diag
 446528; AU076640; Hs.15243; nucleolar protein 1 (120kD); lung, test; diag
 446608; N75217; Hs.175622; ESTs; uter, fibro; diag
 446626; AW292180; Hs.156142; ESTs; pros; diag

- 446636; AC002563; Hs.15767; citron (rho-interacting, serin; lung; CTL+s.m.
 446644; NM_003272; Hs.21065; transmembrane 7 superfamily me; mela; mAb
 446673; NM_016361; Hs.15871; LPAP for lysophosphatidic acid; blad; diag
 446727; AB011095; Hs.16032; KIAA0523 protein; angio; CTL+s.m.
 446733; AA853360; Hs.26040; ESTs, Weakly similar to fatty; breast; s.m.
 446755; AW451473; Hs.16134; serine/threonine kinase 10; mela; CTL+s.m.
 446791; AI632278; Hs.195922; ESTs; test; diag
 446839; BE091926; Hs.16244; mitotic spindle coiled-coil re; test; diag
 446856; AI814373; Hs.164175; ESTs; lung; diag
 446868; AV660737; Hs.348297; ESTs; panc; diag
 446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G; lung; mAb
 446932; AA961459; Hs.125644; ESTs; fibro; diag
 446967; AI699629; Hs.156781; ESTs; fibro; diag
 446979; AI654443; Hs.197683; ESTs; test; diag
 446984; AB020722; Hs.16714; Rho guanine exchange factor (G; angio; CTL+s.m.
 446989; AK001898; Hs.16740; hypothetical protein FLJ11036; lung, headnk; diag
 446998; N99013; Hs.278966; Homo sapiens mRNA; cDNA DKFZp5; panc, fibro; diag
 446999; AA151520; Hs.351416; hypothetical protein MGC4485; headnk; diag
 447004; AW296958; Hs.157539; FGENESH predicted secreted pro; glio; diag
 447078; AW885727; Hs.9914; ESTs; lung; diag
 447126; AW150632; Hs.170307; Ral guanine nucleotide exchange; angio; diag
 447164; AF026941; Hs.17518; vipirin; similar to inflammat; colon, lung, breast, stom, hepC, esoph, mela; diag
 447178; AW594641; Hs.192417; ESTs; mela; diag
 447188; H65423; Hs.17631; hypothetical protein DKFZp434E; test; diag
 447210; AF035269; Hs.17752; phosphatidylserine-specific ph; pros, mela; s.m.
 447269; AW247017; Hs.36978; melanoma antigen, family A, 3; lung, mela; mAb+CTL
 447334; AA515032; Hs.91109; ESTs; blad; diag
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392; lung, blad, panc, headnk, mela; mAb+s.m.
 447350; AJ375572; Hs.172634; v-erb-a avian erythroblastic t breast, ovar, uter; diag
 447377; X77343; Hs.334334; transcription factor AP-2 alpha; breast, lung, mela; CTL+s.m.
 447395; AI418412; Hs.184793; Homo sapiens cDNA: FLJ21880 f; panc; diag
 447437; U07225; Hs.339; purinergic receptor P2Y, G-pro; blad; mAb
 447499; AW262580; Hs.147674; protocadherin beta 16; pros, glio, ovar; mAb+s.m.
 447532; AK000614; Hs.18791; hypothetical protein FLJ20607; lung, blad; CTL+s.m.
 447534; AW953935; Hs.288655; ESTs; lung, test; diag
 447578; AA912347; Hs.136585; ESTs, Weakly similar to JC5314; ovar; s.m.
 447595; AW379130; Hs.18953; phosphodiesterase 9A; pros; CTL+s.m.
 447604; AW089933; Hs.301342; hypothetical protein MGC4342; mela; diag
 447636; Y10043; Hs.19114; high-mobility group (nonhiston; lung; CTL+s.m.
 447733; AF157482; Hs.19400; MAD2 (mitotic arrest deficient; test; diag
 447749; T53260; Hs.8297; ESTs; renal; diag
 447761; AF061573; Hs.19492; protocadherin 8; EWS, glio; mAb
 447768; X86400; Hs.19520; FYD domain-containing ion tra; renal; mAb
 447818; W79940; Hs.355279; Homo sapiens clone 24570 mRNA; renal; diag
 447835; AW591623; Hs.164129; ESTs, Weakly similar to I38022; renal, ovar, uter; diag
 447881; BE620886; Hs.355279; GCN1 (general control of amino; renal; diag
 447937; AL109716; Hs.20034; Homo sapiens mRNA full length; mela; mAb
 447993; AW139525; Hs.170362; ESTs; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 448030; N30714; Hs.325960; membrane-spanning 4-domains, s; panc, leuk, renal, stom lung; mAb
 448045; AJ297436; Hs.20166; prostate stem cell antigen; blad, panc, pros; mAb
 448105; AW591433; Hs.298241; Transmembrane protease, serine; breast, panc, colon, lung, ovar, stom; mAb+diag+s.m.
 448133; AA723157; Hs.73769; folate receptor 1 (adult); ovar, fibro; mAb
 448140; AF146761; Hs.20450; BCM-like membrane protein prec; fibro, mela, leuk; mAb
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase; test; CTL+s.m.
 448181; AF272833; Hs.279763; hypothetical protein FLJ10504; test; diag
 448204; AI475124; Hs.170561; ESTs; sarc; diag
 448231; AI701916; Hs.202509; ESTs; angio; diag
 448258; BE386983; Hs.343214; hypothetical protein FLJ20396; mela, ovar; mAb
 448262; AW880830; Hs.186273; ESTs; blad; diag
 448275; BE514434; Hs.20830; kinesin-like 2; ovar, esoph, mela; diag
 448278; W07369; Hs.11782; ESTs; lung; diag
 448290; AK002107; Hs.20843; Homo sapiens cDNA FLJ11245 f; pros; diag
 448321; NM_005883; Hs.20912; adenomatous polyposis coli lik; glio; CTL+s.m.
 448357; N20169; Hs.108923; RAB38, member RAS oncogene fam; lung, mela; diag
 448410; AK000227; Hs.21126; hypothetical protein FLJ20220; mela; diag
 448437; AW470125; Hs.220529; gbxxw60c04.x1 NCL_CGAP_Pan1 Ho; panc, colon; diag
 448499; BE613280; Hs.77550; p53-regulated DDA3; glio; diag
 448569; BE382657; Hs.21486; signal transducer and activator; panc, headnk, fibro, cerv, mela, renal; CTL+s.m.
 448588; AI970276; Hs.156905; KIAA1676; test; CTL+s.m.
 448595; AB014544; Hs.21572; KIAA0644 gene product; breast, glio; mAb
 448664; AI879317; Hs.334691; splicing factor 3a, subunit 1; mela; CTL+s.m.
 448674; W31178; Hs.154140; ovary-specific acidic protein; angio; diag
 448692; AW013907; Hs.167531; methylcrotonoyl-Coenzyme A car; pros, pros; s.m.
 448706; AW291095; Hs.21814; interleukin 20 receptor, alpha; pros, uter, blad, colon; mAb
 448719; AA033627; Hs.21858; trinucleotide repeat containin; mela, sarc; CTL+diag
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate); test; diag
 448811; AI590371; Hs.199460; ESTs; esoph, panc; mAb
 448939; BE267795; Hs.22595; hypothetical protein FLJ10637; test; CTL+s.m.
 448966; AW372914; Hs.86149; phosphoinositid 3-phosphate-b; mela; CTL+s.m.
 448981; AI968719; Hs.195387; ESTs; test; diag
 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA); pros, cerv, colon, lung, stom, blad, headnk, ovar, breast; mAb
 448993; AI471630; Hs.355952; KIAA0144 gene product; lung, blad; diag
 448999; AF179274; Hs.22791; transmembrane protein with EGF; pros, glio; mAb

- 449003; X76342; Hs.389; alcohol dehydrogenase 7 (class); lung, headnk; s.m.
 449019; AI949095; Hs.67776; ESTs, Weakly similar to T22341; blad, lung; diag
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; blad, colon, ovar; s.m.
 449040; NM_012191; Hs.22919; putative tumor suppressor; lung; CTL+s.m.
 449078; AK001256; Hs.22975; KIAA1576 protein; mel; diag
 449101; AA205847; Hs.23016; G protein-coupled receptor; lung, headnk; mAb
 449109; AW270992; Hs.120949; ESTs, Weakly similar to ALU7_H; sarc; diag
 449156; AF103907; Hs.171353; prostate cancer antigen 3, non; pros; mAb+CTL
 449207; AL044222; Hs.23255; nucleoporin 155kD; lung; diag
 449228; AJ403107; Hs.148590; protein related with psoriasis; lung; diag
 449230; BE613348; Hs.356392; melanoma cell adhesion molecu; lung, cerv, headnk, blad, ovar, colon; mAb
 449317; AW293413; Hs.132906; 19A24 protein; mel; mAb
 449318; AW236021; Hs.78531; Homo sapiens, Similar to RIKEN; headnk, lung, angio; CTL+s.m.
 449322; AI638616; Hs.195566; ESTs; test; diag
 449338; H73444; Hs.394; adrenomedullin; renal; diag
 449394; AA004368; Hs.18160; Homo sapiens cDNA FLJ11550 fis; angio; mAb
 449437; AJ702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fi; test; diag
 449448; D60730; Hs.57471; ESTs; blad, lung, headnk, breast; diag
 449467; AW205006; Hs.197042; ESTs; lung; diag
 449494; AW237014; Hs.315369; aquaporin 4; fibro; diag
 449569; AI658634; Hs.195389; ESTs; test; diag
 449592; AI655494; Hs.195718; ESTs; panc; diag
 449618; AI076459; Hs.15978; KIAA1272 protein; angio; diag
 449625; NM_014253; Hs.349094; odz (odd Oz/ten-m, Drosophila); pros; diag
 449650; AF055575; Hs.23838; calcium channel, voltage-depen; pros; mAb
 449680; AI033821; Hs.12160; ESTs; renal; diag
 449961; AW265634; Hs.133100; ESTs; glio, esoph, lung, blad; diag
 449976; H06350; Hs.135056; Human DNA sequence from clone; lung; diag
 450096; AI682088; Hs.79375; single-minded (Drosophila) hom; pros; CTL
 450098; W27249; Hs.8109; hypothetical protein FLJ21080; breast, lung, stom, uter; diag
 450149; AW969781; Hs.132683; Zic family member 2 (odd-paire; sarc; CTL+s.m.
 450152; AJ138635; Hs.22968; Intron of VEGFR; renal; diag
 450377; AB033091; Hs.355925; KIAA1265 protein; ovar, colon; diag
 450382; AA397658; Hs.60257; Homo sapiens cDNA FLJ13598 fis; pros; diag
 450400; AI694722; Hs.279744; ESTs; panc; diag
 450431; AW136797; Hs.266041; ESTs; test; diag
 450451; AW591528; Hs.202072; ESTs; uter, endo; diag
 450506; NM_004460; Hs.418; fibroblast activation protein; panc, esoph; diag
 450534; AI570189; Hs.25132; KIAA0470 gene product; angio; CTL+s.m.
 450581; AF081513; Hs.25195; TGF-beta 4; uter, cerv, test; diag
 450635; AW403954; Hs.25237; mesenchymal stem cell protein; blad; mAb
 450642; R39773; Hs.7130; copine IV; pros; diag
 450656; AA010539; Hs.18912; unnamed protein product; fibro, uter; CTL+s.m.
 450663; H43540; Hs.25292; ribonuclease H1, large subunit; mel; s.m.
 450676; AJ147155; Hs.279727; ESTs; sarc; diag
 450684; AA872605; Hs.25333; Interleukin 1 receptor, type I; blad, lung, headnk; mAb
 450690; AA296696; Hs.333418; FKDY domain-containing ion tra; mel; diag
 450693; AW450461; Hs.203965; ESTs; pros, uter; diag
 450719; AI068837; Hs.21349; ESTs, Weakly similar to RB88_H; test; diag
 450737; AW007152; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 450785; AA852713; Hs.108885; Homo sapiens, alpha-1 (VI) col; sarc; CTL+s.m.
 450832; AW970602; Hs.105421; ESTs; lung; diag
 451027; AW519204; Hs.40808; Homo sapiens, Similar to RIKEN; pros, uter, glio; diag
 451035; AU076785; Hs.430; plastin 1 (I isoform); panc; diag
 451050; AW937420; Hs.351869; ESTs; mel; diag
 451099; R52795; Hs.25954; Interleukin 13 receptor, alpha; glio, fibro, mel; mAb
 451106; BE382701; Hs.25960; N-MYC oncogene; test, ovar; CTL+s.m.
 451110; AI955040; Hs.265398; PAR-6 beta (partitioning def; breast, ovar, lung, colon; CTL+s.m.
 451181; AI796330; Hs.207461; ESTs; panc; diag
 451253; H48299; Hs.26126; claudin 10; lung, ovar, panc; mAb
 451291; R39288; Hs.6702; ESTs; lung; diag
 451295; AI557212; Hs.17132; ESTs, Moderately similar to I5; panc; diag
 451320; AW118072; Hs.350251; diacylglycerol kinase, zeta (1; lung; s.m.
 451346; NM_006338; Hs.26312; glioma amplified on chromosome; ovar; mAb
 451386; AB029006; Hs.26334; spastic paraplegia 4 (autosoma; lung; diag
 451398; AI793124; Hs.144479; ESTs; breast, ovar; diag
 451411; AA017492; Hs.135655; EST; pros; diag
 451497; H83294; Hs.284122; Wnt inhibitory factor-1; uter, fibro, pros, colon, sarc; diag
 451541; BE279383; Hs.26557; plakophilin 3; lung, blad, ovar; diag
 451592; AB05416; Hs.213897; ESTs; lung, headnk; diag
 451635; AA018899; Hs.127179; cryptic gene; panc; diag
 451663; AI872360; Hs.209293; ESTs; pros; diag
 451720; AW970985; Hs.290853; ESTs; pros; diag
 451743; AW074266; Hs.336428; ESTs; lung; diag
 451820; AW058357; Hs.199248; ESTs; panc; mAb
 451844; T61430; ; gbyc06a03.s1 Stratagene lung; blad; diag
 451982; F13036; Hs.27373; Homo sapiens mRNA; cDNA DKFZp6; pros, blad; mAb
 451999; AW176401; Hs.380623; DEAD/H (Asp-Glu-Ala-Asp/His) b; test; CTL+s.m.
 452046; AB018345; Hs.27657; KIAA0802 protein; lung, uter; CTL+s.m.
 452208; AA024792; Hs.31895; hypothetical protein MGC4093; renal; diag
 452240; AI591147; Hs.61232; ESTs; blad, lung, headnk, panc, cerv; diag
 452243; AL355715; Hs.28555; programmed cell death 9 (PDCD9; breast; diag
 452244; N33530; Hs.176674; ESTs; mel; diag

- 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S; test; CTL+s.m.
 452295; BE379936; Hs.28866; programmed cell death 10; lung; diag
 452298; AI039243; Hs.278585; ESTs; angio; diag
 452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590; lung, panc, blad, stom, esoph, fibro, colon; s.m.
 452316; AA298484; Hs.61265; ESTs, Moderately similar to G7; blad; diag
 452340; NM_002202; Hs.505; ISL1 transcription factor, LIM; panc, pros; CTL+s.m.
 452353; C18825; Hs.29191; epithelial membrane protein 2; pros, breast; mAb
 452355; N54926; Hs.29202; G protein-coupled receptor 34; glio, fibro, panc; mAb
 452367; U71207; Hs.29279; eyes absent (Drosophila) homolog; lung, pros, ovar, uter; CTL+s.m.
 452416; AA026115; Hs.114777; ESTs; fibro; diag
 452461; N78223; Hs.108105; transcription factor; blad, lung, headnk, ovar, glio, stom, colon, cerv; CTL+s.m.
 452571; W31518; Hs.34665; ESTs; stom, lung, panc, colon, fibro; diag
 452594; AU076405; Hs.29981; solute carrier family 26 (sulf; ovar; mAb
 452613; AA61559; Hs.23459; ESTs; lung; diag
 452679; Z42387; Hs.63883; transmembrane, prostate androg; pros, colon, panc, pros; mAb
 452705; H49805; Hs.246005; ESTs; panc; diag
 452717; AW160399; Hs.30376; hypothetical protein; pros; diag
 452721; AJ269529; Hs.301871; solute carrier family 37 (glyc; pros; mAb
 452732; BE300078; Hs.80449; Homo sapiens, clone IMAGE:3535; blad; diag
 452744; AI267652; Hs.246107; Homo sapiens mRNA; cDNA DKFZp4; melar; diag
 452792; AB037765; Hs.30652; KIAA1344 protein; pros, uter, breast; diag
 452795; AW392555; Hs.18878; hypothetical protein FLJ21620; renal, headnk, colon, lung, panc; CTL
 452796; AB011100; Hs.30656; KIAA0528 gene product; test; diag
 452833; BE559681; Hs.30735; KIAA0124 protein; lung, melar; CTL+s.m.
 452865; AJ924046; Hs.119567; ESTs, Weakly similar to A47582; lung; diag
 452899; M96739; Hs.30956; nescient helix loop helix 1; sarc; CTL+s.m.
 452924; AW580939; Hs.97199; complement component C1q recep; angio; diag
 452933; AW391423; Hs.288555; Homo sapiens cDNA: FLJ22425 f1; angio; CTL+s.m.
 452934; AA581322; Hs.4213; hypothetical protein MGC16207; lung, blad; diag
 452955; AW390282; Hs.31130; transmembrane 7 superfamily me; pros; mAb+s.m.
 453008; AJ362575; Hs.303171; ESTs; pros; diag
 453028; AB006532; Hs.31442; RecQ protein-like 4; blad, lung, test; CTL+s.m.
 453085; AW954243; Hs.351573; KIAA0251 protein; angio; diag
 453096; AW294631; Hs.351270; ESTs; pros; diag
 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog; lung, headnk, colon; mAb
 453107; NM_016113; Hs.279746; vanilloid receptor-like prota; melar; mAb
 453134; AA032211; Hs.118493; ESTs; blad; diag
 453142; AA033648; Hs.7473; Homo sapiens gap junction prot; fibro; mAb
 453160; AI263307; Hs.356901; H2B histone family, member L; lung, panc, pros; diag
 453210; AL133161; Hs.32360; hypothetical protein FLJ10867; lung; CTL+s.m.
 453216; AL137566; Hs.32405; progesterone receptor (PR); blad; mAb+s.m.
 453256; AI565587; Hs.32556; KIAA0379 protein; melar; diag
 453310; X70697; Hs.553; solute carrier family 6 (neuro; fibro; mAb
 453321; AI984381; Hs.232521; ESTs; blad; diag
 453323; AF034102; Hs.32951; solute carrier family 29 (nuc; ovar; CTL+s.m.
 453331; AI240665; Hs.352537; ESTs; breast, lung, panc, esoph; mAb+diag+s.m.
 453344; BE349075; Hs.44571; ESTs; melar; diag
 453348; BE272318; Hs.8595; hypothetical protein FLJ12438; test; CTL+s.m.
 453365; AA035211; Hs.17404; SOX7 SRY (sex determining reg; angio, blad; CTL+s.m.
 453370; AI470523; Hs.139336; ATP-binding cassette, sub-fam; pros; mAb
 453389; BE273848; Hs.32963; cadherin 6, type 2, K-cadherin; renal, ovar, blad; mAb+s.m.
 453392; U23752; Hs.32964; SRY (sex determining region Y); ovar, lung, glio, sarc; CTL+s.m.
 453459; BE047032; Hs.257789; ESTs; ovar, cerv, blad, uter, panc, angio, lung; diag
 453464; AI884911; Hs.32989; receptor (calcitonin) activity; pros; mAb
 453633; AA357001; Hs.34045; hypothetical protein FLJ20764; lung, esoph, test; diag
 453637; NM_002589; Hs.34073; BH-protocadherin (brain-heart); headnk; mAb
 453642; AJ370936; Hs.34074; dipeptidylpeptidase VI; glio; mAb
 453779; N35187; Hs.43388; 28kD interferon responsive pro; melar; diag
 453789; AA628517; Hs.118502; ESTs; angio; diag
 453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1; glio, lung, uter, headnk, cerv, panc, pros, sarc; mAb
 453883; AI638516; Hs.347524; cofactor required for Sp1 tran; blad, lung; diag
 453884; AA355925; Hs.36232; KIAA0186 gene product; lung, ovar, test, esoph; diag
 453912; AL121031; Hs.356843; SWI/SNF related, matrix associ; melar; diag
 453922; AF053308; Hs.36708; budding uninhibited by benzimid; colon, stom, lung, test; CTL+s.m.
 453935; AI633770; Hs.42572; ESTs; panc; diag
 453941; U39817; Hs.36820; Bloom syndrome; lung, cerv, headnk; CTL+s.m.
 453984; AI981486; Hs.249196; ESTs; lung; diag
 453986; BE148734; Hs.63325; transmembrane protease, serine; colon, blad, lung, ovar, panc, headnk; mAb+diag+s.m.
 453985; N44545; Hs.251865; ESTs; test; diag
 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 famit; lung, headnk; s.m.
 454042; H22570; Hs.47860; hypothetical protein FLJ20093; lung; diag
 454066; X00356; Hs.37058; calcitonin/calcitonin-related; lung; diag
 454071; AI041793; Hs.42502; ESTs; breast; diag
 454077; AC005952; Hs.37062; insulin-like 3 (Leydig cell); test; diag
 454098; W27953; Hs.217493; Plakophilin; lung; diag
 454117; BE410100; Hs.40368; adaptor-related protein complex; melar; CTL+s.m.
 454360; L78207; Hs.54470; ATP-binding cassette, sub-fam; glio; mAb
 454429; BE273437; Hs.301408; hypothetical protein PP3501; melar; mAb
 454439; AW819152; Hs.154320; DKFZP566O1646 protein; lung; diag
 454478; AW805749; Hs.372783; superoxide dismutase 2, mitocho; melar; s.m.
 455601; AI368680; Hs.816; SRY (sex determining region Y); lung, cerv, esoph; s.m.
 456034; AW450979; ; gb:U1-H-B13-ala-a-12-0-U1s1 N; blad, fibro; diag
 456062; AI866286; Hs.71962; ESTs, Weakly similar to B36298; fibro, ovar, uter; diag

- 456177; NM_012391; Hs.79414; prostate epithelium-specific E; breast, pros; diag
 456266; L29073; Hs.198726; cold shock domain protein A; panc; CTL+s.m.
 456321; NM_001327; Hs.87225; cancer/testis antigen; lung; CTL
 456553; AA721325; Hs.189058; ESTs, Highly similar to Simla; panc; diag
 456723; Z43902; Hs.4748; adenylate cyclase activating p; glio; mAb+s.m.
 456736; AW248217; Hs.1619; achaele-scute complex (Drosoph); lung; diag
 456759; BE259150; Hs.127792; della (Drosophila)-like 3; glio; lung; mAb
 456847; AJ360456; Hs.86088; ESTs; test; diag
 456938; X52509; Hs.161640; tyrosine aminotransferase; breast; s.m.
 456977; AK000252; Hs.169758; hypothetical protein FLJ20245; angio; diag
 457200; U33749; Hs.197764; thyroid transcription factor 1; fibro; CTL+s.m.
 457211; AW972565; Hs.32399; ESTs, Weakly similar to S51797; mela; pros; CTL+s.m.
 457292; AJ921270; Hs.281462; hypothetical protein FLJ14251; blad; mAb
 457313; AF047002; Hs.241520; transcriptional coactivator; test; CTL+s.m.
 457411; AW085961; Hs.130093; iroquois-class homeobox protei; breast; fibro; diag
 457465; AW301344; Hs.122908; DNA replication factor; test; mela; diag
 457498; AJ732230; Hs.191737; ESTs; pros; diag
 457561; AA331517; Hs.286055; chimerin (chimaerin) 2; glio; mAb
 457590; AI612809; Hs.5378; hypothetical protein MGC10724; ovar; diag
 457669; AU077186; Hs.108885; Homo sapiens, alpha-1 (VI) col; sarc; CTL+s.m.
 458092; W67353; Hs.350558; KIAA0251 protein; lung; diag
 458124; AW005548; Hs.124590; ESTs; fibro; diag
 458435; AI418718; Hs.144121; ESTs, Weakly similar to T46916; glio; diag
 458471; AV648609; Hs.194240; ESTs; renal, panc, hepC; diag
 458933; AI638429; Hs.24763; RAN binding protein 1; lung; test; diag
 459373; BE408266; Hs.301406; hypothetical protein PP3501; mela; mAb
 459578; AW612538; Hs.304491; EST; mela; diag
 459702; AJ204995; ; gb:an03c03.x1 Stratagene schiz; blad; fibro; diag
 459705; BE082764; Hs.270252; ESTs, Weakly similar to androg; fibro; mAb+s.m.

TABLE 3B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
103739	49403_2	AA115173 AA075709 AA076354 AA083101 AA076396 AA085391 AA070684 AA083368 AA075779 AA075221 AA076395 AA650486 AA083500
108282	108971_1	AA065143 AA065142
113230	2327174_1	AI820546 AI821336 T61430
118417	35983_1	AF080229 AF080232 U87593 U87591 U87590 AI636743 AI633818 AW206802 AI583718 AF080231 AF080234 AF080233 AL535594
		AI818326 AF080230 S46404 AJ970376 AA63992 AW665466 BF512210 U87595 U87589 BE550633 AI572574 BE467547 AI680833 AW614951
		N29366 N25695 H69001 U87596 BE673974 AI797496 AI701526 AA703396 AW139734 H92278 N66048 BE219539 BE671665 AI624817 BE466611
		AI206344 AA574397 BF593413 BG231271 BF773517 U87594 BF062180 BE466420 AI887798 BF674385 AA204735 AW496808 AA204833
		AA207155 BI004756 AA206262 AI365204 H77608 AW590511
121335	1369289_1	AA404418 AI217248
126872	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
322521	14637_1	AF147347 T55603 T55426
322975	1784168_1	C16391 C16413
323332	245301_1	AI829520 AI791832 AI791823 AA229315 AA228414 AA229211
323817	887879_1	AA410943 BF366582 AA334202 AA332882 BF371899 AW948953
324261	1026976_1	AL044891 AI908240 AA393080 AW748403 BE069341 BF330573
406685	0_0	M18728
409051	107934_1	AA075419 AA082953 AA080912 AA062835 AA071252 AA084926 AA078992 AA113913 AA081881 AA070343 AA083821 AA062836 AA113892
		AA075318 AA076594 AA078900 AA134801 AA063293 AA083403 AW974305
409123	108378_1	AA070050 AA070823 AA053403
409745	MH1944_5	BI030997 AA921874 AW188822 BI027862 BI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722
		BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006591 BI006590 BI007763 BI007762
		BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
411880	1139083_1	BE088101 T05590 AW872477
413804	1556661_1	BE168256 BE168190 T64682
414221	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
417886	1031334_1	AA210987 D57294 AA214584 AA207006 D56572
427260	11272_50	AA401424 AA400100 AA663848
427298	115241_1	AA933717 BF061897 AW628327 AA641788 AA400495
427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165
		AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
429163	1238297_1	AW974271 AA592975 AA447312 AA884766
432189	112710_1	AA527941 AA635266 AI810608 AI620190
432222	539529_1	BG207209 BE166299 AI204995 BG195355 AW969908 AA528756 AW440776 BI044354
432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104
		AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279
		BE748870 BG315540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849
		AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859
		BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928
		AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
432415	11371_1	BG166382 AW161086 N42363 BE935013 BE934998 BG291451 AV700520 BG152773 AI224956 AI079635 AW054706 AA843979 AI744193 F04060
		T23457 F04044 AA723859 AA977643 AA283764 AI123609 N21561 BF055052 BE856661 AI804220 AA843394 AI472045 AI740490 AA578830
		H09495 AI283334 AA609495 AI122773 AW162643 AW161798 BF940077 AI808825 AI360866 AI123189 R40236 R20726 AW975899 BE764052
		N31709 N31708 AI031947 AW194138
434414	35978_1	AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW851851 AW858362 AI817548 BF771300 AA113928 AA223422
		AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754288

				AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175
				BF854337
5	434596	14701_1		AF147374 T59538 T59589 T59598 T59542
	434609	14739_1		AF147390 R76593 R76594
	438966	1242593_1		AW979074 AA834841 AA826650
	438993	2580163_1		AI926361 AA834879 AA828995
	439092	919640_1		AW978407 AA830149 M85983 AW503637 BF352096
10	439780	49082_1		AL109688 R23665 R26578
	440151	1879911_1		AA868167 F21558 F31418 F35624
	444163	682245_1		BG403189 AI148521 AI184746 AI126098 R05933 BI057330
	451844	2327174_1		AI820546 AI821336 T61430
	456034	685586_1		AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
15	459702	539529_1		BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
TABLE 3C				
20	Pkey:	Unique number corresponding to an Eos probe set		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
25	Pkey	Ref	Strand	Nt_position
	325372	5866920	Minus	1117061-1117304
	325544	6682452	Plus	171228-171286
	327036	6531965	Plus	319951-320040
	327075	6531965	Plus	4041318-4041431
30	327414	5867750	Plus	102461-102586
	328700	5868264	Plus	764089-764203
	330211	6013592	Plus	59158-59215
	332798	Dunham, I. et al.	Minus	232147-231974
	333769	Dunham, I. et al.	Plus	7696625-7696707
35	333904	Dunham, I. et al.	Minus	8217374-8217261
	334223	Dunham, I. et al.	Minus	12734365-12734269
	334447	Dunham, I. et al.	Plus	14308764-14308824
	335115	Dunham, I. et al.	Minus	21388250-21388146
	335809	Dunham, I. et al.	Plus	26310772-26310909
40	335824	Dunham, I. et al.	Plus	26376860-26376942
	335825	Dunham, I. et al.	Plus	26378175-26378268
	335936	Dunham, I. et al.	Minus	27360474-27360400
	336034	Dunham, I. et al.	Plus	29014404-29014590
	336152	Dunham, I. et al.	Minus	30156053-30155870
45	336536	Dunham, I. et al.	Plus	988418-988185
	338008	Dunham, I. et al.	Plus	7697068-7697236
	338033	Dunham, I. et al.	Plus	8092128-8092271
	338158	Dunham, I. et al.	Minus	11794465-11794343
	338255	Dunham, I. et al.	Minus	15242294-15242231
50	400494	9714719	Plus	169845-170272
	400517	9796686	Minus	49998-50346
	400651	8117978	Minus	81488-81646
	400665	8118496	Plus	16879-17023
	400773	8131629	Minus	44116-44238,48208-48321
55	400844	9188605	Plus	24746-24872,25035-25204
	400846	9188605	Plus	39310-39474
	400881	2842777	Minus	91446-91603,92123-92265
	401093	8516137	Minus	22335-23166
	401234	9929642	Plus	120173-120337
60	401424	8176894	Plus	24223-24428
	401486	7341763	Plus	32585-32756,36281-36540,40791-40933,4401
	401704	3097841	Plus	24712-25374
	401732	1200312	Plus	19346-19525,19625-19708,19897-19973,2006
	401747	9789672	Minus	118596-118816,119119-119244,119609-11976
65	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
	401780	7249190	Minus	28397-28617,28920-29045,29135-29298,2941
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
	401785	7249190	Minus	165776-165998,166189-166314,166408-16656
	401797	6730720	Plus	6973-7118
70	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519
	402145	8018280	Plus	113086-114800
	402199	8576116	Minus	84187-84744
	402230	9966312	Minus	29782-29932
	402239	7690131	Plus	38175-38304,42133-42266
75	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	402265	3287673	Plus	21059-21168
	402305	7328724	Plus	40832-41362
	402420	9796339	Plus	129750-129919
	402424	9796344	Minus	64925-65073
80	402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	402550	7652009	Minus	80413-80673
	402604	9909420	Plus	20393-20767
	402605	9909420	Minus	47680-47973

	402606	9909429	Minus	81747-82094
	402680	8113438	Plus	137634-137768,139702-139893,140475-14059
	402777	9588235	Plus	126786-126948
5	402860	9588237	Minus	76423-76560
	402888	9930892	Minus	54727-54901
	402992	7767907	Minus	42137-42515
	402994	2996643	Minus	4727-4969
	403046	3540153	Minus	55707-55859,56369-56511
10	403047	3540153	Minus	59793-59968
	403071	8954241	Plus	136688-137096
	403088	8954241	Plus	169894-170193,170504-170806
	403171	9838164	Minus	74502-74703
	403328	8469086	Minus	120428-120703
	403329	8516120	Plus	95450-96598
15	403381	9438267	Minus	26009-26178
	403409	9438598	Plus	6860-7054,12573-12771
	403433	9719611	Minus	72225-72437
	403478	9958258	Plus	116458-116564
20	403715	7239669	Plus	85128-85292
	403740	7630882	Plus	86504-87227
	403776	7770611	Minus	1414-1513,1624-1756
	403903	7710671	Minus	101165-102597
	404029	7671252	Plus	108716-111112
25	404049	3688074	Minus	75765-78155
	404210	5006246	Plus	169926-170121
	404240	5002624	Minus	116132-116407,116653-116922
	404253	9367202	Minus	55675-56055
	404286	2326514	Plus	51086-51301
30	404298	9944263	Minus	73591-73723
	404403	7272157	Minus	72053-72238
	404440	7528051	Plus	80430-81581
	404866	9366919	Minus	11743-11929
	404877	1519284	Plus	1095-2107
35	404927	7342002	Plus	68690-69563
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
	405001	6015406	Minus	104646-104819
	405025	7107727	Plus	105267-105343,106184-106294,106387-10653
	405121	8102330	Minus	35816-36004,36587-36684
40	405238	7249119	Minus	51728-51836
	405239	7249119	Plus	144345-144464,144690-144836,151750-15188
	405451	7622517	Minus	145949-146227
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	405546	1054740	Plus	124010-124183
45	405547	1054740	Plus	124361-124520,124914-125050
	405646	4914350	Plus	741-969
	405704	4204244	Plus	138842-139051
	405770	2735037	Plus	61057-62075
	405849	7651817	Minus	17705-18287
50	405932	7767812	Minus	123525-123713
	406081	9123861	Minus	38115-38691
	406137	9166422	Minus	30487-31058
	406173	7230224	Plus	12925-13213
	406348	9255985	Minus	71754-71944
55	406360	9256107	Minus	7513-7673
	406399	9256288	Minus	63448-63554
	406434	9256651	Minus	17803-17931
	406467	9795551	Plus	182212-182958
	406506	7711374	Minus	6843-8077
60	406547	7711513	Minus	172780-174358

65 Table 4A lists about 425 genes up-regulated in breast cancer compared to normal adult tissues and to non-malignant breast tissues. These genes were selected from a starting collection of about 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array. The "average" breast cancer level was set to the 90th percentile value amongst breast cancer specimens. The "average" normal adult tissue level was set to the 75th percentile value amongst non-malignant adult tissues. Certain predicted protein domains are noted.

70 Table 5A lists about 231 genes up-regulated in breast cancer compared to normal adult tissues and to non-malignant breast tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected similarly as for Table 1. The "average" breast cancer level was set to the 90th percentile value amongst breast cancer specimens. The "average" normal adult tissue level was set to the 50th percentile value amongst non-malignant adult tissues. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modifiable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

75 TABLE 4A: ABOUT 425 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES

80 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.ProT.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; =N, less likely to contain. All other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1: Ratio of 90th percentile of tumor to 75th percentile of normal body tissue

Pkey	ExAccn	UniGeneID	Pred.ProT.Domains	UniGeneTitle	R1
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5	419551	AW582256	Hs.91011	TM=M;SS=M	anterior gradient 2 (Xenopus laevis	9.7
	426174	AA547959	Hs.115838		Homo sapiens similar to Echinoidin	7.0
	409340	BE174629	Hs.321130	aa_permeases,pyridoxal_de	melanophilin (MLPH), mRNA	6.8
	428471	X57348	Hs.184510	14-3-3;TM=M;SS=N	stratulin	6.4
	417931	W95642	Hs.82961	trefol;TM=N;SS=M	trefol factor 3 (intestinal)	6.3
	447966	AA340605	Hs.105887	Jacalin;TM=N;SS=M	ESTs, Weakly similar to Homolog of	6.1
	406387				Target Exon	6.0
10	421814	L12350	Hs.108623	EGF,isp_1,vwc,TSPN,isp_3;	thrombospondin 2	5.8
	406867	AA157857	Hs.182265	filament;ZIP;TM=N;SS=M	keratin 19	5.8
	426104	AI204418	Hs.190080		ESTs	5.8
	421481	AW391972	Hs.104696	TM=M;SS=M	KIAA1324 protein	5.8
	422511	AU076442	Hs.117938	Collagen,none	collagen, type XVII, alpha 1	5.7
15	426539	AB011155	Hs.170290	SH3,POZ,Guanylate_kin;TM=	discs, large (Drosophila) homolog 5	5.6
	419693	AA133749	Hs.301350	ATP1G1_PLM_MAT8;TM=Y;SS=M	FXD domain-containing ion transpor	5.5
	419329	AY007220	Hs.288998	S_100;TM=M;SS=N	S100-type calcium binding protein A	5.4
	418344	AA216387			gb:nc16b02.s1 NCL CGAP_Pr1 Homo sap	5.2
	407116	AA130986	Hs.271627		ESTs	5.1
20	417389	BE260964	Hs.82045	PTN_MK;TM=M;SS=Y	midkine (neurite growth-promoting f	5.1
	419452	U33635	Hs.90572	ig,pkinase;TM=Y;SS=M	PTK7 protein tyrosine kinase 7	5.1
	421552	AF026692	Hs.105700	Fz,NTR;TM=N;SS=M	secreted frizzled-related protein 4	5.1
	409453	AJ88516	Hs.95612	cadherin,cadherin,Cadheri	ESTs	5.1
	409632	W74001	Hs.55279	serpin;TM=N;SS=N	serine (or cysteine) proteinase inh	5.1
25	417515	L24203	Hs.82237	zf-B_box,zf-UBR1;TM=M;SS=	ataxia-telangiectasia group D-assoc	5.0
	411573	AB029000	Hs.70823	Sulfatase;TM=M;SS=N	KIAA1077 protein	5.0
	418751	BE389014	Hs.372548	SH2,none	phosphoinositide-3-kinase, regulato	5.0
	422087	X58968	Hs.111301	fn2,hemopexin,Peptidase_M	matrix metalloproteinase 2 (gelatin	5.0
	421143	AB024536	Hs.102171	ig,LRR,LRRNT,LRRCT;TM=M;S	immunoglobulin superfamily containi	4.9
30	408491	AU088063	Hs.7882		ESTs	4.9
	417944	AU077196	Hs.82985	vwc,Collagen,COLFI;TM=N;S	collagen, type V, alpha 2	4.9
	409062	AL157488	Hs.50150		Homo sapiens mRNA; cDNA DKFZp564B18	4.9
	422281	M36803	Hs.346935	hemopexin;TM=N;SS=M	hemopexin	4.9
35	425308	M97639	Hs.155585	ig,kringle,pkinase,Fz;TM=	receptor tyrosine kinase-like orpha	4.8
	408349	BE546947	Hs.44276	homeobox;TM=M;SS=N	homeo box C10	4.8
	449019	AJ949095	Hs.67776		ESTs, Weakly similar to T22341 hypo	4.8
	435551	AA351978	Hs.4943	MAGE,Cys_knot,EGF,laminin	hepatocellular carcinoma associated	4.8
	410687	U24389	Hs.65436	Lysyl_oxidase;TM=N;SS=M	lysyl oxidase-like 1	4.8
	429455	AA72111	Hs.278694	lectin_c	CD209 antigen	4.8
40	414407	AA147026	Hs.76704		ESTs	4.8
	419390	AJ701162	Hs.331904	PMP22_Claudin,PMP22_Claud	hypothetical protein MGC11138	4.7
	453902	BE502341	Hs.3402		ESTs	4.7
	411089	AA456454	Hs.355702		cell division cycle 2-like 1 (PITSL	4.7
45	450172	NM_005864	Hs.24587	SH3,hormone3;TM=M;SS=N	signal transduction protein (SH3 co	4.7
	449717	AB040935	Hs.23964	Glyco_transf_25;TM=N;SS=N	cerebral cell adhesion molecule	4.6
	451529	AJ917901	Hs.208641	actn,none	ESTs	4.6
	435370	AJ954074	Hs.225838	EGF,fn3,fibrinogen_C,toxi	ESTs	4.6
	411761	AJ733848	Hs.71935	zf-C2H2;TM=M;SS=N	putative zinc finger protein from E	4.6
	424223	AJ243706	Hs.143323	PHD,ARID,jmjC,jmjN,zf-C5H	putative DNA/chromatin binding moti	4.6
50	426935	NM_000088	Hs.172928	vwc,Collagen,COLFI;TM=M;S	collagen, type I, alpha 1	4.5
	408796	AA688292	Hs.170345	hormone_rec,zf-C4	ESTs	4.5
	407230	AA157857	Hs.182265	filament;ZIP;TM=N;SS=M	keratin 19	4.4
	422830	AC007954	Hs.121371		hypothetical protein DKFZp434P0111	4.4
	447528	AJ612027	Hs.76277	TB2_DP1_HVA22;TM=Y;SS=M	Homo sapiens, clone MGC:9381, mRNA,	4.4
55	430168	AW968343	Hs.145582	elfhand,elfhand	DKFZP4341735 protein	4.4
	423225	AA852604	Hs.125359	ig,Ribosomal_S19;TM=M;SS=	Thy-1 cell surface antigen	4.4
	414822	AA156542	Hs.72127	homeobox,HLH	ESTs	4.4
	452683	AJ089575	Hs.374574	homeobox,none	progesterone membrane binding prote	4.4
	444784	D12485	Hs.11951	Somatostatin_B,Endonucleas	ectonucleotide pyrophosphatase/phos	4.4
60	453857	AL080235	Hs.35861	TM=Y;SS=M	Ras-induced senescence 1 (RIS1)	4.4
	413859	AW992356	Hs.8364	SAM_PNT,none	Homo sapiens pyruvate dehydrogenase	4.3
	440369	AW176150	Hs.132449		downstream of breast cancer antigen	4.3
	418140	BE613836	Hs.83551	TM=M;SS=M	microfibrillar-associated protein 2	4.3
	441384	AA447849	Hs.288660	7tm_3,none	retinoid acid induced 3	4.3
65	424464	R68537	Hs.17962	homeobox,none	ESTs	4.3
	423582	BE000831	Hs.23837	TGFb_propeptide,TGF-beta,	Homo sapiens cDNA FLJ11812 fis, clo	4.3
	432562	BE531048	Hs.278422	zf-C2H2;TM=M;SS=N	DKFZP586G1122 protein	4.2
	433320	D60647	Hs.250879	rm	ESTs, Highly similar to CTXN RAT CO	4.2
	429165	AW008885	Hs.118258		prostate cancer associated protein	4.2
70	416984	H38765	Hs.80706	Flavodoxin_2;TM=M;SS=N	diaphorase (NADH/NADPH) (cytochrome	4.2
	448913	AA194422	Hs.22564	rm,zf-RanBP,pkinase,GST_	myosin VI	4.2
	430154	AW583058	Hs.234726	serpin;TM=M;SS=M	serine (or cysteine) proteinase inh	4.2
	400496			TM=Y;SS=N	ENSP00000224716-GTP-binding protei	4.2
75	442599	AF078037	Hs.324051	SH3,ank;TM=M;SS=N	RelA-associated inhibitor	4.2
	448520	AB002367	Hs.21355	pkinase,DCX;TM=M;SS=N	doublecortin and CaM kinase-like 1	4.2
	431309	AW451711	Hs.313760	homeobox,none	ESTs, Weakly similar to I38022 hypo	4.2
	426485	NM_006207	Hs.170040	ig;TM=N;SS=M	platelet-derived growth factor rece	4.2
	435858	AF254260	Hs.283009	bZIP;TM=M;SS=N	tufelin	4.2
	446051	BE048061	Hs.37054	Ephrin_A_deamin,dsrm,z-al	ephrin-A3	4.2
80	451982	F13036	Hs.27373	NA;NA	Homo sapiens mRNA; cDNA DKFZp564017	4.2
	450334	AF035969	Hs.24879	PAP2;TM=Y;SS=M	phosphatidic acid phosphatase type	4.1
	431890	X17033	Hs.271986	vwa,Integrin_A_FG-GAP;TM=	integrin, alpha 2 (CD49B, alpha 2 s	4.1
	434449	AW953484	Hs.3849	elfhand,FKBP;TM=M;SS=N	hypothetical protein FLJ22041 simil	4.1
	422699	BE410590	Hs.119257	SH3,HS1_rep;TM=M;SS=N	ems1 sequence (mammary tumor and sq	4.1

5	423057	AW961597	Hs.130816		ESTs, Moderately similar to I38022	4.1
	452053	R53185	Hs.32356	HLH;TM=M;SS=N	ESTs, Weakly similar to TWST_HUMAN	4.1
	450680	AF131784	Hs.25318	ras,none	Homo sapiens clone 25194 mRNA seque	4.1
	418283	S79895	Hs.83942	Peptidase_C1;TM=N;SS=M	cathepsin K (pseudosclerosis)	4.1
	416361	AW204907	Hs.6872		ESTs, Weakly similar to CA13_HUMAN	4.1
	426255	BE262530	Hs.2006	GST_C,GST_N;TM=M;SS=N	glutathione S-transferase M3 (brain	4.1
	408113	T82427	Hs.194101	7tm_3,none	Homo sapiens cDNA: FLJ20869 fis, cl	4.1
	407792	AI077715	Hs.39384	TM=M;SS=Y	putative secreted ligand homologous	4.1
10	422765	AW409701	Hs.1578	BLR;TM=M;SS=N	baculoviral IAP repeat-containing 5	4.1
	429359	W00482	Hs.2399	hemopexin,Peptidase_M10;T	matrix metalloproteinase 14 (membra	4.1
	442572	AI001922	Hs.135121	HSP70	hypothetical protein FLJ22415	4.0
	448826	AI580252	Hs.255665		ESTs, Weakly similar to putative p1	4.0
	419648	T73661	Hs.91877	TM=N;SS=M	thyroid hormone responsive SPOT14 (4.0
15	421485	AA243499	Hs.104800	TM=Y;SS=M	hypothetical protein FLJ10134	4.0
	440273	AI805392	Hs.325335		Homo sapiens cDNA: FLJ23523 fis, cl	4.0
	417363	AW129357	Hs.329700		ESTs	4.0
	451277	AK001123	Hs.26176	TM=Y;SS=M	hypothetical protein FLJ10261	4.0
	421823	N40850	Hs.28625		ESTs	4.0
	452239	AW379378	Hs.356289		protein tyrosine phosphatase, recep	4.0
20	444286	AI625304	Hs.201008		ESTs	4.0
	451541	BE279383	Hs.26557	Armadillo_seg;TM=M;SS=N	plakophilin 3	4.0
	451304	M92642	Hs.26208	Collagen,TSPN;TM=M;SS=M	collagen, type XVI, alpha 1	4.0
	429556	AW139399	Hs.314807	TM=M;SS=N	ESTs	4.0
25	441094	U33819	Hs.7647	zf-C2H2_LIM,PHD,TFIIIS;TM=	MYC-associated zinc finger protein	4.0
	407788	BE514982	Hs.38991	ethand,S_100,S_100,ethand	S100 calcium-binding protein A2	4.0
	451292	AB037716	Hs.26204	SH3;TM=M;SS=N	KIAA1295 protein	3.9
	437762	T78028	Hs.154679	C2,none	synaptotagmin I	3.9
	433399	N46406	Hs.84700	START;TM=M;SS=N	similar to phosphatidylcholine tran	3.9
30	408056	AA312329	Hs.42331	Ephrin;TM=M;SS=M	ephrin-A4	3.9
	404578	AF183810	Hs.26102	zf-C2H2_rubredoxin;TM=M;S	trichorhinophthalangeal syndrome I gene	3.9
	443883	AA114212	Hs.9930	serpin;TM=M;SS=M	serine (or cysteine) proteinase inh	3.9
	445084	H38914	Hs.250848	TM=Y;SS=M	hypothetical protein FLJ14761	3.9
	453880	AI803166	Hs.135121	HSP70,none	ESTs, Weakly similar to I38022 hypo	3.9
35	424125	M31689	Hs.1735	TGF-beta,TGFb_propeptide;	inhibin, beta B (activin AB beta po	3.9
	437377	AL359573	Hs.124940	ras;TM=M;SS=N	GTP-binding protein	3.9
	422562	AI962060	Hs.118397	Zn_carbOpept,F5_F8_type_C	AE-binding protein 1	3.9
	422320	AI745249	Hs.23650	TM=Y;SS=N	ESTs, Weakly similar to AAB47496 NG	3.9
40	433078	AW015188	Hs.121575	asp	Homo sapiens cDNA FLJ12231 fis, clo	3.9
	411894	M57609	Hs.72916	zf-C2H2;TM=N;SS=M	GLI-Kruppel family member GLI3 (Gre	3.9
	425976	C75094	Hs.334514	voltage_CLC;TM=Y;SS=M	NG22 protein	3.9
	418113	AI272141	Hs.83484	HMG_box,homeobox;TM=M;SS=	SRY (sex determining region Y)-box	3.9
	418753	BE217818	Hs.87016		hypothetical protein FLJ22838	3.8
	452679	Z42387	Hs.83883	TM=Y;SS=M	transmembrane, prostate androgen in	3.8
45	421030	AW161357	Hs.101174	tubulin-binding;TM=N;SS=M	microtubule-associated protein tau	3.8
	431567	N51357	Hs.260855	TM=M;SS=N	Homo sapiens cDNA: FLJ21410 fis, cl	3.8
	426363	M58524	Hs.2025	TGF-beta,TGFb_propeptide;	transforming growth factor, beta 3	3.8
	447151	AI022813	Hs.92679	kinesin;TM=M;SS=M	Homo sapiens clone CDABP0014 mRNA s	3.8
	448717	R67419	Hs.21851	HLH,homeobox,none	Homo sapiens cDNA FLJ12900 fis, clo	3.8
50	425867	D60385	Hs.12079	cadherin;TM=Y;SS=M	calysenterin-2	3.8
	423940	NM_012429	Hs.277728	CRAL_TRIO;TM=M;SS=N	SEC14 (S. cerevisiae)-like 2	3.8
	426742	AA383828	Hs.181131		ESTs	3.8
	435818	AA700553	Hs.368614	arf,ras,RecR,none	ESTs	3.8
	420005	AW271106	Hs.133294		ESTs	3.8
55	410867	X63556	Hs.750	EGF,TB,wnt,EB,TIL;TM=N;SS	fibrillin 1 (Marfan syndrome)	3.8
	402531	AB037745	Hs.104696	TM=M;SS=M	KIAA1324 protein	3.8
	449029	N28989	Hs.22891	aa_permeases;TM=Y;SS=M	solute carrier family 7 (cationic a	3.8
	424806	AA382523	Hs.105689	TM=Y;SS=N	MSTP031 protein	3.8
	443933	AI091631	Hs.203845	lon_trans;TM=Y;SS=M	two pore potassium channel KT3.3	3.8
60	432952	AA813887	Hs.188173		Homo sapiens cDNA FLJ12187 fis, clo	3.8
	424036	AA770688	Hs.348495	histone,CBFD_NFYB_HMF;TM=	H2A histone family, member L	3.7
	453828	AW970960	Hs.293821	Pep_M12B_propep,Repolysl	ESTs	3.7
	407112	AA070801	Hs.51615	hormone_rec,zf-C4	ESTs, Weakly similar to ALU7_HUMAN	3.7
	445669	AI570830	Hs.174870		ESTs	3.7
65	446091	AW022192	Hs.200197	homeobox,none	ESTs	3.7
	424651	AA93205	Hs.120785		ESTs	3.7
	409178	BE393948	Hs.50915	trypsin;TM=M;SS=Y	kallikrein 5	3.7
	417059	AL037672	Hs.81071	TM=N;SS=Y	extracellular matrix protein 1	3.7
	431194	D43704	Hs.250712	Ca_channel_B,RepB_protein	calcium channel, voltage-dependent,	3.7
70	430397	AI924533	Hs.105607	HCO3_cotransp;TM=Y;SS=N	bicarbonate transporter related pro	3.7
	418969	W33191	Hs.28907	SH3;TM=M;SS=N	hypothetical protein FLJ20258	3.7
	427378	BE515037	Hs.177556	MAGE;TM=M;SS=N	melanoma antigen, family D, 1	3.7
	424012	AW358377	Hs.137569	SAM,PS3;TM=M;SS=N	tumor protein 63 kDa with strong ho	3.7
	418840	AI821614	Hs.185831		ESTs	3.7
75	433573	AF234887	Hs.57652	7tm_2,EGF,cadherin,lamini	cadherin, EGF LAG seven-pass G-type	3.7
	433430	AI863735	Hs.369982	(thyroglobulin_1),IGFBP_zf-	ESTs	3.7
	422491	AA338548	Hs.117546	TM=M;SS=Y	neuronatin	3.7
	435114	AA775483	Hs.288936	ODC_AZ_Ribosomal_L9_N;TM=	mitochondrial ribosomal protein L9	3.7
	416899	BE262645	Hs.80420	IL8;TM=M;SS=M	small inducible cytokine subfamily	3.7
80	422110	AI376736	Hs.121555	kazal,none	secreted protein, acidic, cysteine-	3.7
	448560	BE613183	Hs.23213	zf-RanBP,MDM2,Ndr	ESTs	3.6
	414945	BE076358	Hs.77667	UPAR_LY6;TM=M;SS=M	lymphocyte antigen 6 complex, locus	3.6
	422119	AI277829	Hs.111862	WD40;TM=M;SS=N	KIAA0590 gene product	3.6
	447335	BE617695	Hs.286192	TM=M;SS=N	hypothetical protein FLJ20940	3.6

5	450663	H43540	Hs.25292	RNase_HII;TM=N;SS=M	ribonuclease HI, large subunit	3.6
	417387	AW021102	Hs.21509	zf-C2H2:none	ESTs	3.6
	450825	AC005954	Hs.25527	PDZ,Guanylate_kin;TM=N;SS	light junction protein 3 (zona occ	3.6
	439755	AW748482	Hs.77873	ig;TM=Y;SS=M	B7 homolog 3	3.6
	439873	BE159253	Hs.300638		ESTs	3.6
	439039	AI656707	Hs.48713		ESTs	3.6
	419235	AW470411	Hs.288433	pkinae:none	neurotrophin	3.6
	445033	AV52402	Hs.72901	ank;TM=N;SS=N	cyclin-dependent kinase inhibitor 2	3.6
10	404394	AF332975	Hs.307004	EGF,m1,vwc,vwd,MAM,Kerat	Zonadhesin	3.6
	452222	AW806287	Hs.21432	Sema,TIG,PSI,GDI	SEX gene	3.6
	422961	Y13620	Hs.122607	TM=M;SS=N	B-cell CLL/lymphoma 9	3.6
	420988	AW006352	Hs.159643		ESTs, Weakly similar to T32554 hypo	3.6
	439680	AW245741	Hs.58451	zf-C2H2,TFIIIS,KRAB;TM=M;S	ESTs, Weakly similar to A35659 krue	3.6
15	426815	D59505	Hs.351344	ig,SET,PHD,zf-CXXC,Adap_c	ESTs, Weakly similar to K1C1_HUMAN	3.6
	437446	AA789945	Hs.101302	tn3,vwa,Collagen,TSPN;TM=	ESTs, Moderately similar to CA1C RA	3.6
	421690	AW162667	Hs.106857	efhand;TM=M;SS=N	calbindin 2, (29kd, calretinin)	3.5
	453939	AA418160	Hs.86043		Homo sapiens cDNA FLJ13558 fis, clo	3.5
	426158	NM_001982	Hs.199067	Furin-like, pkinae, Recep_	v-erb-b2 avian erythroblastic leuke	3.5
20	439246	AI498072	Hs.351474	ank, pkinae, UPP0073;TM=N;	membrane-associated tyrosine- and t	3.5
	410653	BE383758	Hs.65238	zf-C3HC4, AIP3;TM=M;SS=N	95 kDa retinoblastoma protein bindi	3.5
	412703	AW984744			gb:RC1-HN0015-040400-011-d03 HN0015	3.5
	427871	AW992405	Hs.352406	TM=M;SS=N	Homo sapiens, clone IMAGE:3507281,	3.5
	444273	AJ903474	Hs.230	LRR, LRRNT;TM=M;SS=M	fibromodulin	3.5
25	434936	AI285970	Hs.183817	UCH-L2	ESTs	3.5
	457869	AI077186	Hs.108885	vwa,Collagen;TM=M;SS=M	Homo sapiens, alpha-1 (VI) collagen	3.5
	422575	AK000546	Hs.118552	PTR2;TM=Y;SS=M	hypothetical protein FLJ20539	3.5
	428343	AL043021	Hs.12705	WD40;TM=N;SS=M	ESTs	3.5
	426716	NM_006379	Hs.171921	ig,Sema,PSI;TM=N;SS=M	sema domain, immunoglobulin domain	3.5
30	423778	Y09267	Hs.132821	FMO-like, pyr_redox;TM=Y;S	flavin containing monooxygenase 2	3.5
	451558	NM_001089	Hs.26630	ABC_tran,SRP54;TM=Y;SS=M	ATP-binding cassette, sub-family A	3.5
	407926	AW956382	Hs.59771	TYA;TM=N;SS=M	ESTs	3.5
	447041	AL135480	Hs.250705		Homo sapiens cDNA FLJ11685 fis, clo	3.5
	419073	AW372170	Hs.183918	death,ZU5;TM=N;SS=M	Homo sapiens cDNA FLJ12797 fis, clo	3.5
35	446945	AJ193115	Hs.16611	TM=M;SS=N	tumor protein D52-like 1	3.5
	416322	BE019494	Hs.79217	P5CR,NAD_Gly3P_dh,Octopin	pyrroline-5-carboxylate reductase 1	3.5
	447347	AA570056	Hs.122730	NA;NA	ESTs, Moderately similar to KIAA121	3.5
	448984	AW751955	Hs.22753	TM=M;SS=N	hypothetical protein FLJ22318	3.5
	421778	AA428000	Hs.283072	NA;NA	actin related protein 2/3 complex,	3.5
40	423363	BE544348	Hs.127562	homeobox;TM=M;SS=N	homeo box C11	3.5
	432545	X52486	Hs.3041	cyclin:none	uracil-DNA glycosylase 2	3.5
	408495	W68796	Hs.237731		ESTs	3.5
	406851	AA609784	Hs.352392	ig,MHC_II_beta;TM=M;SS=Y	major histocompatibility complex, c	3.5
	418736	T18979	Hs.87908	helicase_CAT_hook,SNF2_N	Snf2-related CBP activator protein	3.4
45	410197	NM_005518	Hs.59889	HMG_CoA_synth;TM=N;SS=N	3-hydroxy-3-methylglutaryl-Coenzyme	3.4
	453597	BE281130	Hs.33713	KH-domain,Ribosomal_S3_C,	myo-inositol 1-phosphate synthase A	3.4
	417259	AW903838	Hs.81800	EGF,ig,lectin_c,sushi,Xii	chondroitin sulfate proteoglycan 2	3.4
	453985	N44545	Hs.251865	PH:none	ESTs	3.4
	412634	U55984	Hs.356531		heat shock 90kd protein 1, alpha	3.4
50	407204	R41933	Hs.140237	histone,histone	ESTs, Weakly similar to ALU1_HUMAN	3.4
	444371	BE540274	Hs.239	Fork_head;TM=M;SS=N	forkhead box M1	3.4
	447334	AA515032	Hs.91109		ESTs	3.4
	426530	U24578	Hs.278625	A2M,NTR,ANATO,A2M_N,preny	complement component 4A	3.4
	419749	X73508	Hs.93029	kazal,thyroglobulin_1;TM=	sparc/osteonectin, cwcv and kazal	3.4
55	423595	R82826	Hs.220702	homeobox:none	ESTs	3.4
	406673	M34996	Hs.198253	ig,MHC_II_alpha;TM=M;SS=M	major histocompatibility complex, c	3.4
	434241	AF119913		TM=N;SS=M	Homo sapiens PRO3077 mRNA, complete	3.4
	412490	AW803564	Hs.288850		Homo sapiens cDNA: FLJ22528 fis, cl	3.4
60	452277	AL049013	Hs.28783	ank;TM=M;SS=N	KIAA1223 protein	3.4
	431457	NM_012211	Hs.256297	FG-GAP,vwa;TM=Y;SS=M	Integrin, alpha 11	3.4
	421777	BE552088	Hs.108196	TM=M;SS=N	HSPC037 protein	3.4
	453082	H18835	Hs.31608	ion_trans;TM=Y;SS=M	hypothetical protein FLJ20041	3.4
	414085	AA114016	Hs.75746	aldedh;TM=N;SS=M	aldehyde dehydrogenase 1 family, me	3.4
	440300	N39760	Hs.8859	TM=M;SS=N	Homo sapiens, Similar to RIKEN cDNA	3.4
65	400290	H18836	Hs.31608	Cys_Jmol	hypothetical protein FLJ20041	3.4
	433339	AF019226	Hs.8036	ras,arf;TM=M;SS=N	glioblastoma overexpressed	3.4
	419301	AA236168	Hs.132957	TM=Y;SS=M	tenomodulin protein	3.4
	414792	BE314949	Hs.87128	TM=Y;SS=M	hypothetical protein FLJ23309	3.4
70	451428	AW083384	Hs.11067		ESTs, Highly similar to T46395 hypo	3.4
	432210	AI567421	Hs.273330	EGF,kazal,laminin_EGF,Jam	Homo sapiens, clone IMAGE:3544662,	3.4
	452242	R50956	Hs.159993		glycosyltransferase	3.4
	450676	AI147155	Hs.279727		ESTs	3.4
	413014	AW250533	Hs.75139	TM=M;SS=N	partner of RAC1 (arlapin 2)	3.4
75	427919	AA173942	Hs.326416	CTF_NFI:none	Homo sapiens mRNA; cDNA DKFZp564H19	3.4
	424005	AB033041	Hs.137507	TM=Y;SS=N	vang (van gogh, Drosophila)-like 2	3.4
	422072	AB018255	Hs.111138	RhoGAP;TM=M;SS=N	KIAA0712 gene product	3.4
	440995	T57773	Hs.10263		ESTs	3.4
80	426150	NM_003658	Hs.167218	homeobox;TM=N;SS=M	Bart-like homeobox 2	3.3
	416877	BE386266	Hs.85658	zf-C2H2;TM=M;SS=N	hypothetical protein FLJ23436	3.3
	452191	AU076408	Hs.28309	UDPG_MGDP_dh,UDPG_MGDP_dh	UDP-glucose dehydrogenase	3.3
	450273	AW296454	Hs.24743	rm:none	hypothetical protein FLJ20171	3.3
	456177	NM_012391	Hs.79414	Ets,SAM_PNT;TM=M;SS=N	prostate epithelium-specific Ets tr	3.3
	423062	NM_003655	Hs.5637	chromo;TM=N;SS=M	ESTs	3.3
	421848	X15830	Hs.108885	vwa,Collagen;TM=M;SS=M	collagen, type VI, alpha 1	3.3

5	433577	AW007080	Hs.284192		ESTs	3.3
	409636	AA305729	Hs.18272	Aa_trans;TM=Y;SS=N	amino acid transporter system A1	3.3
	404730	AA486704	Hs.33287	CTF_NFL:none	Nuclear factor I/B	3.3
	422940	BE077458		Sec7,PHANF_receptor,lig_	gb:RC1-BT0606-090500-015-b04 BT0606	3.3
	410001	AB041036	Hs.57771	trypsin;TM=M;SS=M	kallikrein 11	3.3
	427461	AA531527	Hs.332040	TM=Y;SS=M	hypothetical protein MGC13010	3.3
	453468	W00712	Hs.32990	TM=M;SS=N	DKFZP566F084 protein	3.3
	443807	W52930	Hs.9822	HAT;TM=N;SS=M	HCNP protein; XPA-binding protein 2	3.3
10	456034	AW450979			gb:U1-H-B13-ala-a-12-0-UI.s1 NCI_CG	3.3
	424307	AW293399	Hs.356377		nuclear receptor co-repressor 1	3.3
	412755	BE144306	Hs.179891		ESTs, Weakly similar to P4HA_HUMAN	3.3
	429690	AW956329	Hs.23721	sugar_tr,Ribosomal_S25	ESTs	3.3
	423472	AF041260	Hs.129057	TM=M;SS=N	breast carcinoma amplified sequence	3.3
15	424118	BE269041	Hs.140452	perlepin;TM=N;SS=M	cargo selection protein (mannose 6	3.3
	437275	AW976035	Hs.292396	Frizzled,Fz	ESTs, Weakly similar to A47582 B-ca	3.3
	437464	AA323296	Hs.97837		Homo sapiens mRNA; cDNA DKFZp547J04	3.3
	433592	NM_004642	Hs.3436	TM=M;SS=N	deleted in oral cancer (mouse, homo	3.3
	434931	AW968941	Hs.166254		hypothetical protein DKFZp566I133	3.3
20	451691	AI809278	Hs.208152	C2	ESTs	3.3
	430433	AA478883	Hs.273766	VWV:none	ESTs	3.3
	429343	AK000785	Hs.199480	VHS,ENTH,UIIM;TM=N;SS=M	Homo sapiens, Similar to epsin 3, c	3.3
	450835	BE262773	Hs.25584	ArfGap;TM=N;SS=M	hypothetical protein FLJ10767	3.3
	414591	AI888490	Hs.248107		ESTs, Weakly similar to ALU8_HUMAN	3.3
25	452579	AA131657	Hs.23830	CN_hydrolase	ESTs	3.3
	409960	BE261944	Hs.355264		hexokinase 1	3.3
	406850	AI624300	Hs.172928	wvc,Collagen,COLFI;TM=M;S	collagen, type I, alpha 1	3.3
	453874	AW591783	Hs.36131		collagen, type XIV, alpha 1 (unduli	3.2
	425964	AW889928	Hs.9071	homeobox:none	progesterone membrane binding prote	3.2
30	428412	AA428240	Hs.126083		ESTs	3.2
	430316	NM_000875	Hs.239176	tn3,Furin-like,pkinase,Ra	insulin-like growth factor 1 recept	3.2
	440087	W28969	Hs.7718	KOW,Ribosomal_S4e,S4_rnm;	hypothetical protein FLJ22678	3.2
	449933	AW157098	Hs.324104	DUF176,efhand;TM=M;SS=N	Human DNA sequence from clone RP1-6	3.2
	441128	AA570256	Hs.348504	TM=Y;SS=M	ESTs, Weakly similar to T23273 hypo	3.2
35	434182	W20309	Hs.8107	G-gamma;TM=M;SS=N	G-protein gamma-12 subunit	3.2
	422737	M26939	Hs.119571	Collagen,COLFI;TM=N;SS=M	collagen, type III, alpha 1 (Ehlers	3.2
	408202	AA227710	Hs.43658	OLF;TM=M;SS=N	DKFZP586L151 protein	3.2
	424971	AA479005	Hs.154036	PH;TM=M;SS=N	tumor suppressing subtransferable c	3.2
	407869	AI827976	Hs.24391	efhand;TM=M;SS=N	hypothetical protein FLJ13612	3.2
40	444734	NM_001360	Hs.11806	ERG4_ERG24;TM=Y;SS=M	7-dehydrocholesterol reductase	3.2
	426991	AK001536	Hs.214410		Homo sapiens cDNA FLJ10674 fis, clo	3.2
	414081	AW969976	Hs.365706	glc;TM=N;SS=Y	matrix Gla protein	3.2
	408795	AW749126	Hs.170345	hormone_rec,zf-C4	hypothetical protein FLJ13710	3.2
	452345	AA293279	Hs.29173	DSPc;TM=M;SS=N	hypothetical protein FLJ20515	3.2
45	437879	BE262082	Hs.5694	TM=N;SS=N	hypothetical protein FLJ10305	3.2
	407872	AB039723	Hs.40735	Fz,Frizzled,7tm_2,DUF81;T	frizzled (Drosophila) homolog 3	3.2
	427289	AI097346	Hs.323878	aminotran_5,SDF:none	phosphoserine aminotransferase	3.2
	432375	BE536069	Hs.2962	efhand,S_100;TM=N;SS=M	S100 calcium-binding protein P	3.2
	429415	NM_002593	Hs.202097	CUB,NTR;TM=N;SS=M	procollagen C-endopeptidase enhance	3.2
50	412774	AA120865	Hs.380149	hormone_rec,zf-C4	ESTs	3.2
	445942	T80334	Hs.13479	TM=M;SS=N	hypothetical protein FLJ20847	3.2
	439456	AI752409	Hs.109314	zf-C2H2;TM=N;SS=M	hypothetical protein FLJ20980	3.2
	414774	X02419	Hs.77274	krtgla,trypsin,plant_thi	plasminogen activator, urokinase	3.2
	433336	AF017986	Hs.31386	Fz,NTR;TM=N;SS=M	secreted frizzled-related protein 2	3.2
55	439905	AW799755	Hs.110953	HLH;TM=M;SS=N	retinoic acid induced 1	3.2
	420251	AW374968	Hs.379829		Human DNA sequence from clone RP5-1	3.2
	413004	T35901	Hs.75117	TM=M;SS=N	interleukin enhancer binding factor	3.2
	418686	Z36830	Hs.87268	annexin;TM=M;SS=N	annexin A8	3.2
	410279	BE271977	Hs.61809	ras;TM=M;SS=N	hypothetical protein FLJ14117	3.2
60	424391	BE550112	Hs.158549		ESTs, Weakly similar to T2D3_HUMAN	3.2
	440409	AW294316	Hs.125608	thioredo	ESTs	3.2
	452689	F33868	Hs.284176	transferrin,KH-domain_rnm	transferrin	3.2
	418154	BE165866	Hs.352403	hormone_rec,zf-C4:none	nuclear receptor subfamily 1, group	3.2
	434384	AA631910	Hs.370133		ESTs	3.2
65	413436	AF238083	Hs.68061	DAGKc;TM=M;SS=N	sphingosine kinase 1	3.2
	431663	NM_016569	Hs.267182	T-box;TM=M;SS=N	TBX3-iso protein	3.2
	432874	W94322	Hs.279651	SH3;TM=M;SS=Y	melanoma inhibitory activity	3.2
	436252	AI539519	Hs.142827		Homo sapiens cDNA FLJ11562 fis, clo	3.2
70	421044	AF061871	Hs.101302	fn3,vwa,Collagen,TSPN;TM=	Human DNA sequence from clone RP1-2	3.2
	419102	AA234098	Hs.42424		ESTs, Weakly similar to 2004399A ch	3.2
	419359	AL043202	Hs.90073	CAS_CSE1;TM=M;SS=N	chromosome segregation 1 (yeast hom	3.2
	441859	AW194364	Hs.9877	Amino_oxidase,FAD_binding	interleukin-4 induced gene-1 protel	3.1
	426418	M90464	Hs.169825	Collagen,C4,VPR;TM=N;SS=M	collagen, type IV, alpha 5 (Alport	3.1
	413076	U10564	Hs.75188	pktnase;TM=M;SS=N	wee1 (S. pombe) homolog	3.1
75	407874	AI766311	Hs.289047	COQ7	Homo sapiens cDNA FLJ14059 fis, clo	3.1
	448019	AW947164	Hs.195641		ESTs, Moderately similar to I38022	3.1
	427024	AA397572	Hs.348802		chromosome 11 open reading frame 14	3.1
	410281	AF076612	Hs.166186	wvc,W2,MA3,MIF4G	Homo sapiens clone 23928 mRNA seque	3.1
	447205	BE617015	Hs.11006	LEA,perlepin;TM=M;SS=N	ESTs, Moderately similar to T17372	3.1
80	434433	AW629759			gb:uh70e05.y1 NCI_CGAP_GU1 Homo sap	3.1
	439737	AI751438	Hs.41271	C1q,Collagen:none	Homo sapiens mRNA full length inser	3.1
	450157	AW961576	Hs.60178	PH,Band_41,RhoGEF:none	ESTs	3.1
	445989	H97754	Hs.11108		ESTs	3.1
	442213	N36110	Hs.305971	sugar_tr;TM=Y;SS=M	solute carrier family 2 (facilitate	3.1

	402496				Target Exon	3.1
	438974	AF089816	Hs.6454	PDZ;TM=N;SS=M	chromosome 19 open reading frame 3	3.1
	439335	AA742697	Hs.62492	TM=N;SS=M	NM_052853:Homo sapiens secretoglobi	3.1
5	412276	BE262621	Hs.73798	MIF,sugar_tr,none	macrophage migration inhibitory fac	3.1
	416950	AL049798	Hs.80552		dermatopontin	3.1
	456157	AW979153	Hs.336881	transmembrane4,none	ESTs	3.1
	452753	AA028049	Hs.277728	CRAL_TRIO,none	SEC14 (S. cerevisiae)-like 2	3.1
	414420	AA043424	Hs.76095	TM=M;SS=N	immediate early response 3	3.1
10	446229	AI744964	Hs.14449	TM=M;SS=N	KIAA1609 protein	3.1
	453143	AA382234	Hs.356289	serpin;TM=N;SS=M	protein tyrosine phosphatase, recep	3.1
	411441	AL042355	Hs.70202	WD40;TM=M;SS=N	WD repeat domain 10	3.1
	422921	BE062045	Hs.351625	AAA,hormone_rec,zf-C4	Homo sapiens cDNA: FLJ23260 fis, cl	3.1
	444441	AW613841	Hs.301394	IRK;TM=Y;SS=N	hypothetical protein MGC3101	3.1
15	436729	BE621807	Hs.351316	TM=Y;SS=M	transmembrane 4 superfamily member	3.1
	427890	AA435761	Hs.373623	RFX_DNA_binding,none	ESTs	3.1
	444838	AV651680	Hs.208558	integrin_a,FG-GAP,none	ESTs	3.1
	427876	AI494291	Hs.369171		ESTs	3.1
	413040	AA193338	Hs.12321	Na_Ca_Ex;TM=Y;SS=M	sodium calcium exchanger	3.1
20	427515	T79526	Hs.179516	EMP24_GP25L;TM=Y;SS=M	integral type I protein	3.1
	451092	AI207256	Hs.13766	filament;TM=N;SS=N	Homo sapiens mRNA for FLJ00074 prot	3.1
	442222	AI061301	Hs.164773	trypsin,kringle,UPAR_LYG	ESTs	3.1
	452613	AA461599	Hs.23459		ESTs	3.1
	447191	NM_014521	Hs.17667	SH3;TM=M;SS=N	SH3-domain binding protein 4	3.1
25	412890	T85247	Hs.351875	COX6C;TM=M;SS=M	cytochrome c oxidase subunit VIc	3.1
	418313	BE244231	Hs.84038	TM=Y;SS=N	CGI-06 protein	3.1
	440006	AK000517	Hs.6844	AAA,NB-ARC,PAAD_DAPIN;NA;	NALP2 protein; PYRIN-Containing APA	3.1
	434042	AI589941	Hs.8254		Homo sapiens, Similar to tumor diff	3.1
	420576	AA297634	Hs.54925		KIAA1858 protein	3.1
30	432269	NM_002447	Hs.2942	pkinese,Sema,PSI,TIG,AA_E	macrophage stimulating 1 receptor (3.1
	424927	AW973666	Hs.153850		hypothetical protein C321D2.4	3.1
	440100	BE382685	Hs.158549		ESTs, Weakly similar to T2D3_HUMAN	3.1
	452408	AA306477	Hs.29379	TM=M;SS=N	hypothetical protein FLJ10687	3.1
	441362	BE614410	Hs.23044	TM=N;SS=N	RAD51 (S. cerevisiae) homolog (E co	3.1
35	418444	AI902899	Hs.85155	zf-CCCH;TM=M;SS=N	butyrate response factor 1 (EGF-res	3.1
	423464	NM_016240	Hs.128856	Collagen;TM=Y;SS=N	CSR1 protein	3.1
	424604	AW865388	Hs.151076	TM=M;SS=N	KIAA1243 protein	3.1
	420059	AF161486	Hs.94769	ras,none	RAB23, member RAS oncogene family	3.1
	453271	AA803424	Hs.6786	LIM;TM=M;SS=N	ESTs	3.1
40	411274	NM_002776	Hs.69423	trypsin;TM=M;SS=N	kallikrein 10	3.1
	434095	AA011117	Hs.3745	EGF,F5_F8_type_C;TM=N;SS=	milk fat globule-EGF factor 8 prote	3.1
	403439			ank;TM=M;SS=N	NM_031419:Homo sapiens molecule po	3.1
	413244	AW955951	Hs.159265	BTB,Pep_M12B_propep,Repro	kruppel-related zinc finger protein	3.1
	411756	BE294350	Hs.71891	pkinese,F5_F8_type_C;TM=Y	discooidin domain receptor family, m	3.1
45	409007	AL122107	Hs.49599		Homo sapiens mRNA; cDNA DKFZp434G08	3.1
	452547	AA335295	Hs.74120	LEA;TM=M;SS=N	adipose specific 2	3.1
	414359	M62194	Hs.75929	cadherin,Cadherin_C_term;	cadherin 11, type 2, OB-cadherin (o	3.1
	433212	BE218049	Hs.121820		ESTs	3.1
	449123	D50920	Hs.23105	TM=M;SS=N	KIAA0130 gene product	3.1
50	431176	AI026984	Hs.293662	MCPsignal,Janinin_B,Janin	ESTs	3.0
	419245	AI732742	Hs.87440		ESTs	3.0
	434493	AA635305	Hs.375591		ESTs	3.0
	449177	BE616694	Hs.288042		hypothetical protein FLJ14299	3.0
	430449	AA352723	Hs.241471	WH1;TM=M;SS=N	RNB6	3.0
55	452887	AI702223	Hs.107253	K-box;TM=N;SS=M	hypothetical protein DKFZp761F241	3.0
	451678	AA374181	Hs.26799		DKFZP564D0764 protein	3.0
	445457	AF168793	Hs.12743	Cam_acyltransf;TM=M;SS=N	camitine O-octanoyltransferase	3.0
	407597	AA043925	Hs.339352	fn3,lg;TM=Y;SS=M	Homo sapiens brother of CDO (BOC) m	3.0
	431629	AU077025	Hs.265827	TM=M;SS=Y	interferon, alpha-inducible protein	3.0
60	432302	AA345857	Hs.274307	TIG;TM=M;SS=N	KIAA1442 protein	3.0
	442549	AI751601	Hs.8375	MATH,zf-TRAF,zf-C3HC4;TM=	TNF receptor-associated factor 4	3.0
	437959	AI472068	Hs.375604	elf5_elf2B,W2;TM=M;SS=N	KIAA1856 protein	3.0
	447400	AK000322	Hs.18457	zf-C3HC4;TM=Y;SS=M	hypothetical protein FLJ20315	3.0
	411734	AW374954	Hs.71779		Homo sapiens DNA from chromosome 19	3.0
65	443547	AW271273	Hs.356487	fn3,none	hypothetical protein FLJ12666	3.0
	417000	BE277919	Hs.305019	TM=Y;SS=M	ESTs, Weakly similar to ALU7_HUMAN	3.0
	416987	D86957	Hs.80712	GTP_CDC;TM=N;SS=M	KIAA0202 protein	3.0
	424494	U78575	Hs.149255	PIP5K;TM=N;SS=M	phosphatidylinositol 4-phosphate 5-	3.0
	414496	W73853	Hs.355424	pkinese,F5_F8_type_C,adh_	ESTs	3.0
70	413336	AI569936	Hs.296178	Occludin;TM=M;SS=N	hypothetical protein FLJ22637	3.0
	434314	BE392921	Hs.3797	ras,art;TM=M;SS=N	RAB26, member RAS oncogene family	3.0
	401038			TM=M;SS=N	C11000425:gi14507721[refNP_003310.	3.0
	418245	AA088767	Hs.83883	TM=Y;SS=M	transmembrane, prostate androgen in	3.0
75	407688	W25317	Hs.37616		Human D9 splice variant B mRNA, com	3.0
	456906	AF117646	Hs.156637	zf-C3HC4,Cbl_N,Cbl_N2,Cbl	Cas-Br-M (murine) ectropic retrovir	3.0
	424744	AW175781	Hs.152720	TM=M;SS=N	M-phase phosphoprotein 6	3.0
	452195	AA994712	Hs.116878		ESTs	3.0
	415988	BE407713	Hs.78943	Pep_LC1-like;TM=N;SS=M	bleomycin hydrolase	3.0
80	418399	AF131781	Hs.84753	TM=N;SS=N	hypothetical protein FLJ12442	3.0
	420568	F09247	Hs.247735	cadherin,lipocalin;TM=M;S	protocadherin alpha 10	3.0
	404661			TM=M;SS=N	C9000306*gi12737280[refXP_005682	3.0
	414152	NM_003248	Hs.75774	EGF,TSPN,isp_3;TM=M;SS=M	thrombospondin 4	3.0
	421307	BE539976	Hs.103305	chromo	Homo sapiens mRNA; cDNA DKFZp434B04	3.0
	444868	BE560471	Hs.12101	TM=N;SS=M	hypothetical protein	3.0

5	450214	BE439763	Hs.227571	RGS;TM=M;SS=N	regulator of G-protein signalling 4	3.0
	452664	AA398859	Hs.18397	TM=M;SS=M	hypothetical protein FLJ23221	3.0
	422105	A1929700	Hs.111680	TM=M;SS=N	endostuffin alpha	3.0
	422278	AF072873	Hs.114218	Fz,Frizzled,7tm_2;TM=Y;SS	frizzled (Drosophila) homolog 6	3.0
	434067	H18913	Hs.124023		Homo sapiens cDNA FLJ14218 fis, clo	3.0
	412676	NM_000165	Hs.74471	connexin,Connexin43;TM=Y;	gap junction protein, alpha 1, 43kD	3.0
	426801	AA486846	Hs.271795		ESTs, Weakly similar to I38022 hypo	3.0
	421983	A1252640	Hs.110364	pro_isomerase,none	peptidylprolyl isomerase C (cycloph	3.0
10	429299	A1620463	Hs.347408	TM=Y;SS=N	hypothetical protein MGC13102	3.0
	408912	AB011084	Hs.48924	Armadillo_seg;TM=M;SS=M	KIAA0512 gene product; ALEX2	3.0
	438746	A1885815	Hs.184727	transferrin,Guanylate_kin	Human melanoma-associated antigen p	3.0

TABLE 4B

15 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

20	Pkey	CAT Number	Accession
	418344	245371_1	AA216387 T63548 AA228676
	412703	1243670_1	AW984759 AW984744
	434241	63414_1	AF119913 AJ207698 R57074
	422940	58443_1	BC012771 BG397153 BF366196 AA337277 AA319285 AW843252
25	456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	434433	111338_1	AA633408 AW749955 AW629759 AJ651005

TABLE 4C

30 Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
35 NL_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
	406387	9256180	Plus	116229-116371,117512-117651
	400496	9743564	Plus	41515-41695
40	402496	9797769	Minus	8515-9103
	403439	9719679	Plus	91463-91632
	401038	7232177	Minus	4277-4469
	404661	9797073	Plus	33374-33675,33769-34008

45 TABLE 5A: ABOUT 231 GENES UP-REGULATED IN BREAST CANCER COMPARED TO NORMAL ADULT TISSUES THAT MAY ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES, PEPTIDES, OR ANTIBODIES

50 Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar accession number, GenBank accession number
UniGeneID: UniGene number
Pred.Protdomains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; =N, less likely to contain. All other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title: UniGene gene title
55 R1: Ratio of 90th percentile tumor to 50th percentile of normal body tissue

	Pkey	ExAccn	UniGeneID	Pred.Protdomains	UniGeneTitle	R1
	409340	BE174629	Hs.321130	aa_permeases,pyridoxal_de	melanophilin (MLPH), mRNA	20.5
	421481	AW391972	Hs.104696	TM=M;SS=M	KIAA1324 protein	16.3
60	419693	AA133749	Hs.301350	ATP1G1_PLM_MAT6;TM=Y;SS=M	FXD domain-containing ion transpor	13.7
	417389	BE260964	Hs.82045	PTN_MK;TM=M;SS=Y	midkine (neurite growth-promoting f	13.7
	414521	D28124	Hs.76307	DAN;TM=M;SS=M	neuroblastoma, suppression of tumor (DAN)	13.7
	438091	AW373062	Hs.351546	hormone_rec,zf-C4,none	nuclear receptor subfamily 1, group	13.4
	413815	AL046341	Hs.75562	pk kinase,F5_F8_type_C;TM=Y	discoidin domain receptor family, m	13.2
65	439180	A1393742	Hs.199067	Furin-like, pk kinase, Recep_	v-erb-b2 avian erythroblastic leuke	13.2
	431441	U81961	Hs.2794	ASC;TM=Y;SS=N	sodium channel, nonvoltage-gated 1	12.5
	452547	AA335295	Hs.74120	LEA;TM=M;SS=N	adipose specific 2	12.4
	452239	AW379378	Hs.356289		protein tyrosine phosphatase, recep	12.1
	441384	AA447849	Hs.286660	7tm_3,none	retinoic acid induced 3	11.9
70	419223	XG0111	Hs.1244	transmembrane4;TM=Y;SS=M	CD9 antigen (p24)	11.7
	413859	AW992356	Hs.8364	SAM_PNT,none	Homo sapiens pyruvate dehydrogenase	11.5
	410687	U24389	Hs.65436	Lysyl_oxidase;TM=N;SS=M	lysyl oxidase-like 1	11.2
	422699	BE410590	Hs.119257	SH3,HS1_rep;TM=M;SS=N	ems1 sequence (mammary tumor and sq	10.1
75	419452	U33635	Hs.90572	lg, pk kinase;TM=Y;SS=M	PTK7 protein tyrosine kinase 7	9.9
	427378	BE515037	Hs.177556	MAGE;TM=M;SS=N	melanoma antigen, family D, 1	9.9
	444784	D12485	Hs.11951	Somatostatin_B,Endonucleas	ectonucleotide pyrophosphatase/phos	9.9
	436972	AA284679	Hs.25640	PMP22_Claudin;TM=Y;SS=M	claudin 3	9.7
	412926	A1879076	Hs.75061	MARCKS;TM=N;SS=M	macrophage myristoylated alanine-r	9.5
80	425280	U31519	Hs.1872	PEPCK;TM=M;SS=N	phosphoenolpyruvate carboxykinase 1	9.5
	432636	AA340864	Hs.278562	PMP22_Claudin;TM=Y;SS=M	claudin 7	9.4
	423778	Y09267	Hs.132821	FMO-like,pyr_redox;TM=Y;S	flavin containing monooxygenase 2	9.4
	424206	NM_003734	Hs.198241	Cu_amine_oxid,Cu_amine_ox	amine oxidase, copper containing 3	9.4
	444797	AB018333	Hs.12002	SH3,SAM;TM=M;SS=N	KIAA0790 protein	9.0

5	402559	AF043329	Hs.173717	PAP2;TM=Y;SS=M	PPAP2B Phosphatidic acid phosphatase type 2B	9.0
	443932	AW888222	Hs.9973	SH2,VW,PID,none	tensin	8.9
	421143	AB024536	Hs.102171	lg.LRR,LRRT,LRCT;TM=M;S	immunoglobulin superfamily containi	8.8
	433592	NM_004642	Hs.3436	TM=M;SS=N	deleted in oral cancer (mouse, homo	8.7
	410668	BE379794	Hs.159651	death,TNFR,c6;TM=Y;SS=M	hypothetical protein	8.7
	433662	W07162	Hs.150826	ras,ABC_tran,arf;TM=M;SS=	RAB25 RAB25, member RAS oncogene fa	8.6
	421853	AL117472	Hs.108924	SH3,Sorb;TM=M;SS=N	SH3-domain protein 5 (ponsin)	8.6
	425335	BE394327	Hs.296267	efhand,kazal,arf,ras,7tm_	folistatin-like 1	8.5
10	400290	H18836	Hs.31608	Cys_knot	hypothetical protein FLJ20041	8.5
	438089	W05391	Hs.351546	hormone_rec,zf-C4,none	nuclear receptor subfamily 1, group	8.4
	426158	NM_001982	Hs.199067	Furin-like,kinase,Recep_	v-erb-b2 avian erythroblastic leuke	8.3
	447191	NM_014521	Hs.17667	SH3;TM=M;SS=N	SH3-domain binding protein 4	8.2
	439941	AI392640	Hs.18272	Aa_trans;TM=Y;SS=N	amino acid transporter system A1	8.2
15	439318	AW837046	Hs.6527	7tm_2,Cytc_asm,GPS;TM=Y;S	G protein-coupled receptor 56	8.1
	442213	N36110	Hs.305971	sugar_tr;TM=Y;SS=M	solute carrier family 2 (facilitate	8.1
	412649	NM_002206	Hs.74369	Integrin_A,FG-GAP;TM=M;SS	integrin, alpha 7	8.1
	448913	AA194422	Hs.22564	rm,zf-RanBP,phkase,GST_	myosin VI	8.1
	420166	AW732276	Hs.95583	transmembrane4;TM=Y;SS=M	transmembrane 4 superfamily member	8.0
20	407102	AA007629	Hs.348601	transport_prot,SWIB,ASC	glycerol-3-phosphate dehydrogenase	7.9
	452516	AA058630	Hs.29759	TM=N;SS=M	RNA POLYMERASE I AND TRANSCRIPT REL	7.9
	413076	U10564	Hs.75188	pkinae;TM=M;SS=N	wee1 (S. pombe) homolog	7.9
	443604	C03577	Hs.9615	efhand;TM=M;SS=N	myosin regulatory light chain 2, sm	7.7
	429002	AW248439	Hs.2340	Armadillo_seg;TM=M;SS=N	junction plakoglobin	7.6
25	432562	BE531048	Hs.278422	zf-C2H2;TM=M;SS=N	DKFZP586G1122 protein	7.6
	426359	AA376409	Hs.10862	adenylatekinase,none	Homo sapiens cDNA: FLJ23313 fis, cl	7.5
	417733	AL048678	Hs.82503	NA;NA	H.sapiens mRNA for 3'UTR of unknown	7.5
	451541	BE279383	Hs.26557	Armadillo_seg;TM=M;SS=N	plakophilin 3	7.4
	443951	F13272	Hs.356835	PMP22_Claudin,none	feritin, light polypeptide	7.4
30	409960	BE261944	Hs.355264		hexokinase 1	7.3
	423184	NM_004428	Hs.1624	Ephrin;TM=M;SS=M	ephrin-A1	7.3
	405121	X04385	Hs.110802	Cys_knot,TGF-beta,vwa,vwc	von Willebrand factor (VWF), mRNA	7.1
	438974	AF089816	Hs.6454	PDZ;TM=N;SS=M	chromosome 19 open reading frame 3	7.1
	417771	AA804698	Hs.82547		retinoic acid receptor responder (I	7.0
35	424118	BE269041	Hs.140452	perilipin;TM=N;SS=M	cargo selection protein (mannose 6	7.0
	402705	X67951	Hs.180909	AhpC-TSA;TM=M;SS=M	peroxiredoxin 1 (PRDX1)	7.0
	417115	AW852792	Hs.334612	Sm,phkase;TM=N;SS=N	small nuclear ribonucleoprotein pol	7.0
	442572	AI001922	Hs.135121	HSP70	hypothetical protein FLJ22415	6.9
	447216	R75812	Hs.169248	cytochrome_c;NA;NA	p75NTR-associated cell death execut	6.9
40	422278	AF072873	Hs.114218	Fz,Frizzled,7tm_2;TM=Y;SS	frizzled (Drosophila) homolog 6	6.9
	414657	AA424074	Hs.76780	TM=M;SS=N	protein phosphatase 1, regulatory (6.9
	447528	AI612027	Hs.76277	TB2_DP1_HVA22;TM=Y;SS=M	Homo sapiens, clone MGC-9381, mRNA,	6.9
	436729	BE621807	Hs.351316	TM=Y;SS=M	transmembrane 4 superfamily member	6.9
	428013	AF151020	Hs.181444	TM=Y;SS=M	hypothetical protein	6.9
45	444143	AW747996	Hs.150399	Bcl-2,none	ESTs, Moderately similar to A56194	6.8
	414443	AI007268	Hs.76144	lg,phkase;TM=Y;SS=N	platelet-derived growth factor rece	6.7
	418751	BE389014	Hs.372548	SH2,none	phosphoinositide-3-kinase, regulato	6.7
	448479	H98115	Hs.21293	UDPGP;TM=M;SS=N	UDP-N-acetylglucosamine pyrophospho	6.6
	410552	X66945	Hs.748	lg,phkase,SH2,SH3,C2,PH,	fibroblast growth factor receptor 1	6.6
50	414883	AA926980	Hs.348669	CKS;TM=N;SS=N	CDC28 protein kinase 1	6.6
	417426	NM_002291	Hs.82124	laminin_EGF,laminin_Nterm	laminin, beta 1	6.6
	428179	AI127772	Hs.279696	pkinae,PX,phkase_C;TM=N	serum/glucocorticoid regulated kina	6.6
	443195	BE148235	Hs.193063	Aa_trans,none	Homo sapiens cDNA FLJ14201 fis, clo	6.5
	424512	X53002	Hs.149846	Integrin_B,EGF;TM=Y;SS=M	Integrin, beta 5	6.5
55	421733	AL119671	Hs.1420	lg,phkase;TM=Y;SS=M	fibroblast growth factor receptor 3	6.5
	428950	BE311879	Hs.194673	DED;TM=M;SS=N	phosphoprotein enriched in astrocyt	6.5
	450172	NM_005864	Hs.24587	SH3,hormona3;TM=M;SS=N	signal transduction protein (SH3 co	6.5
	416078	AL034349	Hs.79005		protein tyrosine phosphatase, recep	6.5
	408912	AB011084	Hs.48924	Armadillo_seg;TM=M;SS=M	KIAA0512 gene product; ALEX2	6.4
60	428373	AI751656	Hs.183986	ig;TM=Y;SS=M	poliovirus receptor-related 2 (herp	6.4
	449029	N28989	Hs.22891	aa_permeases;TM=Y;SS=M	solute carrier family 7 (cationic a	6.4
	406621	X57809	Hs.181125	ig,HSP70,Ppx-GppA;TM=M;SS	immunoglobulin lambda locus	6.4
	431629	AU077025	Hs.265827	TM=M;SS=Y	interferon, alpha-inducible protein	6.4
	428169	AI928984	Hs.182793	photoRC,UPF0118;TM=Y;SS=N	golgi phosphoprotein 2	6.4
65	443337	Y07604	Hs.9235	NDK;TM=N;SS=N	non-metastatic cells 4, protein exp	6.4
	451292	AB037716	Hs.26204	SH3;TM=M;SS=N	KIAA1295 protein	6.4
	425976	C75094	Hs.334514	voltage_CL_C;TM=Y;SS=M	NG22 protein	6.4
	426539	AB011155	Hs.170290	SH3,PDZ,Guanylate_kin;TM=	discs, large (Drosophila) homolog 5	6.3
70	417208	S67773	Hs.81665	lg,phkase;TM=Y;SS=M	v-kit Hardy-Zuckerman 4 feline sarc	6.3
	438278	BE409248	Hs.57988	TFIIIS,RNA_POL_M_15KD,UPFO	hypothetical protein FLJ22357 simil	6.3
	429455	AI472111	Hs.278694	lectin_c	CD209 antigen	6.3
	431685	AW296135	Hs.267659	CH,DAG_PE-bind,PH,RhoGEF,	vav 3 oncogene	6.3
	445033	AV652402	Hs.72901	ant;TM=N;SS=N	cyclin-dependent kinase inhibitor 2	6.3
	411756	BE294350	Hs.71891	pkinae,F5_F8_type_C;TM=Y	discolidin domain receptor family, m	6.3
75	453902	BE502341	Hs.3402		ESTs	6.3
	418005	AI186220	Hs.83164	Collagen,TSPN;TM=M;SS=M	collagen, type XV, alpha 1	6.2
	449924	W30681	Hs.146233	SH3,none	Homo sapiens cDNA: FLJ22130 fis, cl	6.2
	426520	BE545684	Hs.343566	aa_permeases,pyridoxal_de	KIAA0251 protein	6.2
	453064	R40334	Hs.89463		potassium large conductance calcium	6.2
80	448520	AB002367	Hs.21355	pkinae,DCX;TM=M;SS=N	doublecortin and CaM kinase-like 1	6.2
	452683	AI089575	Hs.374574	homeobox,none	progesterone membrane binding prote	6.2
	402575	AF043329	Hs.173717	PAP2;TM=Y;SS=M	PPAP2B Phosphatidic acid phosphat. type 2B	6.2
	444672	Z95636	Hs.11669	laminin_EGF,laminin_G,EGF	laminin, alpha 5	6.2
	450440	AB024334	Hs.25001	14-3-3;TM=M;SS=N	tyrosine 3-monooxygenase/tryptophan	6.2

	432314	AA533447	Hs.285173	Xlink,nona	ESTs	6.1
	438564	AA381553	Hs.198253	ig,MHC_II_alpha,nona	major histocompatibility complex, c	6.1
	444252	R21135	Hs.54985		ESTs	6.1
5	425184	BE278288	Hs.155048	ig;TM=Y;SS=M	Lutheran blood group (Aubergier b an	6.1
	431890	X17033	Hs.271986	vwa;integrin_A,FG-GAP;TM=	integrin, alpha 2 (CD49B, alpha 2 s	6.1
	449475	AJ348027	Hs.129826	transmembrane4;TM=Y;SS=M	hypothetical protein PP1057	6.1
	449538	AJ559444	Hs.104679	TM=M;SS=M	ESTs	6.0
	414496	W73853	Hs.355424	pkinae,F5_F8_type_C,adh_	ESTs	6.0
	414217	AJ309298	Hs.279898	NA;NA	Homo sapiens cDNA: FLJ23165 fis, cl	6.0
10	445333	BE537641	Hs.44278	ras,arf,TK;TM=N;SS=M	hypothetical protein FLJ12538 simil	5.9
	431183	NM_006855	Hs.250596	ER_lumen_recept;TM=M;SS=M	KDEL (Lys-Asp-Glu-Leu) endoplasmic	5.9
	409645	AJ142265	Hs.55498	polyprenyl_synt;TM=M;SS=N	geranylgeranyl diphosphate synthase	5.9
	412276	BE262621	Hs.73798	MIF,sugar_br,none	macrophage migration inhibitory fac	5.9
15	416137	BE279513	Hs.278607	pkinae,UBA,ThiF;TM=M;SS=	ubiquitin activating enzyme E1-like	5.9
	412969	AJ373162	Hs.75103	14-3-3;TM=N;SS=M	tyrosine 3-monooxygenase/tryptophan	5.9
	414504	AW069181	Hs.115175	pkinae,SAM;TM=M;SS=N	sterile-alpha motif and leucine zip	5.9
	433573	AF234887	Hs.57652	7tm_2,EGF,cadherin,lamtni	cadherin, EGF LAG seven-pass G-type	5.9
	436415	BE265254	Hs.343258	Peptidase_M24,Furin-like,	proliferation-associated 2G4, 38kD	5.9
20	413900	AW409747	Hs.55612	TPR,PDZ,VW,Guanylate_kin;	stress-induced-phosphoprotein 1 (Hs	5.9
	441455	AJ271671	Hs.7854	Zip;TM=Y;SS=M	zinc/ferron regulated transporter-fk	5.9
	444006	BE395085	Hs.334762	kl_recept_a,PKD,MHC_J;TM	type I transmembrane protein Fn14	5.8
	408269	AW888219	Hs.44077	CH;TM=M;SS=N	parvin, alpha	5.8
	411372	AJ147861	Hs.213289	Glyco_transf_11,EGF,Jdl_r	low density lipoprotein receptor (f	5.8
25	450825	AC005954	Hs.25527	PDZ,Guanylate_kin;TM=M;SS	tight junction protein 3 (zona oocl	5.8
	456534	X91195	Hs.100623	LIM,PDZ,pkinae;TM=N;SS=M	phospholipase C, beta 3, neighbor p	5.7
	451558	NM_001089	Hs.26630	ABC_tran,SRP54;TM=Y;SS=M	ATP-binding cassette, sub-family A	5.7
	446812	AL042279	Hs.16206	pkinae	uncharacterized hypothalamus protei	5.7
	424307	AW293399	Hs.356377		nuclear receptor co-repressor 1	5.7
30	405484	XM_093451		TM=N;SS=M	C3002124:g[12737280]ref[XP_006682	5.7
	425367	BE271188	Hs.155975	TM=M;SS=Y	protein tyrosine phosphatase, recep	5.7
	444607	AW405635	Hs.293687	PI-PLC-X,PH,PI-PLC-Y	ESTs	5.7
	421456	AW579842	Hs.104557	zf-C2H2,DUF18,efhand,C2_P	hypothetical protein FLJ10697	5.6
	412810	M21574	Hs.74615	ig,pkinae,DUF11;TM=M;SS=	platelet-derived growth factor rece	5.6
35	450334	AF035959	Hs.24879	PAP2;TM=Y;SS=M	phosphatidic acid phosphatase type	5.6
	453880	AJ803166	Hs.135121	HSP70,none	ESTs, Weakly similar to I38022 hypo	5.6
	439578	AW263124	Hs.350547	WD40;TM=M;SS=N	nuclear receptor co-repressor/HDAC3	5.6
	450954	AJ904740	Hs.25691	TM=Y;SS=M	receptor (calcitonin) activity modi	5.6
	414555	N88569	Hs.76422	phoslip;TM=M;SS=Y	phospholipase A2, group IIA (platel	5.6
40	409963	AA133590	Hs.377830	MBOAT,none	calcium/calmodulin-dependent protei	5.6
	450463	AW952018	Hs.201398	C1q,Collagen;TM=M;SS=Y	G protein coupled receptor interact	5.6
	425177	AF127577	Hs.155017	TM=N;SS=M	nuclear receptor interacting protei	5.5
	445496	AB007860	Hs.12802	SH3,ank,PH,ArfGap;TM=M;SS	development and differentiation enh	5.5
	428981	BE313077	Hs.93135	nm	ESTs, Weakly similar to ALU2_HUMAN	5.5
45	424441	X14850	Hs.147097	histone,CBFD_NFYB_HMF;TM=	H2A histone family, member X	5.5
	415662	AW972481	Hs.170610	pkinae,none	ESTs, Highly similar to G01887 MEK	5.5
	422105	AJ929700	Hs.111680	TM=M;SS=N	endosulfine alpha	5.5
	428556	AW139399	Hs.314807	TM=M;SS=N	ESTs	5.5
	408056	AA312329	Hs.42331	Ephrin;TM=M;SS=M	ephrin-A4	5.5
50	425205	NM_005854	Hs.155106	TM=Y;SS=N	receptor (calcitonin) activity modi	5.5
	444633	AF111713	Hs.12284	ig;TM=Y;SS=M	junctional adhesion molecule 1	5.5
	431565	AF161470	Hs.260622	TM=Y;SS=N	butyrate-induced transcript 1	5.5
	429655	U48959	Hs.211582	pkinae,fn3,lg,none	myosin, light polypeptide kinase	5.5
	431886	L77964	Hs.271980	pkinae;TM=M;SS=N	mitogen-activated protein kinase 6	5.5
55	453143	AA382234	Hs.356289	serpin;TM=N;SS=M	protein tyrosine phosphatase, recep	5.4
	451863	AL120634	Hs.331803	cpn60_TCP1,E1-E2_ATPase,C	ATPase, Ca transporting, plasma mem	5.4
	422293	X94453	Hs.114366	aldedh,aakinae;TM=M;SS=N	pymolito-5-carboxylate synthetase	5.4
	432179	X75208	Hs.2913	EPH_b,d,fn3,pkinae,SAM,T	EphB3	5.4
	408048	NM_007203	Hs.42322	Paralemmin;TM=M;SS=N	A kinase (PRKA) anchor protein 2	5.4
60	448153	Y10805	Hs.20521	NusG;TM=N;SS=M	HMT1 (hnRNP methyltransferase, S. c	5.4
	421251	Z28913	Hs.102948	LIM,PDZ;TM=N;SS=M	enigma (LIM domain protein)	5.4
	439039	AJ656707	Hs.48713	pkinae,none	ESTs	5.4
	409882	AJ243191	Hs.55674	HSP20;TM=N;SS=M	heat shock 27kD protein family, mem	5.4
65	451295	AJ557212	Hs.17132	pkinae,DAG_PE-blind,pkina	ESTs, Moderately similar to I54374	5.4
	442549	AJ751601	Hs.8375	MATH,zf-TRAF,zf-C3HC4;TM=	TNF receptor-associated factor 4	5.4
	445930	AF055009	Hs.13456	DAGKc,DAGKa,ank,WD40,bZIP	Homo sapiens clone 24747 mRNA seque	5.4
	453082	H18835	Hs.31608	ion_trans;TM=Y;SS=M	hypothetical protein FLJ20041	5.4
	426432	AF001601	Hs.169857	Arylesterase;TM=M;SS=N	paraoxonase 2	5.4
	415753	U52819	Hs.78781	PDGF;TM=M;SS=M	vascular endothelial growth factor	5.4
70	450778	U81375	Hs.25450	Nucleoside_tran;TM=Y;SS=M	solute carrier family 29 (nucleosid	5.4
	414739	U83867	Hs.77196	efhand,SH3,spectrin;TM=N;	spectrin, alpha, non-erythrocytic 1	5.3
	421233	AA209534	Hs.284243	transmembrane4;TM=Y;SS=M	tetraspan NET-6 protein	5.3
	414774	X02419	Hs.77274	kringle,trysin,plan_thi	plasminogen activator, urokinase	5.3
	414368	W70171	Hs.75939	PRK,CoaE;TM=N;SS=N	uridine monophosphate kinase	5.3
75	448051	BE048061	Hs.37054	Ephrin_A_deamin,dsrm,z-al	ephrin-A3	5.3
	423619	T48691	Hs.249159	7tm_1,7tm_2;TM=Y;SS=M	adrenergic, alpha-2A-, receptor	5.3
	440188	AK001812	Hs.7036	ROK;TM=M;SS=N	N-Acetylglucosamine kinase	5.3
	414135	NM_004419	Hs.2128	Rhodanese,DSPE_Y_phosphat	dual specificity phosphatase 5	5.3
	444838	AV651680	Hs.208558	integrin_A,FG-GAP,none	ESTs	5.3
80	447918	AJ129320	Hs.115175	pkinae,SAM,none	ESTs, Highly similar to JC5818 gamm	5.3
	405517	AF000974	Hs.119498	LIM;TM=M;SS=N	thyroid hormone receptor interactor 6	5.3
	413588	AA971014	Hs.75432	IMPDH_C,CBS,IMPDH_N;TM=M;	IMP (inosine monophosphate) dehydro	5.2
	411089	AA456454	Hs.355702		cell division cycle 2-like 1 (PITSL	5.2
	416157	NM_003243	Hs.342874	zona_pellucida;TM=Y;SS=M	transforming growth factor, beta re	5.2

5	407744	AB020629	Hs.38095	ABC_tran,PRK;TM=Y;SS=M	ATP-binding cassette, sub-family A	5.2
	446108	AL036596	Hs.42322	Paralemmin;TM=M;SS=N	A kinase (PKA) anchor protein 2	5.2
	422034	AC006486	Hs.333069	Ets;TM=M;SS=N	Ets2 repressor factor	5.2
	417098	AB017365	Hs.173859	Frizzled,Fz,7tm_2,toxin_2	frizzled (Drosophila) homolog 7	5.2
	430526	AF181862	Hs.242407	7tm_3;TM=Y;SS=M	G protein-coupled receptor, family	5.2
	414176	BE140638	Hs.75794	7tm_1,CRC8;TM=Y;SS=N	EDG-2 (endothelial differentiation	5.2
	416710	AI268325	Hs.54890	Peptidase_M49,EGF,Ig,Neur	hypothetical protein FLJ23590	5.2
	417896	AA379770	Hs.82890	DAD;TM=Y;SS=M	defender against cell death 1	5.2
10	413244	AW955951	Hs.159265	BTB,Pep_M12B_propep,Rapro	kruppel-related zinc finger protein	5.2
	421837	AF135168	Hs.108802	AAA,cdc48_N,cdc48_2,NB-AR	N-ethylmaleimide-sensitive factor	5.2
	429379	NM_014840	Hs.200598	pkinase,RIO1;TM=M;SS=N	KIAA0537 gene product	5.2
	429619	AL120751	Hs.211568		eukaryotic translation initiation f	5.2
	437275	AW976035	Hs.292396	Frizzled,Fz	ESTs, Weakly similar to A47582 B-ce	5.1
15	421071	AJ311238	Hs.104476	TM=Y;SS=M	ESTs, Weakly similar to CGH1E coll	5.1
	448581	NM_002709	Hs.21537		protein phosphatase 1, catalytic su	5.1
	452568	AA805634	Hs.300870	PI3_PI4_kinase;TM=M;SS=M	Homo sapiens mRNA; cDNA DKFZp547M07	5.1
	452069	AB028949	Hs.183994	Metallophos;TM=M;SS=N	KIAA1026 protein	5.1
	437175	AW968078	Hs.87773	pkinase,pkinase_C,none	protein kinase, cAMP-dependent, cat	5.1
20	437056	AI147061		spectrin,SH3,PH,CH	gb:ok33a11.s1 Scores_NSIF_F8_9W_OT_P	5.1
	450998	BE387614	Hs.25797	rm;TM=M;SS=N	splicing factor 3b, subunit 4, 49kD	5.1
	444441	AW613841	Hs.301394	IRK;TM=Y;SS=N	hypothetical protein MGC3101	5.1
	448528	BE613248	Hs.172084	PHD;TM=M;SS=N	Homo sapiens, clone IMAGE:3627860,	5.1
	452345	AA293279	Hs.29173	DSPc;TM=M;SS=N	hypothetical protein FLJ20515	5.1
25	443412	W84893	Hs.9305		angiotensin receptor-like 1	5.1
	412853	M34175	Hs.74626	Adaptin_N,Alpha_adaptinC2	adaptor-related protein complex 2,	5.1
	439866	AA280717	Hs.6727	rm,NTF2;TM=M;SS=N	Ras-GTPase activating protein SH3 d	5.1
	439975	AW328081	Hs.6817	Ham1p_lke;TM=M;SS=N	inosine triphosphatase (nucleoside	5.1
	435523	T62849	Hs.11090	TM=Y;SS=M	membrane-spanning 4-domains, subfam	5.1
30	433423	BE407127	Hs.8997	HSP70,Ig,Ppx-GppA;TM=M;SS	heat shock 70kD protein 1A	5.1
	412641	M16680	Hs.74335	HSP90,HATPase_c;TM=M;SS=N	heat shock 90kD protein 1, beta	5.1
	431236	AV656840	Hs.285115	fn3;TM=Y;SS=M	interleukin 13 receptor, alpha 1	5.1
	438552	AJ245820	Hs.6314		type I transmembrane receptor (seiz	5.0
	422765	AW409701	Hs.1578	BLR;TM=M;SS=N	baculoviral IAP repeat-containing 5	5.0
35	427502	AJ811865	Hs.7133	TM=M;SS=N	Homo sapiens, clone IMAGE:3161564,	5.0
	414166	AW888941	Hs.75789	DEAD,helicase_C,rm,Ndr,C	N-myc downstream regulated	5.0
	424954	NM_000546	Hs.1846	P53,WD40,IRK;TM=M;SS=N	tumor protein p53 (Li-Fraumeni synd	5.0
	422089	AA523172	Hs.103135	REJ,PLAT,PKD,WSC,LRR	ESTs, Weakly similar to SFR4_HUMAN	5.0
	426636	BE242634	Hs.2055	ThIF,UBACT;TM=M;SS=N	ubiquitin-activating enzyme E1 (A1S	5.0
40	410793	AW581906	Hs.66392	SH3,efhand,C2,PH,RhoGEF,M	intersectin 1 (SH3 domain protein)	5.0

TABLE 5B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

437056 428504_3 AW976398 AH147061 AA765223 AA743380 AI803927

TABLE 5C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
405484	5922025	Plus	199214-199579,199672-199920,200262-20049

TABLE 6A: 777 GENES UP-REGULATED IN COLON CANCER COMPARED TO NORMAL ADULT TISSUES

Table 6A lists 777 genes up-regulated in colon cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" colon cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" colon cancer level was set to the 90th percentile amongst 95 colon cancers. The "average" normal adult tissue level was set to the 90th percentile amongst 209 non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the 209 non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 Rt: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
5	447033	AI357412	Hs.157601	ESTs	31.35
	409041	AB033025	Hs.50081	KIAA1199 protein	29.00
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	26.41
	422330	D30783	Hs.115263	epiregulin	24.38
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	24.00
10	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	23.55
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	22.70
	416209	AA235776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	21.60
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	21.15
	415989	AI267700	Hs.317584	ESTs	20.95
15	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	19.35
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	18.68
	421470	R27496	Hs.1378	annexin A3	18.05
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	17.30
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	17.15
20	450531	AW301032	Hs.203800	ESTs	16.60
	432867	AW016936	Hs.233354	ESTs	16.35
	443211	AI28388	Hs.143555	ESTs	15.80
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	15.10
	406964	M21305	Hs.143655	gb:Human alpha satellite and satellite 3	15.00
25	410355	S58544	Hs.153057	sperm associated antigen 1	14.70
	441377	BE218239	Hs.202656	ESTs	14.45
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	14.35
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	14.35
	440304	BE159984	Hs.125395	ESTs	14.25
30	426427	M86699	Hs.169840	TTK protein kinase	13.60
	451561	N52812	Hs.177403	ESTs	12.80
	434032	AW009951	Hs.206892	ESTs	12.75
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone CO	12.65
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfam	12.55
35	428564	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	12.40
	446232	AJ281848	Hs.194691	retinoic acid induced 3	12.25
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	12.18
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	11.85
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZNS1_HUMAN Z	11.80
40	422011	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	11.65
	452461	N78223	Hs.108106	transcription factor	11.42
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	11.35
	400534				11.00
	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	10.75
45	453688	AW381270	Hs.194110	hypothetical protein PRO2730	10.75
	426890	AA393167	Hs.41294	ESTs	10.60
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	10.55
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	10.50
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	10.50
50	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	10.40
	425761	AW664214	Hs.195729	ESTs	10.25
	404567				10.15
	428536	AI143139	Hs.2288	visinin-like 1	10.10
	414972	BE263782	Hs.77695	KIAA0008 gene product	10.05
55	459504	BE514127		gb:601315974F1 NIH_MGC_8 Homo sapiens cD	9.95
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	9.90
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	9.85
	442353	BE379594	Hs.49135	ESTs, Moderately similar to ALU7_HUMAN A	9.85
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	9.78
60	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	9.73
	420900	AL045633	Hs.44269	ESTs	9.68
	438639	AJ278360	Hs.31409	ESTs	9.55
	439521	AJ808955	Hs.58248	ESTs	9.55
	445676	AJ247763	Hs.16928	ESTs	9.50
65	408489	AI082437	Hs.26690	ESTs	9.50
	418738	AW388633	Hs.66882	solute carrier family 7, (cationic amino	9.37
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	9.00
	423349	AF010258	Hs.127428	homeo box A9	8.96
	400195	NA		NA	8.90
70	411765	H43346		gb:yp09a04.r1 Soares breast 3NtHBst Homo	8.90
	418895	AA894638	Hs.14600	ESTs	8.85
	424653	AW977534	Hs.151469	calcium/calmodulin-dependent serine prot	8.80
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	8.75
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	8.65
75	414559	AV656184	Hs.76452	C-reactive protein, pentraxin-related	8.64
	445436	AI224105	Hs.151408	ESTs	8.50
	403776				8.50
	433447	U29195	Hs.3281	neuronal pentraxin II	8.50
	407168	R45175	Hs.117183	ESTs	8.31
80	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	8.30
	422505	AL120862	Hs.124165	ESTs	8.25
	458242	BE299588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	8.20
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	8.15
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	8.10
	409687	T51125	Hs.8493	ESTs	8.05

	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	8.00
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	7.93
	406360	NA		NA	7.80
5	443450	N66045	Hs.133529	ESTs	7.75
	414422	AA147224	Hs.337232	ESTs	7.75
	442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	7.70
	438604	AA811896	Hs.44604	ESTs	7.60
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	7.55
	400250	NA		NA	7.53
10	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	7.50
	404996				7.50
	450459	AI697193	Hs.299254	Homo sapiens cDNA: FLJ23597 fis, clone L	7.45
	445019	AI205540	Hs.281295	ESTs	7.30
15	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	7.25
	448816	AB033052	Hs.22151	KIAA1226 protein	7.25
	444361	W76027	Hs.23920	hypothetical protein FLJ11105	7.25
	449370	AK002114	Hs.23495	hypothetical protein FLJ11252	7.20
	433859	AW896758	Hs.273789	ESTs	7.20
20	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	7.20
	456120	AA535244	Hs.78305	RAB2, member RAS oncogene family	7.20
	419751	AW195581	Hs.93121	KIAA0761 protein	7.16
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	7.15
	456553	AA721325	Hs.189058	ESTs, Highly similar to Similar to a C.a	7.15
25	421373	AA808229	Hs.167771	ESTs	7.10
	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	7.00
	423248	AA380177	Hs.125845	ribulose-5-phosphate-3-epimerase	6.96
	444798	BE242144	Hs.12013	ATP-binding cassette, sub-family E (OABP	6.95
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	6.95
30	413573	AI733859	Hs.149089	ESTs	6.95
	442660	AW138174	Hs.130651	ESTs	6.93
	427878	C05766	Hs.181022	CGI-07 protein	6.90
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	6.85
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp586I1518 (f	6.82
35	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	6.80
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	6.80
	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	6.75
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	6.75
40	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	6.71
	401644				6.70
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	6.70
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	6.69
	406747	AI925153	Hs.217493	annexin A2	6.65
45	445191	AF048686	Hs.12393	dTDP-D-glucose 4,6-dehydratase	6.60
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	6.60
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	6.55
	427072	H38046	Hs.303193	ESTs	6.55
	452588	AA889120	Hs.110637	homeo box A10	6.53
50	439809	R41396	Hs.101774	hypothetical protein FLJ23045	6.50
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE; Human selen	6.50
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	6.50
	423685	BE350494	Hs.49753	uvet autoantigen with coiled coil domai	6.50
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	6.50
55	410908	AA121686	Hs.10592	ESTs	6.47
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	6.47
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.45
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	6.42
	451389	N73222	Hs.279009	matrix Gla protein	6.40
60	438202	AW169287	Hs.22588	ESTs	6.40
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	6.40
	425860	L29339	Hs.1964	solute carrier family 5 (sodium/glucose	6.37
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.36
	436539	AI005457	Hs.275048	ESTs	6.35
65	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	6.34
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	6.32
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	6.31
	407237	AA169872	Hs.6216	Homo sapiens hepatocellular carcinoma-as	6.30
	413597	AW302885	Hs.117183	ESTs	6.30
70	429529	AA454190	Hs.24283	ESTs, Moderately similar to reduced expr	6.30
	409916	BE313525	Hs.57435	solute carrier family 11 (proton-coupled	6.25
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	6.20
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.20
	438050	BE262816	Hs.6061	protein kinase, AMP-activated, beta 1 no	6.20
75	416857	AA188775	Hs.292453	ESTs	6.20
	409683	U33317	Hs.711	defensin, alpha 6, Paneth cell-specific	6.18
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	6.15
	420096	AA775910	Hs.95011	syntrophin, beta 1 (dystrophin-associate	6.15
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.15
80	433393	AF038564	Hs.98074	itchy (mouse homolog) E3 ubiquitin prote	6.11
	424745	AA214618	Hs.152759	activator of S phase kinase	6.10
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	6.10
	454438	AA224053	Hs.172405	cell division cycle 27	6.08
	407771	AL138272	Hs.62713	ESTs	6.08

5	416057	AI927382	Hs.29857	ESTs	6.05
	442917	AA314907	Hs.85950	ESTs	6.00
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	6.00
	453700	AB009426	Hs.560	apolipoprotein B mRNA editing enzyme, ca	5.96
	412246	AI160873	Hs.69233	zinc finger protein	5.96
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	5.95
	418668	AW407987	Hs.173518	M-phase phosphoprotein homolog	5.95
	418421	AA134006	Hs.79306	eukaryotic translation initiation factor	5.95
10	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	5.90
	409913	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	5.90
	429201	X03178	Hs.198246	group-specific component (vitamin D bind	5.87
	408908	BE296227	Hs.250822	serine/threonine kinase 15	5.86
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	5.86
15	432298	AL118812	Hs.274293	Homo sapiens mRNA; cDNA DKFZp761G1111 (f	5.85
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.85
	441645	AI222279	Hs.201555	ESTs, Weakly similar to T23406 hypotheti	5.85
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	5.85
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	5.85
20	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.82
	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	5.80
	459309	AA040820	Hs.5672	hypothetical protein AF140225	5.80
	410060	NM_001448	Hs.58367	glypican 4	5.79
	423806	AA331247	Hs.86617	ESTs	5.77
25	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	5.75
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	5.75
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.75
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypotheti	5.75
	442957	AI949552	Hs.49397	ESTs	5.75
30	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	5.70
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.70
	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	5.70
	415385	R17798	Hs.7535	COBW-like protein	5.70
	409757	NM_001898	Hs.123114	cystatin SN	5.69
35	433687	AA743891		gb:ny57g01.s1 NCL CGAP_Pr18 Homo sapiens	5.68
	424492	AI133482		gb:HA2093 Human fetal liver cDNA library	5.60
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	5.60
	438777	AA825487	Hs.142179	ESTs	5.60
	417235	AA810278	Hs.24250	ESTs	5.60
40	451177	AI969716	Hs.13034	ESTs	5.60
	415227	AW821113	Hs.72402	ESTs	5.58
	436217	T53925	Hs.107	fibrinogen-like 1	5.56
	452881	AW135220	Hs.241921	ESTs	5.55
	426010	AA136553	Hs.1975	hypothetical protein FLJ21007	5.55
45	426235	AI631964	Hs.34447	ESTs	5.55
	445640	AW969526	Hs.31704	ESTs, Weakly similar to KIAA0227 [Hsapi	5.53
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked mol	5.52
	442980	AA857025	Hs.6878	kinesin-like 1	5.50
50	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.50
	453884	AA355925	Hs.36232	KIAA0186 gene product	5.47
	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.47
	419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	5.47
	420218	AW958037	Hs.286	ribosomal protein L4	5.45
	421155	H87879	Hs.102267	lysyl oxidase	5.45
55	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	5.45
	456435	AI880384	Hs.270747	ESTs, Weakly similar to ALU2_HUMAN ALU S	5.45
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	5.44
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	5.42
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	5.41
60	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	5.41
	453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	5.35
	430217	N47863	Hs.336901	ribosomal protein S24	5.33
	417372	T99755	Hs.334728	ESTs	5.30
	415139	AW975942	Hs.48524	ESTs	5.30
65	412140	AA219691	Hs.73625	RAB6 Interacting, kinesin-like (rabkines	5.29
	424086	AI351010	Hs.102267	lysyl oxidase	5.27
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.27
	417576	AA339449	Hs.82285	phosphoribosylglycnamide formyltransfer	5.26
	452131	AI860677	Hs.72325	Human DNA sequence from clone RP1-187J11	5.25
70	436016	AA805465	Hs.121536	Human DNA sequence from clone RP11-472E5	5.25
	449347	AV649748	Hs.295901	KIAA0493 protein	5.25
	445038	AI635444	Hs.143917	dJ467N11.1 protein	5.25
	453921	AI824009	Hs.44577	ESTs	5.25
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	5.25
75	421076	AW007988	Hs.233299	ESTs, Weakly similar to I38022 hypotheti	5.25
	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	5.24
	433384	AI021992	Hs.124244	ESTs	5.23
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	5.21
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	5.20
80	441795	N58115	Hs.21137	AD024 protein	5.20
	449416	AI651016	Hs.246311	ESTs	5.20
	418379	AA218940	Hs.137516	fidgetin-like 1	5.20
	426753	T89832	Hs.170278	ESTs	5.18
	422109	S73265	Hs.1473	gastrin-releasing peptide	5.17

5	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	5.17
	416806	NM_000288	Hs.79993	peroxisomal biogenesis factor 7	5.17
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	5.15
	427728	AJ245600	Hs.180545	Homo sapiens mRNA for hypothetical prote	5.15
	447713	AI420733	Hs.207083	ESTs	5.15
	425739	T19016	Hs.159410	molybdopterin synthase sulfurylase	5.15
	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	5.15
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	5.13
10	441139	AW449009	Hs.126647	ESTs	5.13
	451121	AW973795	Hs.128927	Homo sapiens cDNA FLJ13903 fis, clone TH	5.10
	435202	AI971313	Hs.170204	KIAA0551 protein	5.10
	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	5.10
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	5.09
	422805	AA436989	Hs.121017	H2A histone family, member A	5.07
15	411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	5.06
	435496	AW340171	Hs.265399	ESTs, Weakly similar to transformation-r	5.06
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	5.05
	413293	AL047483	Hs.302498	GTP-binding protein homologous to Saccha	5.05
	445236	AK001676	Hs.12457	hypothetical protein FLJ10814	5.05
20	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.05
	441675	AI914329	Hs.5461	ESTs	5.00
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	5.00
	401480	NA	NA	NA	5.00
25	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	4.95
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	4.92
	414718	H95348	Hs.107987	ESTs	4.91
	419139	AI123517	Hs.269940	ESTs	4.90
	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	4.90
30	425420	BE536911	Hs.234545	hypothetical protein NUF2R	4.90
	408758	NM_003686	Hs.47504	exonuclease 1	4.90
	439741	BE379646	Hs.6904	Homo sapiens mRNA full length insert cDN	4.90
	418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	4.90
	433927	AI557019	Hs.116467	small nuclear protein PRAC	4.89
35	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	4.88
	455777	AA524285	Hs.154172	ESTs, Moderately similar to BCGF_HUMAN B	4.87
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (tr	4.87
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	4.86
	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (R	4.85
40	418396	AI765805	Hs.26691	ESTs	4.85
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	4.84
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	4.80
	406414				4.75
	430178	AW449612	Hs.152475	ESTs	4.71
45	411901	AA165730	Hs.6966	Human DNA sequence from clone RP1-187J11	4.70
	404025	NA		NA	4.70
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	4.68
	436662	AI582393	Hs.126695	ESTs	4.68
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	4.68
	410044	BE568742	Hs.58169	highly expressed in cancer, rich in leuc	4.65
50	431041	AA490967	Hs.197955	KIAA0704 protein	4.65
	417860	AW408557	Hs.235498	hypothetical protein FLJ14075	4.65
	410658	AW105231	Hs.192035	ESTs	4.65
	425895	AI269484	Hs.161427	zinc finger protein 215	4.65
55	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	4.65
	436397	AA715013	Hs.169835	ESTs	4.60
	439225	AA192669	Hs.45032	ESTs	4.60
	423197	T91418	Hs.125156	transcriptional adaptor 2 (ADA2, yeast,	4.60
	413374	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	4.60
60	412723	AA648459	Hs.335951	hypothetical protein AF301222	4.59
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	4.59
	452795	AW392555	Hs.18878	hypothetical protein FLJ21620	4.58
	430704	AW813091	Hs.335799	ESTs	4.56
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	4.55
65	433326	AI379486	Hs.159430	ESTs	4.55
	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferri	4.55
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	4.55
	423343	AA324643	Hs.246106	ESTs	4.55
	416467	H57585	Hs.37467	ESTs	4.55
70	408867	AA437199	Hs.656	cell division cycle 25C	4.54
	419423	D26488	Hs.90315	KIAA0007 protein	4.54
	414132	AI801235	Hs.48480	ESTs	4.53
	423948	AW392342	Hs.263077	centrosomal P4.1-associated protein; unc	4.53
	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acylt	4.50
75	451009	AA013140	Hs.115707	ESTs	4.50
	431064	AI903735		gb:MR-BT035-200199-031 BT035 Homo sapien	4.50
	432725	AL137496	Hs.9001	ESTs	4.50
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	4.50
	410486	AW235094	Hs.69233	zinc finger protein	4.50
80	428532	AF157326	Hs.184786	TBP-interacting protein	4.50
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	4.50
	408380	AF123050	Hs.44532	diubiquitin	4.49
	423936	U77629	Hs.135639	achaete-scute complex (Drosophila) homol	4.47
	434294	AJ271379	Hs.76194	ribosomal protein S5	4.47

	442875	BE623003	Hs.23625	Homo sapiens clone TCCTA00142 mRNA sequ	4.46
	447102	BE167434	Hs.98471	ESTs, Weakly similar to T18712 hypothe	4.45
	410142	AA081924	Hs.124918	KIAA1795 protein	4.45
5	434894	AW977850	Hs.23856	hypothetical protein MGC5297	4.45
	420092	AA814043	Hs.88045	ESTs	4.45
	400115	NA		NA	4.45
	430957	H16791	Hs.31445	ESTs	4.41
	438078	AI016377	Hs.131693	ESTs	4.41
10	412359	AW837985		gb:QV3-LT0048-140200-083-e05 LT0048 Homo	4.40
	429774	AI522215	Hs.50883	KIAA1804 protein	4.40
	426214	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	4.40
	419790	U79250	Hs.93201	glycerol-3-phosphate dehydrogenase 2 (mi	4.40
	450480	X82125	Hs.25040	zinc finger protein 239	4.40
15	421211	AA284966	Hs.266308	mosaic serine protease	4.40
	419251	X07876	Hs.89791	wingless-type MMTV integration site fami	4.40
	434414	AI798376		gb:tr34b07.x1 NCJ_CGAP_Ov23 Homo sapiens	4.37
	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT	4.35
	410568	AW162948	Hs.64542	cleavage and polyadenylation specific fa	4.35
20	459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	4.35
	448243	AW369771	Hs.52620	integrin, beta 8	4.35
	438069	N80701	Hs.33790	ESTs	4.35
	446152	AI292036	Hs.150028	ESTs	4.34
	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	4.32
25	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	4.30
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	4.30
	422835	BE218705	Hs.121378	metallothionein-like 5, testis-specific	4.30
	418845	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	4.30
	439619	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypothe	4.30
30	458076	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	4.30
	450192	AA263143	Hs.24596	RAD51-interacting protein	4.29
	443232	AF161521	Hs.9081	phenylalanyl-tRNA synthetase beta-subuni	4.28
	413881	L00190	Hs.75599	serine (or cysteine) proteinase inhibito	4.26
	434217	AW014795	Hs.23349	ESTs	4.26
35	409723	AW885757	Hs.257862	ESTs	4.25
	417956	AA210704	Hs.190465	ESTs	4.25
	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypothe	4.25
	409928	AL137163	Hs.57549	hypothetical protein dJ47384	4.24
	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	4.22
40	424583	AF017445	Hs.150926	fructose-1-phosphate guanylyltransferase	4.20
	429436	AA452934	Hs.279813	hypothetical protein	4.20
	424625	AW904466	Hs.321197	PDZ domain protein (Drosophila InaD-like	4.20
	448912	D83781	Hs.22559	KIAA0197 protein	4.20
	442671	AI005668	Hs.134779	EST	4.20
45	411893	R82845	Hs.273789	ESTs	4.20
	456281	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	4.20
	421106	AA877124	Hs.172844	ESTs	4.20
	451401	AI793163		gb:tr52g03.y5 NCJ_CGAP_Co8 Homo sapiens	4.20
	404516	NA		NA	4.20
50	414968	C16096	Hs.22826	tropomodulin 3 (ubiquitous)	4.20
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	4.20
	419229	AI827237	Hs.282884	ESTs	4.18
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	4.16
55	453911	AW503857	Hs.4007	Sarcoplasmic-associated protein	4.16
	433159	AB035898	Hs.150587	kinesin-like protein 2	4.15
	419247	S65791	Hs.89764	fragile X mental retardation 1	4.15
	432491	AA662910	Hs.42635	hypothetical protein DKFZp434K2435	4.15
	422093	AF151852	Hs.111449	CGI-94 protein	4.15
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	4.15
60	446999	AA151520	Hs.334822	hypothetical protein MGC4485	4.15
	414538	AW612228	Hs.107987	ESTs	4.14
	453931	AL121278	Hs.25144	ESTs	4.12
	427718	AI798680	Hs.25933	ESTs	4.11
	453863	X02544	Hs.572	orosomucoid 1	4.10
65	440209	H05049	Hs.22269	neurexin 3	4.10
	435148	AI918049	Hs.124961	ESTs	4.10
	409732	NM_016122	Hs.56148	NY-REN-58 antigen	4.10
	448692	AW013907	Hs.167531	methylenetetrahydrofolate-Coenzyme A carboxylase 2	4.10
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypothe	4.10
70	444188	AI393165	Hs.699	peptidylprolyl isomerase B (cyclophilin	4.10
	457059	BE561665	Hs.177677	exosome component Rrp40	4.10
	407162	N63855	Hs.142634	zinc finger protein	4.10
	406117				4.10
	434370	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	4.09
75	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MA	4.08
	448666	NM_014953	Hs.323346	KIAA1008 protein	4.07
	450375	AA009547	Hs.8850	a disintegrin and metalloproteinase doma	4.07
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	4.07
	456030	AA136106	Hs.184852	KIAA1553 protein	4.05
80	434082	AI373481	Hs.131715	hypothetical protein PR01777	4.05
	443646	AI085198	Hs.164226	ESTs	4.05
	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	4.05
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	4.05
	432619	AW291722	Hs.278526	related to the N terminus of tre	4.05

5	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	4.05
	423573	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	4.04
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-assoc	4.04
	424176	AL137273	Hs.142307	hypothetical protein	4.04
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.04
	418203	X54942	Hs.83758	CDC28 protein kinase 2	4.03
	435420	AI928513	Hs.59203	ESTs	4.03
	406666	V00495	Hs.184411	albumin	4.02
10	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	4.00
	449448	D60730	Hs.57471	ESTs	4.00
	421037	AI684808	Hs.197653	ESTs	4.00
	448310	AI480316		gb:tm26h09.x1 Soares_NFL_T_GBC_S1 Homo s	4.00
	408155	AB014528	Hs.43133	KIAA0628 gene product	4.00
15	413841	M34276	Hs.75576	plasminogen	3.98
	400110	NA		NA	3.98
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.97
	443715	AI583187	Hs.9700	cyclin E1	3.97
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.97
20	450164	AI239923	Hs.30098	ESTs	3.97
	451592	AI805416	Hs.213897	ESTs	3.95
	402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome delta	3.95
	426199	AA371865	Hs.97090	ESTs	3.95
	414148	BE084049		gb:PM0-BT0651-270400-003-f02 BT0651 Homo	3.95
25	417006	AW673606	Hs.80758	aspartyl-tRNA synthetase	3.94
	449532	W74653	Hs.271593	ESTs, Moderately similar to A47582 B-cel	3.93
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	3.93
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	3.92
	423337	NM_004655	Hs.127337	axin 2 (conductin, axl)	3.91
30	416185	AW975861	Hs.47367	KIAA1785 protein	3.91
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	3.90
	432596	AJ224741	Hs.278461	matrinin 3	3.90
	451229	AW967707	Hs.48473	ESTs	3.90
	413583	AL120806	Hs.5888	ESTs	3.90
35	432702	AW973953	Hs.293744	ESTs	3.90
	437207	T27503	Hs.15929	hypothetical protein FLJ12910	3.90
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	3.90
	423697	BE088697	Hs.131834	Homo sapiens mRNA; cDNA DKFZp434B0328 (f	3.90
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	3.90
40	432289	AI860145	Hs.55118	ESTs	3.89
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	3.88
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.88
	433042	AW193534	Hs.281895	Homo sapiens cDNA FLJ11660 fis, clone HE	3.88
	410094	BE147897	Hs.55593	general transcription factor IIF, polype	3.88
45	441826	AW503603	Hs.129915	phosphotriesterase related	3.87
	444059	R69743	Hs.116774	integrin, alpha 1	3.86
	426262	AI792141	Hs.196270	folate transporter/carrier	3.85
	452641	AW952893	Hs.237825	signal recognition particle 72kD	3.85
50	454403	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	3.85
	448315	AW290912	Hs.20797	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.85
	411343	U77949	Hs.69563	CDC6 (cell division cycle 6, S. cerevisi	3.85
	409734	BE161664	Hs.56155	hypothetical protein	3.85
	454014	AW016670	Hs.233275	ESTs	3.84
	453116	AI276680	Hs.146086	ESTs	3.83
55	449508	AK001566	Hs.23618	hypothetical protein FLJ10704	3.82
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	3.82
	435040	AI932350	Hs.152825	ESTs	3.81
	426249	F05422	Hs.168352	nucleoporin-like protein 1	3.81
	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	3.81
60	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.81
	437631	AA764749	Hs.267245	hypothetical protein FLJ14803	3.80
	429118	H20669	Hs.35406	ESTs, Highly similar to unnamed protein	3.80
	405769				3.80
65	438295	AI394151	Hs.37932	ESTs	3.80
	453628	AW243307	Hs.83937	hypothetical protein	3.80
	450098	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	3.80
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.76
	423881	AK001720	Hs.134403	hypothetical protein FLJ10858	3.75
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	3.75
70	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.75
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.74
	420726	K02402	Hs.1330	coagulation factor IX (plasma thrombopla	3.74
	418413	R95735	Hs.117753	ESTs, Weakly similar to A48666 cell prol	3.73
	443354	AW970672	Hs.9247	protein kinase, AMP-activated, alpha 1 c	3.73
75	406667	M12523	Hs.184411	albumin	3.72
	436411	AW674352		gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD	3.72
	417246	AI760098	Hs.21411	ESTs	3.72
	410564	NM_008033	Hs.65370	lipase, endothelial	3.71
	432686	BE223007	Hs.152460	Homo sapiens cDNA FLJ12909 fis, clone NT	3.70
80	442881	AI023175	Hs.167022	ESTs	3.70
	432356	AA831032	Hs.111670	ESTs, Highly similar to JC2257 protyl ol	3.70
	450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	3.70
	405460	NA		NA	3.70
	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.70

	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-4	3.70
	425282	AW163518	Hs.155485	huntingtin interacting protein 2	3.69
	439857	AA847194	Hs.232002	ESTs	3.69
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfamily	3.69
5	444471	AB020684	Hs.11217	KIAA0877 protein	3.69
	419559	Y07828	Hs.91096	ring finger protein	3.69
	437641	AA811452	Hs.291911	ESTs	3.68
	455364	H72176	Hs.4273	hypothetical protein FLJ13159	3.67
10	417791	AW965339	Hs.111471	ESTs	3.66
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	3.66
	432023	AW273128	Hs.330144	EST	3.66
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.65
	450600	BE079478	Hs.24880	ESTs	3.65
	420595	AA278865	Hs.88523	ESTs	3.65
15	404477	NA	NA	NA	3.65
	457003	S78234	Hs.172405	cell division cycle 27	3.65
	443055	AV653742	Hs.15536	hypothetical protein DKFZp761J139	3.65
	452220	BE158006	Hs.212296	ESTs	3.65
20	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	3.65
	457465	AW301344	Hs.122908	DNA replication factor	3.64
	436149	AI754308	Hs.159452	ESTs	3.63
	433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	3.63
	427920	Z11502	Hs.181107	annexin A13	3.63
	424641	AB001106	Hs.151413	glia maturation factor, beta	3.63
25	428514	BE616533	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.62
	411975	AI916058	Hs.144583	ESTs	3.61
	409239	AA740875	Hs.44307	ESTs, Moderately similar to I38022 hypot	3.61
	429628	H09604	Hs.13268	ESTs	3.61
	449722	BE280074	Hs.23960	cyclin B1	3.60
30	426389	AW135714	Hs.283127	ESTs, Weakly similar to T19201 hypotheti	3.60
	419945	AW290975	Hs.118923	ESTs	3.60
	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp566D0923 (f	3.60
	420585	AW505139	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	3.60
35	407809	AW082279	Hs.244106	ESTs	3.60
	457708	AA805443	Hs.179909	hypothetical protein FLJ22995	3.60
	427943	AW959075	Hs.238797	ESTs, Moderately similar to I38022 hypot	3.60
	428771	AB028992	Hs.193143	KIAA1069 protein	3.60
	446638	AL133063	Hs.15783	Homo sapiens mRNA; cDNA DKFZp434P1115 (f	3.59
40	416688	T85017	Hs.1192	KIAA0074 protein	3.59
	436961	AW375974	Hs.156704	ESTs	3.58
	430514	AA318501	Hs.241587	megakaryocyte-enhanced gene transcript 1	3.58
	415245	N59650	Hs.27252	ESTs	3.57
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	3.55
45	423508	AW504297	Hs.129711	hepatitis A virus cellular receptor 1	3.55
	401165	NA	NA	NA	3.55
	415382	AI743539	Hs.72465	ESTs, Weakly similar to non-lens beta ga	3.55
	433968	AL157518	Hs.90421	PRO2463 protein	3.55
	421528	AB037837	Hs.105461	hypothetical protein FLJ20357	3.55
50	443325	BE398006	Hs.90462	Homo sapiens, clone IMAGE:4132043, mRNA,	3.55
	444355	BE383686	Hs.191621	ESTs, Moderately similar to ALU6_HUMAN A	3.55
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.55
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	3.55
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	3.55
55	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.54
	434208	AW136973	Hs.288518	ESTs, Weakly similar to S69890 mitogen i	3.54
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.53
	432542	AW083920	Hs.16098	claudin 2	3.53
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	3.52
60	423441	R68649	Hs.278359	absent in melanoma 1 like	3.51
	452940	AA029722	Hs.2173	fucosyltransferase 4 (alpha (1,3) fucosy	3.51
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheti	3.50
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.48
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.48
65	449915	NM_004529	Hs.404	myeloid/lymphoid or mixed-lineage leukem	3.47
	427975	AI536065	Hs.122460	ESTs	3.46
	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	3.45
	404253				3.45
	435567	AW504944	Hs.162990	Homo sapiens cDNA FLJ14193 fis, clone NT	3.45
70	432158	W33165	Hs.22883	UDP-glucose:glycoprotein glucosyltransfe	3.45
	417315	AI080042	Hs.336901	ribosomal protein S24	3.45
	419140	AI982647	Hs.215725	ESTs	3.44
	446901	AI347274		gbt05d02.x1 NCI_CGAP_Co16 Homo sapiens	3.43
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	3.42
75	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.42
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	3.41
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.41
	419131	AA405293	Hs.41167	ESTs	3.41
	430264	AA470519		gbtnc71f10.s1 NCI_CGAP_Pr1 Homo sapiens	3.40
80	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	3.40
	453531	AA417940	Hs.271400	ESTs, Weakly similar to JCS795 CDEP prot	3.40
	444826	AI674482	Hs.148441	ESTs	3.40
	445354	AV653485	Hs.6390	Homo sapiens clone FLB3344 PRO0845 mRNA,	3.40
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-	3.40

	418939	AW530803	Hs.89497	lamin B1	3.40
	418134	AA397769	Hs.86617	ESTs	3.40
	430544	AA481066	Hs.105153	Homo sapiens, clone IMAGE:3461987, mRNA,	3.39
5	427927	AI879165	Hs.2227	CCAAT/enhancer binding protein (C/EBP),	3.39
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.39
	410406	AI969703	Hs.1466	glycerol kinase	3.38
	408494	AA554714	Hs.187578	Homo sapiens cDNA FLJ11639 fis, clone HE	3.38
	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypothesi	3.38
10	446432	AI377320	Hs.150058	ESTs	3.36
	456653	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	3.35
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.35
	428261	AW006855	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	3.35
	421039	NM_003478	Hs.101299	cullin 5	3.35
15	407819	R42185	Hs.274803	ESTs	3.35
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	3.35
	433361	AW469373	Hs.300141	ribosomal protein L39	3.35
	435022	AW183385	Hs.54627	ESTs, Weakly similar to FTDH_HUMAN 10-FO	3.35
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	3.35
20	454018	AW016892	Hs.100855	ESTs	3.35
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	3.35
	453941	U39817	Hs.36820	Bloom syndrome	3.34
	411560	AW851186	Hs.179909	hypothetical protein FLJ22995	3.33
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	3.33
25	438008	AA775026	Hs.203802	ESTs	3.33
	421246	AW582962	Hs.102897	CGI-47 protein	3.33
	451707	AW051061	Hs.60973	ESTs	3.33
	457574	H88717	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC0	3.31
	443613	AI079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapi	3.31
30	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	3.31
	438746	AI885815	Hs.184727	ESTs	3.30
	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	3.30
	427738	NM_000318	Hs.180612	peroxisomal membrane protein 3 (35kD), Ze	3.30
	458855	AW361299	Hs.107000	hypothetical protein FLJ11294	3.30
35	417221	AW379029	Hs.118338	ESTs, Weakly similar to unnamed protein	3.30
	424770	AA425562	Hs.11065	Homo sapiens HDCME13P mRNA, partial cds	3.30
	417720	AA205625	Hs.208067	ESTs	3.29
	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease,	3.29
	452862	AW378065	Hs.8687	ESTs	3.28
40	414343	AL038166	Hs.323378	coated vesicle membrane protein	3.28
	437222	AL117588	Hs.12778	ESTs	3.28
	422665	AJ011812	Hs.119018	transcription factor NRF	3.28
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.28
	446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	3.27
45	447829	AJ433029	Hs.164104	ESTs	3.27
	427576	BE242611	Hs.2173	fucosyltransferase 4 (alpha (1,3) fucosy	3.27
	456132	BE219771	Hs.237146	hypothetical protein FLJ12752	3.26
	407305	AA715284		gb:mv35f03.r1 NCI_CGAP_Br5 Homo sapiens	3.26
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.26
50	424581	M52062	Hs.150917	catenin (cadherin-associated protein), a	3.25
	445592	AV654382	Hs.17947	ESTs, Weakly similar to T16534 hypothesi	3.25
	453320	AW450240	Hs.257274	ESTs	3.25
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.25
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	3.25
55	410659	AI080175	Hs.68826	ESTs	3.25
	446202	AI279706	Hs.149474	ESTs	3.25
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	3.25
	439262	AA832333	Hs.333045	ESTs	3.25
	401823	NA		NA	3.25
60	441264	AA927170	Hs.23290	ESTs	3.25
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	3.24
	408321	AW405882	Hs.44205	coristatin	3.24
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked mol	3.24
	404519				3.24
65	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	3.23
	422660	AW297582	Hs.103267	hypothetical protein FLJ22548 similar to	3.23
	427961	AW293165	Hs.143134	ESTs	3.22
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	3.22
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	3.21
70	458652	AW375610	Hs.117102	hypothetical protein FLJ13046 similar to	3.21
	426472	BE246138	Hs.30853	ESTs	3.21
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.21
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.21
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.20
75	443162	T49951	Hs.9029	DKFZP434G032 protein	3.20
	431678	AW072372	Hs.267446	hypothetical protein FLJ11184	3.20
	430439	AL133561	Hs.241426	DKFZP434B061 protein	3.20
	407201	N31998	Hs.164256	hypothetical protein FLJ20657	3.20
	437905	AW363121	Hs.175596	ESTs, Weakly similar to T26935 hypothesi	3.20
80	434160	BE551196	Hs.114275	ESTs	3.20
	407995	AI094748	Hs.100134	hypothetical protein FLJ12787	3.20
	412966	BE243311	Hs.8024	IK cytokine, down-regulator of HLA II	3.19
	414386	X00442	Hs.75990	haptoglobin	3.19
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothesi	3.18

	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.18
	433764	AW753676	Hs.39982	ESTs	3.17
	459370	AA889982	Hs.271826	ESTs, Weakly similar to I38022 hypoteli	3.17
5	429516	AI982722	Hs.120845	ESTs	3.17
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.16
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.16
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.16
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.15
10	443830	AI142095	Hs.143273	ESTs	3.15
	413516	BE145907		gb:MR0-HT0208-221299-204-e12 HT0208 Homo	3.15
	433527	AW235613	Hs.133020	ESTs	3.15
	427986	N45214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone H	3.15
	457453	Z70695	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.15
15	427687	AW003867	Hs.1570	histamine receptor H1	3.15
	455068	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp5648176 (fr	3.15
	441720	AI346487	Hs.28739	ESTs	3.15
	419569	AI971651	Hs.91143	jagged 1 (Alagille syndrome)	3.15
	445921	AW015211	Hs.146181	ESTs	3.15
20	429957	AW204530	Hs.99500	ESTs	3.15
	403137				3.14
	425268	AI807883	Hs.180059	Homo sapiens cDNA FLJ20553 fis, clone KA	3.14
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	3.14
	439635	AA477288	Hs.94891	hypothetical protein FLJ22729	3.14
25	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.14
	439277	R80061	Hs.164478	hypothetical protein FLJ21939 similar to	3.13
	443584	AI807036	Hs.267245	hypothetical protein FLJ14803	3.13
	406668	T62745	Hs.184411	albumin	3.13
	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	3.13
30	437594	AA761431	Hs.74335	heat shock 90kD protein 1, beta	3.13
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	3.13
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	3.13
	414080	AA135257	Hs.47783	B aggressive lymphoma gene	3.11
	450209	AW008921	Hs.13138	Homo sapiens, clone IMAGE:3448343, mRNA,	3.11
35	441790	AW294909	Hs.132208	ESTs	3.11
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	3.10
	449664	R06212	Hs.127733	ESTs	3.10
	435979	W03698	Hs.83513	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.10
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	3.10
40	402963				3.10
	428967	AW978441	Hs.296100	ESTs	3.10
	455838	BE145808		gb:MR0-HT0208-101299-103-f11 HT0208 Homo	3.10
	407502	U52096		gb:Human zinc finger protein (kr-znf1) m	3.10
	426853	U32974	Hs.172777	baculoviral IAP repeat-containing 4	3.10
45	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	3.10
	421056	AI076890	Hs.146847	TRAF family member-associated NFKB activ	3.10
	420617	AK001652	Hs.99423	ATP-dependent RNA helicase	3.10
	421841	AA908197	Hs.108850	MAK-related kinase	3.10
	429534	AW976987	Hs.163327	ESTs, Weakly similar to 2109260A B cell	3.10
50	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	3.10
	433037	NM_014158	Hs.279938	HSPC057 protein	3.09
	443183	R16258	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	3.09
	457726	AI217477	Hs.194591	ESTs	3.09
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	3.08
55	433013	AI697890	Hs.127337	axin 2 (conductin, axil)	3.08
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.08
	420276	AA290938	Hs.190561	ESTs, Highly similar to SORL1_HUMAN SORT1	3.07
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.07
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	3.07
60	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1, c	3.07
	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	3.07
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	3.06
	436554	AI985810	Hs.301173	ESTs	3.06
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	3.06
65	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	3.06
	445413	AA151342	Hs.12677	CGI-147 protein	3.06
	452909	NM_015368	Hs.30985	pannexin 1	3.06
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	3.05
	425942	AU077195	Hs.164036	glucosamine (N-acetyl)-6-sulfatase (Sanf	3.05
70	406333				3.05
	428454	U55936	Hs.184376	synaptosomal-associated protein, 23kD	3.05
	411864	AW948147		gb:RCO-MT0013-280300-031-e03 MT0013 Homo	3.05
	458632	AI744445	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	3.05
	448292	BE281316	Hs.47334	hypothetical protein FLJ14495	3.05
75	459055	N23235	Hs.30567	ESTs, Weakly similar to B34087 hypoteli	3.05
	402167				3.05
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	3.05
	437828	AW976806	Hs.73149	paired box gene 8	3.05
	404232				3.05
80	418164	AI761820	Hs.41074	ESTs, Weakly similar to I39294 McLeod sy	3.05
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.05
	452787	AW294022	Hs.222707	KIAA1718 protein	3.05
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	3.05
	410718	AI920783	Hs.191435	ESTs	3.04

5	419195	AF110908	Hs.297660	TNF receptor-associated factor 3	3.04
	446861	AI695519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	3.03
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	3.02
	452834	AI638627	Hs.105585	KIAA1688 protein	3.02
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	3.02
	416568	H64844	Hs.138558	ESTs	3.02
	425834	NM_001639	Hs.1957	amyloid P component, serum	3.02
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	3.01
10	412719	AW016610	Hs.129911	ESTs	3.01
	439686	AA922936	Hs.110039	ESTs	3.01
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	3.01
	429703	T93154	Hs.28705	ESTs	3.00
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.00
	415261	T40928	Hs.8346	ESTs	3.00
15	419435	AI200540	Hs.14877	ESTs, Weakly similar to (define not ava	3.00
	429985	NM_015836	Hs.227274	tryptophanyl tRNA synthetase 2 (mitochon	3.00
	423038	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.00
	407182	AA312551	Hs.230157	ESTs	3.00
20	424202	BE350295	Hs.15032	RAN binding protein 17	3.00
	444585	AW170015	Hs.6594	ESTs	3.00
	420552	AK000492	Hs.98806	hypothetical protein	3.00
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	3.00
	441928	AI370188	Hs.211454	ESTs	3.00
25	430888	BE155293	Hs.76064	ribosomal protein L27a	3.00
	417805	AI867277	Hs.183733	ESTs	3.00
	447175	AI365208	Hs.293806	ESTs	3.00
	417177	NM_004458	Hs.81452	fatty acid-Coenzyme A ligase, long-chain	3.00
	435447	AI872932		gb:wm72e03.x1 NCL CGAP_U12 Homo sapiens	3.00
30	405394				3.00
	454975	AW848047		gbcL3-CT0214-291299-052-A12 CT0214 Homo	3.00
	441535	AL135735	Hs.7885	phosphatidylinositol binding clathrin as	3.00
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.00

TABLE 6B

	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
40			
	Pkey	CAT number	Accession
45	411765	125700_1	H43346 AA248302 AA095182
	411864	1262055_1	AW948147 BE092318 AW948138 AW948130 AW948148 AW948129 AW948136 AW948152 AW948144 AW948137 AW948160
	412359	129085_1	AW837985 AW837938 AA101955 AW837913 AW837935
	413516	1374595_1	BE145907 BE145796 BE145803 BE145851 BE145923 BE145812 BE145809 BE145852 BE145856
	414148	142133_1	BE084049 AW292907 AA135984
50	424492	240008_1	AI133482 AI207619 AA341626
	430264	315008_1	AA470519 BE303010 BE302954 BE384120
	431064	327472_1	AI903735 AA491283 AI694953 AW976903 AA761362
	433687	373061_1	AA743991 AA604852 AW272737
	434414	38585_1	AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231
55			AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139
			AA149776 AA699829 AW879188 AW813557 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730
			AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957
			N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659
			BE081531 H59570
60	435447	406400_1	AI872932 AA682306 BE220163 W88695 T81307 H91447
	436411	419334_1	AW674352 AA715374 Z25205
	443613	575391_1	AI079358 W23287
	446901	697809_1	AI347274 AW844024
	448310	757918_1	AI480316 AW847535
65	451401	868474_1	AI793163 AW875182 AW875178 AW875176
	454403	1170435_1	BE065985 BE065944 BE066008 BE066083 BE066093
	454975	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905
			AW848214
	455838	1374605_1	BE145808 BE145807 BE181883
70	TABLE 6C		
	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.	
	Strand:	Indicates DNA strand from which exons were predicted.	
	Nt_position:	Indicates nucleotide positions of predicted exons.	
75			

	Pkey	Ref	Strand	NL_position
5	400534	6981826	Minus	278537-279292
	401165	9438376	Minus	168244-168423
	401480	7321503	Plus	166120-166347,166451-166557,169651-169832
	401644	8576138	Plus	82655-83959
	401823	2262095	Minus	42575-42697,43189-43287,45830-45974
10	402167	8571795	Plus	109122-110357
	402963	5419653	Minus	12950-15959
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403776	7770611	Minus	1414-1513,1624-1756
	404025	7341444	Plus	131740-131905
15	404232	8218045	Minus	71800-71956
	404253	9367202	Minus	55675-56055
	404477	8080699	Plus	113390-113577
	404516	8151967	Plus	114153-114322
	404519	8152000	Plus	12817-13000
20	404567	7249169	Minus	101320-101501
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	405394	6624123	Minus	31900-32373
	405460	7684569	Minus	52223-52389
	405769	3046270	Minus	76844-77193
25	406117	9142932	Plus	54304-54584
	406333	9213235	Plus	64689-64798
	406360	9256107	Minus	7513-7673
	406414	9256407	Plus	49593-49850

30 TABLE 7A: 516 GENES UP-REGULATED IN COLON CANCER COMPARED TO NORMAL COLON

Table 7A lists 516 genes up-regulated in colon cancer compared to normal colon. These were selected as for Table 6A except for using all CEP and colon sample in the normal body tissue list as the normal samples in determining the denominator value and the ratio was equal to or greater than 5.0.

35 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal colon

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
45	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	57.52
	406667	M12523	Hs.184411	albumin	49.94
	409041	AB033025	Hs.50081	KIAA1199 protein	49.18
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	42.22
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	34.64
50	429201	X03178	Hs.198246	group-specific component (vitamin D bind	33.38
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	33.10
	447033	AI357412	Hs.157601	ESTs	31.24
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	26.84
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	25.40
55	413841	M34276	Hs.75576	plasminogen	24.68
	428187	AI687303	Hs.285529	G protein-coupled receptor 49	24.00
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	23.18
	452862	AW378065	Hs.8687	ESTs	21.34
	415989	AI267700	Hs.317584	ESTs	20.92
60	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	19.22
	421470	R27496	Hs.1378	annexin A3	17.92
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	17.36
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	17.28
	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	17.08
65	421462	AF016495	Hs.104624	aquaporin 9	17.02
	424252	AK000520	Hs.143811	hypothetical protein FLJ20513	16.98
	452823	AB012124	Hs.30696	transcription factor-like 5 (basic helix	16.70
	432340	AA534222		gbmj21d02.s1 NCI_CGAP_AA1 Homo sapiens	16.64
	433447	U29195	Hs.3281	neuronal pentraxin II	16.59
70	414386	X00442	Hs.75990	haptoglobin	16.19
	425260	L47726	Hs.1870	phenylalanine hydroxylase	16.08
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	15.82
	439518	W76326		gbzdf60d04.r1 Soares_fetal_heart_NbHH19W	15.80
	443211	AI128388	Hs.143655	ESTs	15.78
75	439608	AW864696	Hs.301732	hypothetical protein MGC5306	15.52
	414559	AV656184	Hs.76452	C-reactive protein, pentraxin-related	15.42
	412719	AW016610	Hs.129911	ESTs	15.24
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	15.18
	448974	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (f	15.03

	416402	NM_000715	Hs.1012	complement component 4-binding protein,	14.60
	453863	X02544	Hs.572	orosomucoid 1	14.35
	441243	AI767056	Hs.193002	ESTs	14.30
5	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	14.30
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	13.91
	433213	AW665130	Hs.137190	ESTs	13.80
	428261	AW006855	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	13.52
	438578	AA811244	Hs.164168	ESTs	13.40
10	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	13.36
	417006	AW673605	Hs.80758	aspartyl-tRNA synthetase	13.00
	449199	AI990122	Hs.196988	ESTs	12.98
	436393	AW022213	Hs.143617	ESTs	12.90
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	12.83
	451561	N52812	Hs.177403	ESTs	12.72
15	420734	AW972872	Hs.293736	ESTs	12.70
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfam	12.50
	441377	BE218239	Hs.202656	ESTs	12.45
	435981	H74319	Hs.188620	ESTs	12.38
20	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	12.38
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	12.38
	459370	AA889882	Hs.271826	ESTs, Weakly similar to I38022 hypothe	12.34
	430290	AI734110	Hs.136355	ESTs	12.30
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	12.26
25	450628	AW382884	Hs.204715	ESTs	12.24
	446232	AI281848	Hs.194691	retinoic acid induced 3	12.16
	428223	AA424313	Hs.98402	ESTs	12.08
	432582	AI623817	Hs.168457	ESTs	12.08
	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	12.02
30	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	12.01
	407202	N58172	Hs.109370	ESTs	11.84
	422109	S73265	Hs.1473	gastrin-releasing peptide	11.68
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ111980 fis, clone HE	11.68
	447532	AK000614	Hs.18791	hypothetical protein FLJ20607	11.67
35	443162	T49951	Hs.9029	DKFZP434G032 protein	11.67
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	11.62
	446372	AB020644	Hs.14945	long fatty acyl-CoA synthetase 2 gene	11.46
	453909	AW004045	Hs.203365	ESTs	11.42
	416655	AW968813	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	11.34
40	452903	AI953425	Hs.246911	ESTs, Weakly similar to I38022 hypothe	11.32
	433011	H07960	Hs.306044	CGI-05 protein	11.30
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	11.22
	455777	AA524285	Hs.154172	ESTs, Moderately similar to BCGF_HUMAN B	11.20
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	11.08
45	407168	R45175	Hs.117183	ESTs	10.91
	407633	NM_007069	Hs.37189	similar to rat HREV107	10.90
	400534				10.88
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	10.76
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 14	10.68
50	440526	AI832243	Hs.211471	ESTs	10.63
	427544	AI767152	Hs.181400	ESTs, Weakly similar to I78885 serine/th	10.62
	447974	R76886		gb:yi64b03.s1 Soares placenta Nb2HP Homo	10.52
	431958	X53629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	10.52
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	10.50
55	457065	AI476318	Hs.192480	ESTs	10.40
	408950	AA707814	Hs.14945	long fatty acyl-CoA synthetase 2 gene	10.38
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	10.34
	414718	H95348	Hs.107987	ESTs	10.29
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	10.28
60	404567				10.14
	428538	AI143139	Hs.2288	vishin-like 1	10.06
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothe	10.05
	437267	AW511443	Hs.258110	ESTs	10.00
	420583	H77859	Hs.65450	reticulin 4	10.00
65	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	9.99
	425071	NM_013989	Hs.154424	deiodinase, liothyronine, type II	9.97
	449555	AI021987	Hs.59970	ESTs	9.91
	459504	BE514127		gb:601315974F1 NIH_MGC_8 Homo sapiens cD	9.90
	434609	R76593		gb:yi60c11.r1 Soares placenta Nb2HP Homo	9.90
70	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	9.88
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	9.84
	448105	AI800470	Hs.171941	ESTs	9.64
	439192	AW970536	Hs.105413	ESTs	9.64
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	9.61
75	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	9.50
	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	9.44
	440404	AI015881	Hs.324527	mitochondrial ribosomal protein S5	9.40
	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	9.35
80	401742	NA		NA	9.30
	416393	N54037	Hs.262869	plasminogen-like	9.28
	413339	AI818080	Hs.194290	ESTs	9.28
	437641	AA811452	Hs.291911	ESTs	9.28
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	9.22
	431319	AA873350	Hs.302232	ESTs	9.21

	434008	AA740878	Hs.112982	ESTs	9.20
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	9.16
	419668	XD4430	Hs.93913	interleukin 6 (interferon, beta 2)	9.16
5	413597	AW302885	Hs.117183	ESTs	9.15
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	9.14
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	9.14
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	9.05
	456653	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	8.98
10	450164	AI239923	Hs.30098	ESTs	8.95
	432867	AW016936	Hs.233364	ESTs	8.93
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	8.92
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	8.92
	452712	AW638616		gb:RC5-LT0054-140200-013-DD1 LT0054 Homo	8.90
	419131	AA406293	Hs.41167	ESTs	8.86
15	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	8.82
	418895	AA894638	Hs.14600	ESTs	8.82
	422665	AJ011812	Hs.119018	transcription factor NRF	8.82
	409757	NM_001898	Hs.123114	cystatin SN	8.78
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	8.74
20	412446	AI768015	Hs.92127	ESTs	8.71
	433285	AW975944	Hs.237396	ESTs	8.68
	414538	AW612228	Hs.107987	ESTs	8.64
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	8.62
25	430835	AI240006	Hs.192326	ESTs	8.60
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	8.59
	445537	AJ245571	Hs.12844	EGF-like domain, multiple 6	8.52
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	8.52
	428355	BE256452	Hs.2257	vitronectin (serum spreading factor, som	8.50
	444478	W07318	Hs.240	M-phase phosphoprotein 1	8.47
30	439398	AA284267	Hs.221504	ESTs	8.44
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	8.43
	403776				8.42
	418973	AA233056	Hs.191518	ESTs	8.42
35	445436	AI224105	Hs.151408	ESTs	8.38
	417958	AA767382	Hs.193417	ESTs	8.34
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	8.34
	425761	AW664214	Hs.196729	ESTs	8.33
	449419	R34910	Hs.119172	ESTs	8.29
40	407007	U22961		gb:human mRNA clone with similarity to L	8.28
	420900	AL045633	Hs.44269	ESTs	8.25
	452503	AB000509	Hs.29736	TNF receptor-associated factor 5	8.23
	458242	BE295588	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H	8.18
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	8.16
45	432363	AA534489		gb:776g11.s1.NCL_CGAP_Co3 Homo sapiens	8.16
	418738	AW388533	Hs.6682	solute carrier family 7, (cationic amino	8.12
	446155	AI563695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y7	8.10
	418379	AA218940	Hs.137516	fidgetin-like 1	8.07
	424560	AA158727	Hs.150555	protein predicted by clone 23733	8.06
50	453116	AI276680	Hs.146086	ESTs	8.04
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	8.04
	409587	T51125	Hs.8493	ESTs	8.00
	407790	AI027274	Hs.288941	Homo sapiens cDNA FLJ14866 fis, clone PL	8.00
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	8.00
55	418036	Z37976	Hs.83337	latent transforming growth factor beta b	7.99
	422762	AL031320	Hs.119976	Human DNA sequence from clone RP1-20N2 o	7.96
	421633	AF121860	Hs.106260	sorting nexin 10	7.92
	432542	AW083920	Hs.16098	claudin 2	7.86
	414869	AA157291	Hs.21479	ubiquitin 1	7.84
60	419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	7.80
	406666	V00495	Hs.184411	albumin	7.78
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.78
	439616	BE018635	Hs.58582	Homo sapiens cDNA FLJ12789 fis, clone NT	7.77
	406360	NA		NA	7.76
65	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	7.76
	431510	AA580082	Hs.112264	ESTs	7.76
	414312	AA155694	Hs.191060	ESTs	7.71
	443450	N66045	Hs.133529	ESTs	7.70
	449870	AI672487	Hs.15423	hypothetical protein HDCMC04P	7.64
70	425681	AB018297	Hs.159183	KIAA0754 protein	7.63
	408897	N50204	Hs.283709	lipopolysaccharide specific response-7 p	7.62
	443285	AI301918	Hs.334264	ESTs	7.60
	420807	AA280827	Hs.57846	ESTs	7.60
	424650	AW576156	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	7.60
75	410718	AI920783	Hs.191435	ESTs	7.60
	430848	AW021726		gb:U27e02.y1 Morton Fetal Cochlea Homo	7.60
	434294	AJ271379	Hs.76194	ribosomal protein S5	7.60
	445808	AV655234	Hs.298083	ESTs, Moderately similar to PC4259 ferri	7.56
	438604	AA811896	Hs.44604	ESTs	7.54
80	458997	AW937420	Hs.69662	ESTs	7.54
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	7.54
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	7.52
	445640	AW959626	Hs.31704	ESTs, Weakly similar to KIAA0227 (H.sapi	7.49
	404996				7.48

	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	7.48
	433859	AW896758	Hs.273789	ESTs	7.44
	423952	AW877787	Hs.136102	KIAA0853 protein	7.44
5	431193	AW749505	Hs.295770	KIAA1719 protein	7.43
	413530	AA130158	Hs.19977	ESTs, Moderately similar to ALU8_HUMAN A	7.40
	417479	AJ057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC	7.40
	424613	AL079850	Hs.151236	highly charged protein	7.37
	417720	AA205625	Hs.208067	ESTs	7.35
10	449347	AV649748	Hs.295901	KIAA0493 protein	7.34
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	7.34
	447499	AW262580	Hs.147674	protocadherin beta 16	7.32
	426890	AA393167	Hs.41294	ESTs	7.31
	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	7.28
	445019	AI205540	Hs.281295	ESTs	7.28
15	419474	AW968619	Hs.155849	ESTs	7.24
	417015	M83772	Hs.80876	flavin containing monooxygenase 3	7.24
	411765	H43346		gbyp09a04.r1 Soares breast 3NbH8st Homo	7.24
	448816	AB033052	Hs.22151	KIAA1226 protein	7.18
	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	7.18
20	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	7.18
	420777	AA280223	Hs.130865	ESTs	7.16
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	7.14
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	7.14
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	7.14
25	448706	AW291095	Hs.21814	interleukin 20 receptor, alpha	7.13
	441124	T97717	Hs.119563	ESTs	7.12
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	7.10
	446432	AI377320	Hs.150058	ESTs	7.10
	439295	AW206091	Hs.253536	ESTs	7.08
30	436902	AW247145	Hs.192729	ESTs	7.08
	428679	AA431765		gbzw80c03.s1 Soares_testis_NHT Homo sap	7.08
	414865	AA157155	Hs.274414	hypothetical protein FLJ14457	7.08
	421373	AA808229	Hs.167771	ESTs	7.06
	432435	BE218886	Hs.282070	ESTs	7.05
35	427933	AW974943	Hs.190571	ESTs	7.04
	436330	NM_004413	Hs.109	dipeptidase 1 (renal)	7.04
	433800	AI034381	Hs.135150	lung type-I cell membrane-associated gly	7.01
	418763	AK000219	Hs.88367	hypothetical protein FLJ20212	6.98
40	446322	N23033	Hs.155814	ESTs	6.98
	442577	AA292998	Hs.163900	ESTs	6.96
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	6.94
	412280	AW205116	Hs.272814	hypothetical protein DKFZp434E1723	6.92
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	6.90
45	429125	AA446854	Hs.271004	ESTs, Weakly similar to L38022 hypothe	6.90
	453204	R10799	Hs.191990	ESTs	6.90
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.88
	427878	C05766	Hs.181022	CGI-07 protein	6.88
	454438	AA224053	Hs.172405	cell division cycle 27	6.86
50	424402	M53108	Hs.1769	lutalinizing hormone/choriogonadotropin r	6.86
	438394	BE379823	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	6.84
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	6.80
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	6.80
	419629	AB020695	Hs.91662	KIAA0888 protein	6.80
55	451686	AA059246	Hs.110293	ESTs	6.80
	430829	AW451999	Hs.194024	ESTs	6.78
	446501	AI302616	Hs.150819	ESTs	6.78
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	6.78
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	6.76
60	437773	U24186	Hs.283018	replication protein A complex 34 kd subu	6.73
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	6.72
	425478	AB007953	Hs.268840	ESTs	6.70
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	6.70
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	6.67
65	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	6.62
	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.62
	450638	AK001826	Hs.25245	hypothetical protein FLJ11269	6.60
	450480	X82125	Hs.25040	zinc finger protein 239	6.58
	445191	AF048686	Hs.12393	dTDP-D-glucose 4,6-dehydratase	6.56
70	414575	H11257	Hs.229568	Homo sapiens clone IMAGE:451939, mRNA se	6.54
	432639	AW973785		gb:EST385886 MAGE resequences, MAGM Homo	6.54
	410116	AW630671	Hs.58636	squamous cell carcinoma antigen recogniz	6.54
	449894	AK001578	Hs.24129	CLLL7 protein	6.53
	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	6.53
75	424745	AA214618	Hs.152759	activator of S phase kinase	6.52
	441801	AW242799	Hs.86366	ESTs	6.52
	435542	AA687376	Hs.269533	ESTs	6.51
	427072	H38046	Hs.303193	ESTs	6.50
	418051	AW192535	Hs.19479	ESTs	6.46
80	436217	T53925	Hs.107	fibrinogen-like 1	6.46
	439809	R41396	Hs.101774	hypothetical protein FLJ23045	6.46
	430704	AW813091	Hs.335799	ESTs	6.44
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.43
	417057	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	6.41

	428392	H10233	Hs.2265	secretory granule, neuroendocrine protel	6.40
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypotheti	6.40
	438202	AW169287	Hs.22588	ESTs	6.38
5	458311	AF069478		gb:AF069478 Homo sapiens astrocytoma lb	6.36
	451389	N73222	Hs.279009	matrix Gla protein	6.36
	427899	AA829286	Hs.332053	serum amyloid A1	6.35
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	6.34
	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	6.34
10	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	6.32
	433908	AW298141	Hs.157975	ESTs	6.32
	430114	AA847744	Hs.99540	ESTs	6.32
	434032	AW009951	Hs.206892	ESTs	6.31
	444656	AI277924	Hs.145199	ESTs	6.30
15	433607	AA602004	Hs.23260	ESTs	6.26
	440659	AF134160	Hs.7327	claudin 1	6.25
	435663	AI023707	Hs.134273	ESTs	6.24
	409916	BE313625	Hs.57435	solute carrier family 11 (proton-coupled	6.24
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like	6.24
20	447500	AI381900	Hs.159212	ESTs	6.24
	407237	AA169872	Hs.6216	Homo sapiens hepatocellular carcinoma-as	6.22
	417715	AW969587	Hs.86366	ESTs	6.22
	423276	AC003034	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	6.20
	438138	R98299	Hs.177502	ESTs	6.20
25	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	6.20
	416857	AA188775	Hs.292453	ESTs	6.20
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	6.18
	429598	AA811257	Hs.269710	ESTs	6.18
	426921	AA037145	Hs.172865	cleavage stimulation factor, 3' pre-RNA,	6.18
30	438940	AF075045	Hs.271609	ESTs	6.18
	400195	NA		NA	6.15
	430473	AW130690	Hs.59962	ESTs	6.12
	452291	AF015592	Hs.28853	CDG7 (cell division cycle 7, S. cerevisi	6.10
	420096	AA775910	Hs.95011	syntrophin, beta 1 (dystrophin-associate	6.10
35	427513	AI476318	Hs.192480	ESTs	6.10
	448934	AI568134	Hs.225592	ESTs, Highly similar to T51146 ring-box	6.10
	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	6.08
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	6.08
	424856	AA347746	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	6.08
40	409048	H59990	Hs.37699	ESTs	6.08
	427674	NM_003528	Hs.2178	H2B histone family, member Q	6.08
	452689	F33868	Hs.284176	transferrin	6.06
	453804	AA300204	Hs.35276	KIAA0852 protein	6.06
	442875	BE623003	Hs.23625	Homo sapiens clone TCCTA00142 mRNA sequ	6.05
45	408243	Y00787	Hs.624	interleukin 8-	6.04
	420721	AA927802	Hs.159471	ZAP3 protein	6.04
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	6.04
	435420	AI928513	Hs.59203	ESTs	6.04
	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hypot	6.04
50	407746	AK001952	Hs.38114	hypothetical protein FLJ11100	6.02
	442116	AI884570	Hs.128813	ESTs	6.00
	423568	NM_005256	Hs.129818	growth arrest-specific 2	6.00
	422011	U30246	Hs.110736	solute carrier family 12 (sodium/potassi	5.99
	441794	AW197794	Hs.253338	ESTs	5.99
55	434739	AA804487	Hs.144130	ESTs	5.98
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	5.96
	420218	AW958037	Hs.286	ribosomal protein L4	5.96
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	5.94
	445546	AW468821	Hs.156054	ESTs	5.94
60	439095	AA830185	Hs.269680	ESTs	5.94
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	5.94
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.94
	417246	AI760098	Hs.21411	ESTs	5.94
	433190	M26901	Hs.3210	renin	5.92
65	418744	AI887288	Hs.196379	ESTs, Weakly similar to putative p150 [H	5.92
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	5.92
	434342	AI791138	Hs.116768	ESTs	5.92
	406668	T62745	Hs.184411	albumin	5.92
	418668	AW407987	Hs.173518	M-phase phosphoprotein homolog	5.90
70	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	5.90
	408867	AA437199	Hs.656	cell division cycle 25C	5.90
	409913	BE243842	Hs.283077	centrosomal P4.1-associated protein; unc	5.88
	450380	AI863675	Hs.114017	ESTs	5.88
	413026	AA809485	Hs.124219	hypothetical protein FLJ12934	5.88
75	454653	AW812227		gb:RC2-ST0173-201099-011-g09 ST0173 Homo	5.87
	457876	AI821940	Hs.264622	ESTs, Moderately similar to ALU8_HUMAN A	5.86
	437222	AL117588	Hs.12778	ESTs	5.86
	455530	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	5.86
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	5.84
80	409045	AA633082	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	5.84
	441645	AI222279	Hs.201555	ESTs, Weakly similar to T23406 hypotheti	5.84
	401352				5.84
	419088	AI538323	Hs.52620	integrin, beta 8	5.84
	431379	AA504264	Hs.182937	peptidylprolyl isomerase A (cyclophilin	5.83

	439580	AF086401	Hs.293847	ESTs, Moderately similar to S65657 alpha	5.82
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT	5.82
	419220	AA811938	Hs.291759	ESTs	5.82
5	439303	W00605	Hs.102784	ESTs	5.80
	415954	AA171850	Hs.42251	ESTs	5.80
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	5.80
	429945	NM_006729	Hs.226483	diaphanous (Drosophila, homolog) 2	5.80
	439527	AW298119	Hs.202536	ESTs	5.78
10	435380	AA679001	Hs.192221	ESTs	5.78
	424086	AI351010	Hs.102267	lysyl oxidase	5.76
	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	5.76
	428460	AA428865	Hs.98563	ESTs	5.74
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	5.74
	413982	BE503035	Hs.279193	ESTs	5.74
15	453240	AI969564	Hs.166254	hypothetical protein DKFp556I133	5.74
	410505	AW752139	Hs.314323	ESTs	5.72
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.72
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	5.72
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	5.71
20	433384	AI021992	Hs.124244	ESTs	5.70
	415385	R17798	Hs.7535	COBW-Eks protein	5.70
	441894	AA134329	Hs.24170	Homo sapiens, clone IMAGE:3685398, mRNA,	5.70
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	5.68
	448666	NM_014953	Hs.323346	KIAA1008 protein	5.68
25	412246	AI160873	Hs.69233	zinc finger protein	5.68
	426518	Z43039	Hs.170198	KIAA0009 gene product	5.66
	418269	AA806113	Hs.189025	ESTs	5.64
	443316	AI478463	Hs.18443	aldehyde dehydrogenase 8 family, member	5.64
	422805	AA436989	Hs.121017	H2A histone family, member A	5.62
30	442252	AI733395	Hs.129124	ESTs	5.60
	414372	AA143654		gb:zo65a02.r1 Stratagene pancreas (93720	5.60
	435040	AI932350	Hs.152825	ESTs	5.59
	438777	AA825487	Hs.142179	ESTs	5.58
35	433849	BE465884	Hs.280728	ESTs	5.58
	438639	AI278360	Hs.31409	ESTs	5.58
	411274	NM_002776	Hs.69423	kallikrein 10	5.55
	435008	AF150262	Hs.162898	ESTs	5.55
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	5.54
40	452881	AW135220	Hs.241921	ESTs	5.54
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	5.54
	424492	AI133482		gb:HA2093 Human fetal liver cDNA library	5.54
	418971	AA360392	Hs.87113	ESTs	5.52
	453716	AA037675	Hs.152675	ESTs	5.52
45	406972	M32053		gb:Human H19 RNA gene, complete cds.	5.51
	417543	AA203820	Hs.110153	ESTs	5.51
	419423	D26488	Hs.90315	KIAA0007 protein	5.51
	434674	AA831879	Hs.136985	ESTs	5.50
	442980	AA857025	Hs.8878	kinesin-like 1	5.50
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	5.50
50	404227	NA		NA	5.49
	412766	BE544475	Hs.54347	ESTs	5.49
	441708	AI469911	Hs.26498	hypothetical protein FLJ21657	5.49
	408432	AW195262		gb:cn67b05.x1 NCI_CGAP_CML1 Homo sapiens	5.48
55	437440	AA846804	Hs.123694	ESTs	5.48
	410486	AW235094	Hs.69233	zinc finger protein	5.46
	456435	AI890384	Hs.270747	ESTs, Weakly similar to ALU2_HUMAN ALU S	5.44
	437378	AI198823	Hs.160473	ESTs	5.44
	436907	AA737171	Hs.131809	ESTs	5.44
60	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	5.44
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	5.42
	441795	N58115	Hs.21137	AD024 protein	5.42
	452449	AW068658	Hs.20943	ESTs	5.42
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	5.40
65	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	5.40
	441217	AI922183	Hs.213246	ESTs	5.40
	432383	AK000144	Hs.274449	Homo sapiens cDNA FLJ20137 fis, clone CO	5.40
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	5.40
	408690	AW864542		gb:PMW-SN0016-120500-003-h02 SN0016 Homo	5.40
70	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	5.39
	446142	AI754693	Hs.145958	ESTs	5.38
	408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	5.36
	433929	AI375499	Hs.27379	ESTs	5.36
	421155	H87879	Hs.102267	lysyl oxidase	5.34
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	5.34
75	453931	AL121278	Hs.25144	ESTs	5.33
	409091	AW970386	Hs.269423	ESTs	5.33
	416057	AI927382	Hs.29857	ESTs	5.33
	438647	AA813118	Hs.163230	ESTs	5.32
80	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	5.32
	445038	AI635444	Hs.143917	dJ467N1.1 protein	5.30
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	5.30
	403432				5.29
	435820	AA700580	Hs.189000	ESTs	5.28

	401714	NA	NA	5.28
	449508	AK001566	Hs.23618 hypothetical protein FLJ10704	5.28
	413151	H47969	Hs.141971 ESTs, Weakly similar to ALU1_HUMAN ALU S	5.28
5	414853	U31116	Hs.77501 sarcoglycan, beta (43kD dystrophin-assoc	5.28
	417372	T99755	Hs.334728 ESTs	5.28
	443613	AI079356	gb00239b09.s1 Soares_NhHMPv_S1 Homo sapi	5.28
	412610	X90908	Hs.74126 fatty acid binding protein 6, ileal (gas	5.27
	408943	NM_007070	Hs.49105 FKBP-associated protein	5.26
10	415139	AW975942	Hs.48524 ESTs	5.26
	447982	H22953	Hs.137551 ESTs	5.26
	430789	AA632577	Hs.310235 ESTs, Weakly similar to I78885 serine/th	5.24
	453921	AI824009	Hs.44577 ESTs	5.24
	409582	R27430	Hs.271565 ESTs	5.24
15	420911	U77413	Hs.100293 O-linked N-acetylglucosamine (GlcNAc) tr	5.23
	422956	BE545072	Hs.122579 hypothetical protein FLJ10451	5.23
	418661	NM_001949	Hs.1189 E2F transcription factor 3	5.22
	446271	D82484	Hs.330994 ESTs	5.22
	435905	AW997484	Hs.5003 KIAA0456 protein	5.21
20	434551	BE387162	Hs.280858 ESTs, Highly similar to A35661 DNA excis	5.21
	415245	N59650	Hs.27252 ESTs	5.20
	436016	AA808465	Hs.121536 Human DNA sequence from clone RP11-472E5	5.20
	431242	AA987742	Hs.251278 KIAA1201 protein	5.20
	439818	AL360137	Hs.19934 Homo sapiens mRNA full length insert cDN	5.20
25	424281	AA766243	gb00a13b11.s1 NC1_CGAP_GCB1 Homo sapiens	5.20
	449138	AW294215	Hs.195631 ESTs	5.20
	449416	AI651016	Hs.246311 ESTs	5.20
	430092	AI821399	Hs.16514 ESTs	5.20
	436574	AW293527	Hs.126465 ESTs	5.18
30	433377	AI752713	Hs.43845 ESTs	5.18
	440987	AA911705	Hs.130229 ESTs	5.18
	426116	AA868729	Hs.144694 ESTs	5.18
	441928	AI370188	Hs.211454 ESTs	5.17
	432657	AA831815	Hs.270940 ESTs, Weakly similar to I78885 serine/th	5.17
35	438011	BE466173	Hs.145696 splicing factor (CC1.3)	5.16
	437257	AI283085	Hs.290931 ESTs, Weakly similar to YFJ7_YEAST HYPOT	5.16
	423926	X03833	Hs.1722 interleukin 1, alpha	5.16
	433393	AF038564	Hs.98074 itchy (mouse homolog) E3 ubiquitin prote	5.15
	415757	AA830854	Hs.187810 ESTs	5.14
40	420170	U43374	Hs.95631 Human normal keratinocyte mRNA	5.14
	420493	AI635113	Hs.270366 ESTs, Weakly similar to I78885 serine/th	5.12
	425739	T19016	Hs.159410 molybdopter synthase sulfurylase	5.12
	440652	AI216751	Hs.143977 ESTs	5.12
	419705	C04649	Hs.77899 tropomyosin 1 (alpha)	5.12
45	427728	AJ245600	Hs.180545 Homo sapiens mRNA for hypothetical prote	5.12
	416113	AA173525	Hs.118758 ESTs, Weakly similar to RLF [H.sapiens]	5.12
	446223	BE300091	Hs.119699 hypothetical protein FLJ12959	5.11
	407624	AW157431	Hs.248941 ESTs	5.11
	447197	R36075	gb0yh88b01.s1 Soares placenta Nb2HP Homo	5.11
50	452465	AA610211	Hs.34244 ESTs	5.10
	442833	AA328153	Hs.88201 ESTs, Weakly similar to A Chain A, Cryst	5.10
	448952	AI609595	Hs.208038 ESTs	5.10
	408170	AW204516	Hs.31835 ESTs	5.08
	424238	AA337401	Hs.137635 ESTs	5.07
55	421072	AI215069	Hs.89113 ESTs	5.06
	424717	H03754	Hs.152213 wingless-type MMTV integration site fami	5.06
	423654	AI674253	Hs.35828 ESTs	5.06
	436862	AI821940	Hs.264622 ESTs, Moderately similar to ALU8_HUMAN A	5.06
	436554	AI985810	Hs.301173 ESTs	5.05
60	433264	D85782	Hs.3229 cysteine dioxygenase, type I	5.04
	452387	AI680772	Hs.306094 trinucleotide repeat containing 12	5.04
	412666	AL080116	Hs.74420 origin recognition complex, subunit 3 (y	5.03
	430287	AW182459	Hs.125759 ESTs, Weakly similar to LEU5_HUMAN LEUKE	5.03
	413293	AL047483	Hs.302498 GTP-binding protein homologous to Saccha	5.00
65	418217	AI910647	Hs.13442 ESTs	5.00
	401480	NA	NA	5.00
	456179	H75490	Hs.271930 ESTs	5.00

TABLE 7B

70	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers

75	Pkey	CAT number	Accession
	408432	1058667_1	AW195262 R27868 AW811262
	408690	107490_1	AW864542 AA056587 AW882724
	411765	125700_1	H43346 AA248302 AA095182
80	414372	143909_1	AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
	424281	237742_1	AA766243 AA338252 AA338213

5	424492	240008_1	AI133482 AI207619 AA341626
	428679	294049_1	AA431765 AA432015
	430848	324621_1	AW021726 AA487752 AA488085
	432340	345248_1	AA534222 AA632632 T81234
	432363	345469_1	AA534489 AW970240 AW970323
	432639	351744_1	AW973785 H60163 AA557608
	434609	38950_1	R76593 AF147390 R76594
	439518	47334_1	W76326 AF086341 W72300
10	443613	575391_1	AI079356 W23287
	447197	711623_1	R36075 AJ366546 R36167
	447974	745643_1	R76886 AJ453674 R77049
	452712	928309_1	AW838616 AW838660 BE144343 AJ914520 AW888910 BE184854 BE184784
	454653	1228081_1	AW812227 AW812294 AW812092
15	458311	543550_1	AF069478 AF069479 AF069480

TABLE 7C

20	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	NL_position:	Indicates nucleotide positions of predicted exons.

25	Pkey	Ref	Strand	NL_position
	400534	6981826	Minus	278637-279292
	401352	9931258	Minus	26064-26208
30	401480	7321503	Plus	166120-166347,166451-166557,169651-169832
	401714	6715702	Plus	96484-96681
	401742	2911728	Plus	64003-64147
	403432	9719611	Minus	68204-68392
	403776	7770611	Minus	1414-1513,1624-1756
35	404227	7838233	Minus	93110-93259
	404567	7249169	Minus	101320-101501
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
	406360	9256107	Minus	7513-7673

40 Table 8A shows 538 genes significantly down-regulated in colon cancer compared to normal colon. These were selected as for Table 7A and the ratio was equal to or less than than 0.33.

45 TABLE 8A: 538 GENES SIGNIFICANTLY DOWN-REGULATED IN COLON CANCER COMPARED TO NORMAL COLON

50	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
	R1:	Ratio of tumor to normal colon

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
55	421996	AW583807	Hs.1460	glucagon	0.0233
	429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	0.0307
	457407	AA505035	Hs.195651	ESTs	0.0416
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	0.0564
	426651	AJ076646	Hs.171683	nuclear receptor subfamily 1, group H, m	0.0567
60	425920	AL049977	Hs.162209	ctaudin 8	0.0601
	431436	AA505035	Hs.195651	ESTs	0.0607
	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	0.0629
	442009	AI733281	Hs.128320	ESTs	0.0634
	416889	AW250318	Hs.80395	mal, T-cell differentiation protein	0.0707
65	429050	X81333	Hs.194777	meprin A, beta	0.0714
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	0.0735
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	0.0739
	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-prote	0.0769
	443606	H10661	Hs.192124	ESTs, Weakly similar to I38022 hypotheti	0.0838
70	415314	N88802	Hs.5422	glycoprotein M5B	0.0853
	451181	AJ796330	Hs.207461	ESTs	0.0873
	429001	AF098951	Hs.194720	ATP-binding cassette, sub-family G (WHIT	0.0888
	426635	BE395109	Hs.129327	hypothetical protein MGC13057	0.0900
	429350	AJ754634	Hs.131987	ESTs	0.0927
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	0.0931

5	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	0.0951
	441066	AW205427	Hs.190726	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.0957
	431252	NM_005478	Hs.251380	insulin-like 5	0.0985
	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	0.0987
	433546	AI075877	Hs.125461	hypothetical protein FLJ11539	0.1007
	415154	D63175		gb:HUMS018098 Clontech human placenta po	0.1032
	409921	AW600239		gb:EST00009 pGEM-T library Homo sapiens	0.1057
	432440	X63597	Hs.2996	sucrase-isomaltase	0.1107
10	430468	NM_004673	Hs.241519	angiotensin-like 1	0.1114
	427167	AI239507	Hs.99196	hypothetical protein MGC11324	0.1147
	441212	AW242447	Hs.146182	cytosolic beta-glucosidase	0.1167
	423605	AF047826	Hs.129887	cadherin 19, type 2	0.1190
	411381	AW841862	Hs.306831	Homo sapiens cDNA: FLJ22549 fis, clone H	0.1211
	412639	AW961284	Hs.296235	ESTs	0.1239
15	453399	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	0.1240
	403548				0.1248
	421913	AI934365	Hs.109439	osteoglycin (ostecinductive factor, mime	0.1274
	457982	AW856093	Hs.183617	ESTs	0.1277
20	448835	BE277929	Hs.11081	UBX domain-containing 2	0.1277
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	0.1291
	441805	AA285136	Hs.301914	neuronal specific transcription factor D	0.1309
	407639	AW205369	Hs.312830	ESTs	0.1315
	421741	AK001879	Hs.107527	hypothetical protein FLJ11017	0.1325
25	454790	AW820852		gb:RC2-ST0301-120200-011-112 ST0301 Homo	0.1328
	451742	T77609	Hs.117970	ankyrin 2, neuronal	0.1335
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	0.1379
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	0.1393
	416585	X54162	Hs.79386	leiomodulin 1 (smooth muscle)	0.1395
30	435869	AF255910	Hs.54650	junctional adhesion molecule 2	0.1456
	407744	AB020629	Hs.38095	ATP-binding cassette, sub-family A (ABC1	0.1459
	404767				0.1460
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	0.1462
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	0.1463
35	452768	AW069459	Hs.61539	ESTs	0.1466
	418692	AK000268	Hs.87383	hypothetical protein	0.1471
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	0.1471
	407551	Y10516		gb:Hsapiens mRNA for CD58 T3 protein.	0.1486
	402076				0.1487
40	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	0.1500
	442080	AW444761	Hs.44565	ESTs	0.1500
	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	0.1513
	429545	AI824164	Hs.77667	lymphocyte antigen 6 complex, locus E	0.1523
	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo	0.1529
45	435056	AW023337	Hs.5422	glycoprotein M5B	0.1532
	426034	AI276989	Hs.56123	Homo sapiens cDNA FLJ13443 fis, clone PL	0.1538
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	0.1542
	408221	AA912183	Hs.47447	ESTs	0.1552
	425220	AW975317	Hs.162987	ESTs	0.1558
50	445200	AA084460	Hs.12409	somatostatin	0.1558
	443238	T78886	Hs.284450	ESTs	0.1563
	456064	AA256213	Hs.72010	ESTs	0.1582
	428133	AW167727	Hs.11873	ESTs	0.1605
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	0.1615
55	437734	AA693951	Hs.180284	ESTs	0.1637
	414290	AI568801	Hs.71721	ESTs	0.1638
	418935	T28499	Hs.89485	carbonic anhydrase IV	0.1656
	411939	AI365585	Hs.146246	ESTs	0.1660
	442495	R55073	Hs.124130	ESTs	0.1676
60	450693	AW450461	Hs.203965	ESTs	0.1698
	420736	AI263022	Hs.82204	ESTs	0.1718
	405385				0.1745
	404638				0.1751
	427333	AF067797	Hs.176658	aquaporin 8	0.1757
65	404246				0.1763
	433785	BE044593	Hs.112704	ESTs	0.1767
	412056	T28160	Hs.778	guanylate cyclase activator 1B (retina)	0.1769
	406980	S69265		(NONE)	0.1781
	421666	AL036250	Hs.1408	endothelin 3	0.1784
70	452854	AA437061	Hs.14060	prokineticin 1 precursor	0.1795
	400514				0.1805
	454186	BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	0.1808
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	0.1812
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	0.1812
75	412474	AI791451		gb:n150c09.y5 NCI_CGAP_Ov2 Homo sapiens	0.1812
	436008	AI078428	Hs.58785	ESTs	0.1820
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	0.1828
	431728	NM_007351	Hs.268107	multimerin	0.1832
	419746	AW867943	Hs.127216	hypothetical protein FLJ13465	0.1835
80	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	0.1838
	415672	N53097	Hs.193579	ESTs	0.1838
	419050	NM_000036	Hs.89570	adenosine monophosphate deaminase 1 (iso	0.1838
	417342	W40277	Hs.81994	glycophorin C (Gerbich blood group)	0.1842
	413714	AI560944	Hs.71428	ESTs	0.1845

	427061	AB032971	Hs.173392	KIAA1145 protein	0.1847
	405282				0.1848
	400163				0.1855
5	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	0.1863
	447414	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	0.1876
	407891	AA486620	Hs.41135	endomucin-2	0.1895
	437140	AA312799	Hs.283689	activator of CREM in testis	0.1901
	431544	AK000770	Hs.299329	Homo sapiens cDNA FLJ20763 fis, clone CO	0.1904
10	436659	AI217900	Hs.144464	ESTs	0.1905
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	0.1926
	453698	AA037615	Hs.42746	ESTs	0.1928
	423743	AB023148	Hs.173373	KIAA0931 protein	0.1941
	428412	AA428240	Hs.126083	ESTs	0.1942
15	420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT	0.1944
	434683	AW298724	Hs.202639	ESTs	0.1957
	421865	AA609911	Hs.109012	MAX dimerization protein	0.1957
	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheli	0.1969
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	0.1981
20	419758	U31973	Hs.93173	phosphodiesterase 6C, cGMP-specific, con	0.2004
	437740	AA810265	Hs.122915	ESTs	0.2016
	405610				0.2017
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	0.2025
	416961	BE391476	Hs.80617	ribosomal protein S16	0.2041
25	401465				0.2045
	437425	AW183714	Hs.20981	hypothetical protein DKFZp547M238	0.2049
	416231	H30333	Hs.165062	ESTs	0.2049
	401753				0.2050
	433430	AI863735	Hs.186755	ESTs	0.2051
30	432150	AK000224	Hs.272789	hypothetical protein FLJ20217	0.2052
	411644	H92064	Hs.278626	Arg/Abi-interacting protein ArgBP2	0.2059
	403957				0.2063
	435900	AI243036	Hs.16094	ESTs	0.2070
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	0.2075
35	445500	AW451938	Hs.257512	ESTs	0.2075
	419956	AL137939	Hs.400086	ESTs	0.2090
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	0.2093
	423655	AA722425	Hs.182785	ESTs, Moderately similar to 1207289A rev	0.2118
	401381				0.2120
40	426452	AW614271	Hs.121647	ESTs, Highly similar to AC006014.8 simil	0.2122
	433476	AA594394	Hs.152616	ESTs	0.2125
	423405	NM_014151	Hs.128155	HSPC053 protein	0.2130
	442826	AI018777	Hs.131241	ESTs	0.2132
	427060	AW378993	Hs.90286	ESTs	0.2137
	437354	AA749215	Hs.291886	ESTs	0.2137
45	447734	AI421412	Hs.163659	ESTs	0.2144
	424585	AA464840	Hs.131987	ESTs	0.2146
	458016	AW188099	Hs.131813	ESTs	0.2151
	423893	AL031709	Hs.134846	Human DNA sequence from clone 316G12 on	0.2151
	401521				0.2157
50	430130	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp751G02121 (0.2165
	401024				0.2171
	414802	AI793107	Hs.27018	Ris	0.2179
	441083	BE562611		gb:601336446F1 NIH_MGC_44 Homo sapiens c	0.2185
55	417355	D13168	Hs.82002	endothelin receptor type B	0.2186
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	0.2188
	442930	AW881975	Hs.213923	ESTs	0.2193
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	0.2209
	444567	AV654020	Hs.184261	ESTs, Weakly similar to T26686 hypotheli	0.2212
	405654				0.2217
60	415471	F09747	Hs.268707	ESTs	0.2222
	449243	AW295031	Hs.198671	ESTs	0.2229
	436088	AA704687	Hs.191294	ESTs	0.2232
	434098	AA625499		gb:af69g08.r1 Soares_NhHMPu_S1 Homo sapi	0.2242
	427552	NM_005771	Hs.179608	retinol dehydrogenase homolog	0.2243
65	416439	AA180363	Hs.118769	ESTs	0.2244
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	0.2254
	459395	Z30300	Hs.281935	ESTs	0.2257
	439039	AI656707	Hs.48713	ESTs	0.2268
	433575	AA600175	Hs.39720	ESTs	0.2268
70	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	0.2273
	428415	AA337211	Hs.184222	Down syndrome critical region gene 1	0.2283
	441899	AI372588	Hs.8022	TUSA protein	0.2283
	437191	NM_005846	Hs.331555	serine protease inhibitor, Kazal type, 5	0.2290
	434839	AI743069	Hs.134736	ESTs	0.2294
75	435731	AA699581	Hs.186811	ESTs	0.2299
	400865				0.2304
	446294	AI284935		gb:qk55g09.x1 NCL_CGAP_Co8 Homo sapiens	0.2305
	414193	BE260069		gb:601150964F1 NIH_MGC_19 Homo sapiens c	0.2309
80	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	0.2315
	453098	Z25935	Hs.86379	ESTs	0.2315
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	0.2319
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	0.2320
	443482	AW186093	Hs.250385	ESTs	0.2326

5	432134	AI816782	Hs.122583	hypothetical protein FLJ21934	0.2329
	421539	AA292747	Hs.97296	ESTs	0.2330
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	0.2344
	408001	AA046458	Hs.95296	ESTs	0.2347
	409331	M36534	Hs.53973	vasoactive intestinal peptide	0.2351
10	431094	AW972276	Hs.116195	ESTs	0.2354
	429575	AA706003	Hs.99387	ESTs	0.2358
	404958				0.2361
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	0.2364
	452742	AW589945	Hs.97876	hypothetical protein DKFZp564K0322	0.2380
15	417511	AL049176	Hs.82223	chordin-like	0.2381
	404927				0.2387
	430297	AW243166	Hs.129806	ESTs	0.2412
	447482	AB033059	Hs.18705	KIAA1233 protein	0.2415
	418332	R34976	Hs.78293	ESTs	0.2416
20	454145	AA046872	Hs.62798	ESTs	0.2421
	422472	R59096	Hs.279939	mitochondrial carrier homolog 1	0.2424
	404070				0.2427
	421232	AA989220	Hs.292100	ESTs	0.2427
	414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	0.2432
25	412622	AW664708	Hs.171959	ESTs	0.2433
	454430	AI082777	Hs.61384	sema domain, seven thrombospondin repeat	0.2437
	416694	AW161284	Hs.79564	neuronal PAS domain protein 1	0.2443
	426724	AA383623	Hs.293616	ESTs	0.2444
	405073				0.2445
30	401236	H24185	Hs.92918	hypothetical protein	0.2445
	414203	BE262170	Hs.78629	ATPase, Na ⁺ /K ⁺ transporting, beta 1 poly	0.2451
	401776				0.2452
	404696				0.2462
	426666	AW500131	Hs.171763	CD22 antigen	0.2471
35	427078	AI676062	Hs.111902	ESTs	0.2474
	424682	AW604804	Hs.151717	KIAA0437 protein	0.2478
	440383	AA884208	Hs.30484	ESTs	0.2481
	419118	AA234223	Hs.139204	ESTs	0.2494
	443515	AV657547	Hs.286014	Homo sapiens, clone IMAGE:3867243, mRNA	0.2495
40	424648	AA344576		gb:EST50478 Gall bladder I Homo sapiens	0.2499
	404605				0.2500
	446066	AI343931	Hs.149383	ESTs	0.2505
	408345	R93851	Hs.63063	ESTs	0.2506
	418358	L02840	Hs.84244	potassium voltage-gated channel, Shab-re	0.2508
45	416950	AL049798	Hs.80552	dermatopontin	0.2510
	423555	AW958201	Hs.178589	hepatocellular carcinoma antigen gene 52	0.2513
	449833	R82252	Hs.106106	protein kinase (cAMP-dependent, catalytic)	0.2515
	459275	AI808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	0.2519
	406897	M57417		gb:Homo sapiens mucin (mucin) mRNA, part	0.2523
50	422743	BE304678	Hs.119598	ribosomal protein L3	0.2526
	459688	U72671	Hs.151250	intercellular adhesion molecule 5, telen	0.2532
	450880	AK002183	Hs.285885	Homo sapiens cDNA FLJ11321 fis, clone PL	0.2536
	457330	AB013818	Hs.247220	peroxisome biogenesis factor 10	0.2536
	451979	F06972	Hs.27372	BMX non-receptor tyrosine kinase	0.2549
55	440274	R24595	Hs.7122	scrapie responsive protein 1	0.2553
	430097	AI523245	Hs.127638	ESTs	0.2558
	410626	BE407727		gb:601299771F1 NIH_MGC_21 Homo sapiens c	0.2564
	402695				0.2565
	453992	AW014995	Hs.281080	ESTs	0.2569
60	453888	AW450670	Hs.252819	ESTs	0.2569
	401371				0.2574
	456145	BE299427	Hs.21446	KIAA1716 protein	0.2579
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiester	0.2580
	422591	L07648	Hs.118630	MAX-interacting protein 1	0.2582
65	452359	BE167229	Hs.29206	hypothetical protein MGC14376	0.2584
	447569	AI393202	Hs.147554	hypothetical protein FLJ23392	0.2586
	405880				0.2588
	420321	D78761	Hs.96657	hypothetical protein	0.2595
	454415	AK000846	Hs.58679	solute carrier family 7, (cationic amino	0.2602
70	437032	AW867372	Hs.302063	immunoglobulin heavy constant mu	0.2604
	448025	BE502965	Hs.170426	ESTs	0.2605
	444304	AW628433	Hs.271296	ESTs, Weakly similar to I54374 gene NF2	0.2605
	424885	AI333771	Hs.82204	ESTs	0.2608
	425381	D84371	Hs.1898	paraoxonase 1	0.2611
75	457413	AA743462	Hs.165337	ESTs	0.2618
	452078	AA022620	Hs.52170	ESTs	0.2624
	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	0.2628
	401974				0.2639
	411319	BE537094		gb:601063333F1 NIH_MGC_10 Homo sapiens c	0.2646
80	417761	R13727	Hs.21435	ESTs	0.2648
	426132	AA370501		gb:EST82261 Prostate gland I Homo sapien	0.2653
	455771	BE084820	Hs.186711	hypothetical protein FLJ20070	0.2653
	414349	BE512968		gb:601172296F1 NIH_MGC_15 Homo sapiens c	0.2660
	402182				0.2660
	402610				0.2661
	444814	BE010749	Hs.255097	ESTs	0.2663
	450017	W56434	Hs.201608	ESTs	0.2663

	408684	R61377	Hs.12727	hypothetical protein FLJ21610	0.2667
	444209	AJ753134	Hs.146494	ESTs	0.2668
	415022	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid	0.2677
5	416184	R48481	Hs.269177	ESTs, Weakly similar to ALU6_HUMAN ALU S	0.2681
	422909	AA533356		gb:nj67110.s1 NCI_CGAP_Pr10 Homo sapiens	0.2681
	412047	AA934589	Hs.49696	ESTs	0.2693
	426356	BE536836	Hs.98682	hypothetical protein FKSG32	0.2703
	442238	AW135374	Hs.270949	ESTs, Moderately similar to F41925 hypot	0.2709
	402425				0.2710
10	450545	AW135582	Hs.201767	ESTs	0.2710
	417118	U38654	Hs.50477	RAB27A, member RAS oncogene family	0.2725
	419850	F06844		gb:HSC1ME091 normalized infant brain cDN	0.2727
	428020	L19058	Hs.181581	glutamate receptor, ionotropic, kainate	0.2730
	441493	AW070446	Hs.127037	ESTs	0.2733
15	413541	BE147036		gb:QV4-HT0222-091199-024-e10 HT0222 Homo	0.2733
	428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	0.2734
	455597	BE008545	Hs.156110	immunoglobulin kappa constant	0.2740
	447809	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cyc	0.2740
	444195	AB002351	Hs.10587	KIAA0353 protein	0.2743
20	415160	T82802		gb:yd38a04.r1 Soares fetal liver spleen	0.2747
	421823	N40850	Hs.28625	ESTs	0.2755
	434464	BE063921	Hs.295971	ESTs	0.2755
	414376	BE393856	Hs.66915	ESTs, Weakly similar to 16.7Kd protein [0.2756
	430073	U86136	Hs.232070	telomerase-associated protein 1	0.2762
25	432018	AA524447	Hs.152377	ESTs	0.2763
	422854	AW998605		gb:PM0-BN0065-100300-001-b10 BN0065 Homo	0.2768
	416397	H53035	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	0.2775
	442420	AJ024834	Hs.131729	ESTs	0.2775
	410950	AW811633		gb:RC2-ST0158-091099-011-d05 ST0158 Homo	0.2778
30	427114	AJ219896	Hs.97592	ESTs	0.2778
	448466	AJ522109	Hs.171066	ESTs	0.2778
	434445	AJ349306	Hs.11782	ESTs	0.2784
	457115	AA420712		gb:nc63cd07.s1 NCI_CGAP_Pr1 Homo sapiens	0.2785
35	459511	AJ142379		gb:qg64cd01.r1 Soares_testis_NHT Homo sap	0.2786
	421321	NM_005309	Hs.103502	glutamic-pyruvate transaminase [alanine	0.2794
	433633	AJ880516	Hs.84630	ESTs, Weakly similar to 2004399A chromos	0.2799
	440236	AW996722	Hs.125297	ESTs	0.2799
	405691				0.2804
	405334				0.2804
40	403047				0.2809
	412506	AW957159		gb:EST369229 MAGE resequences, MAGD Homo	0.2809
	441042	AA077736		gb:7B48A07 Chromosome 7 Fetal Brain cDNA	0.2815
	434660	AA764768	Hs.121158	hypothetical protein DKFZp434J0113	0.2816
45	444453	AW379394	Hs.145126	ESTs	0.2817
	457736	AK000390	Hs.4205	hypothetical protein FLJ20124	0.2820
	454012	M76424	Hs.37014	carbonic anhydrase VII	0.2821
	427448	BE246449	Hs.2157	Wiskott-Aldrich syndrome (eczema-thrombo	0.2822
	419564	U08989	Hs.91139	solute carrier family 1 (neuronal/epithe	0.2827
	435021	AA922192	Hs.54709	ESTs	0.2828
50	413344	U46024	Hs.75302	myotubular myopathy 1	0.2837
	447787	BE620108		gb:601483015F1 NIH_MGC_69 Homo sapiens c	0.2840
	457290	AA465293	Hs.105069	ESTs	0.2841
	458244	AJ929453	Hs.122489	Homo sapiens cDNA FLJ13289 fs, clone OV	0.2841
55	437483	AL390174		gb:Homo sapiens mRNA; cDNA DKFZp547J184	0.2842
	407938	AA905097	Hs.85050	phospholamban	0.2845
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	0.2846
	428212	AW444451	Hs.134812	ESTs	0.2853
	424433	H04607	Hs.9218	ESTs	0.2857
60	425195	AA352026	Hs.94319	VPS10 domain receptor protein	0.2857
	404769				0.2863
	411620	AW854536		gb:RC3-CT0255-200100-024-a08 CT0256 Homo	0.2868
	428746	AW503820	Hs.192861	Spi-B transcription factor (Spi-1/PU.1 r	0.2870
	431822	AA516049		gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens	0.2872
65	441290	VZ7501	Hs.89605	cholinergic receptor, nicotinic, alpha p	0.2874
	422033	AW245805	Hs.110903	claudin 5 (transmembrane protein deleted	0.2877
	421935	AA131632	Hs.109672	CMP-NeuAc;(beta)-N-acetylglactosaminide	0.2878
	447955	BE544271	Hs.288390	hypothetical protein FLJ22795	0.2880
	405364				0.2881
70	422165	AL041199	Hs.1481	histidine decarboxylase	0.2882
	431087	H12723	Hs.290791	ESTs	0.2882
	450610	AA010370	Hs.60386	nuclear RNA export factor 3	0.2882
	445627	AW818475	Hs.7363	ESTs	0.2883
	436144	AW881250	Hs.148367	ESTs	0.2886
	445152	AJ214667	Hs.283597	ESTs	0.2891
75	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	0.2891
	455614	AJ693369	Hs.202274	ESTs	0.2899
	419683	AA248897	Hs.48784	ESTs	0.2900
	411886	AL046810	Hs.20021	vesicle-associated membrane protein 1 (s	0.2904
	430770	AA755694	Hs.123296	ESTs	0.2913
80	444459	AJ680624	Hs.148676	ESTs	0.2913
	444918	AJ202262	Hs.283362	ESTs	0.2915
	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	0.2915
	435598	AA689470	Hs.163026	ESTs	0.2921

	413056	BE063031		gb:MR0-BT0265-231199-002-e09 BT0265 Homo	0.2922
	443998	AI620661	Hs.296276	ESTs	0.2924
	424412	H15512	Hs.10043	hypothetical protein FLJ13074	0.2925
5	421204	AW081587	Hs.165051	ESTs	0.2928
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	0.2938
	440507	H06994		gb:yl81b07.r1 Soares infant brain 1N18 H	0.2943
	445555	AW974013	Hs.260809	ESTs	0.2945
	438570	AW888554	Hs.84298	CD74 antigen (invariant polypeptide of m	0.2948
10	447195	T73745	Hs.279870	ESTs, Weakly similar to A46010 X-linked	0.2950
	423267	AL137416	Hs.126177	Homo sapiens mRNA; cDNA DKFZp434O192 (fr	0.2956
	421920	BE551245	Hs.1438	gamma-aminobutyric acid (GABA) receptor,	0.2956
	412177	Z23091	Hs.73734	glycoprotein V (platelet)	0.2959
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	0.2959
15	433745	AF075320	Hs.28980	hypothetical protein FLJ14540	0.2969
	417935	R53697	Hs.170044	ESTs	0.2970
	420874	NM_000055	Hs.1327	butyrylcholinesterase	0.2973
	413537	BE146866		gb:QV4-HT0222-211099-014-f06 HT0222 Homo	0.2973
	445194	AI215667	Hs.175044	ESTs	0.2974
20	454135	AW135965	Hs.246783	ESTs	0.2976
	403418				0.2986
	457605	AV657778	Hs.3314	selenoprotein P, plasma, 1	0.2989
	408896	AI610447	Hs.48778	riban protein	0.2993
	448542	BE256176	Hs.278712	eukaryotic translation initiation factor	0.2994
25	417945	R29072		gb:F1-101D 22 week old human fetal liver	0.2994
	412518	BE047637	Hs.173739	hypothetical protein FLJ10297	0.2996
	424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	0.2997
	430778	D90337	Hs.247916	natriuretic peptide precursor C	0.3000
	451531	AA018311	Hs.114762	ESTs	0.3003
30	444926	AI202492	Hs.212933	ESTs, Weakly similar to CLD4_HUMAN CLAUD	0.3003
	407366	AF026942		gb:Homo sapiens cly33 mRNA, partial sequ	0.3012
	459456	AA486036	Hs.190124	ESTs	0.3012
	417111	AW016321	Hs.82306	desitin (actin depolymerizing factor)	0.3012
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	0.3012
35	451959	AA056203	Hs.27337	hypothetical protein FLJ20623	0.3012
	410482	AW772187	Hs.191859	ESTs	0.3013
	417700	M36542	Hs.1101	POU domain, class 2, transcription facto	0.3018
	404414				0.3019
	432247	AA531287	Hs.105805	ESTs	0.3023
40	453471	AL037887	Hs.208179	ESTs	0.3028
	417481	AA203281	Hs.21798	ESTs	0.3029
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	0.3032
	448744	AL135424	Hs.9469	pleckstrin homology domain-containing, f	0.3033
	429223	BE264152	Hs.221994	ESTs	0.3034
45	404501	AW247252	Hs.75514	nucleoside phosphorylase	0.3037
	406829	AW419128	Hs.84298	CD74 antigen (invariant polypeptide of m	0.3039
	438839	AW297945	Hs.128490	ESTs	0.3039
	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	0.3042
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	0.3045
50	458789	AL157468	Hs.325825	Homo sapiens cDNA FLJ20848 fs, clone AD	0.3048
	443294	AI733625	Hs.133053	ESTs	0.3050
	447023	AA356764	Hs.17109	integral membrane protein 2A	0.3052
	458583	AI479646	Hs.157081	hypothetical protein MGC4170	0.3056
	414567	BE281057	Hs.184519	hypothetical protein FLJ12949	0.3057
55	445123	AI762911	Hs.145369	ESTs	0.3064
	412682	AW983772		gb:RC3-HN0002-060400-012-h09 HN0002 Homo	0.3065
	434361	AF129755	Hs.117772	ESTs	0.3071
	414026	BE241713		gb:TCAAP1E0472 Pediatric acute myelogeno	0.3072
	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	0.3073
60	408350	AW183350	Hs.250127	ESTs	0.3074
	401042				0.3077
	422586	AA312704	Hs.59457	hypothetical protein FLJ22127	0.3077
	438692	AB007950	Hs.6360	KIAA0481 gene product	0.3077
	447452	BE618258	Hs.102480	Homo sapiens, clone IMAGE:3869590, mRNA,	0.3083
65	444414	AW293214	Hs.8752	transmembrane protein 4	0.3085
	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fs, clone L	0.3088
	430410	AF099144	Hs.250700	trypsin beta 1	0.3090
	419299	AI311085	Hs.52406	hypothetical protein FLJ22573	0.3091
	400672				0.3094
70	444010	AW976457	Hs.282887	ESTs	0.3096
	451699	AL118571	Hs.121557	ESTs, Weakly similar to DP1_HUMAN POLYPO	0.3096
	432471	BE244667	Hs.296155	CGI-100 protein	0.3105
	405277				0.3106
	456765	AI497900	Hs.33067	ESTs	0.3106
75	452090	AA022684	Hs.124673	Homo sapiens cDNA FLJ11477 fs, clone HE	0.3106
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	0.3106
	406592				0.3106
	423621	BE002904		gb:QV4-BN0090-070400-163-c07 BN0090 Homo	0.3107
80	417919	AI928203	Hs.86379	ESTs	0.3110
	414484	BE314385		gb:601154649F1 NIH_MGC_19 Homo sapiens c	0.3110
	457439	AW410408	Hs.271167	L-tyrosine oxidase	0.3116
	426449	AL134009	Hs.169936	Homo sapiens mRNA; cDNA DKFZp586N1918 (f	0.3116
	419942	U25138	Hs.93841	potassium large conductance calcium-acti	0.3119
	458544	AI631036	Hs.196843	ESTs	0.3119

5	447778	BE620592	Hs.71190	ESTs, Weakly similar to S16506 hypothe	0.3121
	449097	BE271708	Hs.95110	ESTs, Weakly similar to A55943 1-phospha	0.3125
	429338	AW170591	Hs.13967	ESTs, Weakly similar to PSM_HUMAN PROSTA	0.3125
	451385	AA017656		gb:ze39h01.1 Soares retina N2b4HR Homo	0.3125
	446404	AA019961	Hs.26216	LOC50627	0.3130
10	446616	R65964	Hs.241559	ESTs, Weakly similar to ALU8_HUMAN ALU S	0.3132
	409404	BE220053	Hs.129056	ESTs	0.3135
	417318	AW953937	Hs.12891	ESTs	0.3139
	443980	AI459140	Hs.259087	ESTs	0.3140
	459138	AI903291		gb:RC-BT029-080199-047 BT029 Homo sapien	0.3142
15	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	0.3143
	434704	AW135276	Hs.192311	ESTs	0.3143
	414214	D49958	Hs.75819	glycoprotein M6A	0.3145
	446378	AI905699	Hs.239760	citrate synthase	0.3145
	459233	AI939966		gb:MR0-CT0015-160799-002-b06 CT0015 Homo	0.3146
20	428193	NM_004235	Hs.7934	Kruppel-like factor 4 (gut)	0.3148
	426515	BE394222	Hs.231444	Homo sapiens, Similar to hypothetical pr	0.3150
	426597	AA382250	Hs.145601	ESTs	0.3153
	459729	AL037285	Hs.289848	EST, Weakly similar to ALU4_HUMAN ALU SU	0.3157
	405071				0.3160
25	407457	AJ242724		gb:Homo sapiens mRNA for partial putativ	0.3162
	409922	AW505582	Hs.130732	KIAA1575 protein	0.3172
	438219	AI916151	Hs.257194	ESTs	0.3173
	412944	AA384110	Hs.197143	ESTs	0.3175
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	0.3178
30	426662	AA879474	Hs.122710	ESTs	0.3178
	444391	AL137597	Hs.11114	hypothetical protein dJ1181N3.1	0.3179
	432168	AK000563	Hs.272805	hypothetical protein FLJ20556	0.3181
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	0.3183
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	0.3185
35	448812	H30775	Hs.22140	BM88 antigen	0.3188
	411288	AW835511		gb:QV0-LT0015-180200-127-d02 LT0015 Homo	0.3189
	422884	AW860975	Hs.13256	ESTs	0.3190
	405535				0.3195
	458663	AV658444	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	0.3195
40	455353	W26786		gb:15d7 Human retina cDNA randomly prime	0.3195
	414540	BE379050	Hs.306969	Homo sapiens, clone MGC:10782, mRNA, com	0.3195
	428568	AC004755	Hs.184922	Homo sapiens chromosome 19, fosmid 37502	0.3195
	428106	BE620016	Hs.182470	PTD010 protein	0.3198
	411856	H67899	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	0.3202
45	445682	AW378397		gb:RC3-HT0220-031299-012-g05 HT0220 Homo	0.3205
	437568	AI954795	Hs.156135	ESTs	0.3205
	448943	AI608810	Hs.193288	ESTs	0.3205
	431999	AL133573	Hs.272312	Homo sapiens mRNA; cDNA DKFZp434J2235 (f	0.3207
	419279	AA235900	Hs.87500	ESTs	0.3208
50	405913				0.3209
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	0.3212
	424729	AF063012	Hs.152531	heart and neural crest derivatives expre	0.3212
	440020	AI480204	Hs.177131	ESTs	0.3213
	429082	AL135682	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	0.3215
55	433663	AF083131	Hs.229535	CATX-15 protein	0.3215
	400641				0.3216
	406140				0.3216
	415280	R56473	Hs.268715	ESTs	0.3217
	447635	AI668669	Hs.195362	ESTs	0.3217
60	401887				0.3217
	400767				0.3221
	457713	H47495	Hs.13810	hypothetical protein MGC15504	0.3221
	448758	AB018311	Hs.21917	KIAA0768 protein	0.3222
	444750	AW242684	Hs.243623	ESTs	0.3223
65	411466	AW847669		gb:IL3-CT0213-280100-056-G10 CT0213 Homo	0.3226
	432749	NM_014438	Hs.276909	interleukin 1, eta	0.3231
	408112	AW451982	Hs.248613	ESTs	0.3231
	433234	AB040928	Hs.65366	KIAA1495 protein	0.3231
	422831	R02504	Hs.332943	ESTs	0.3234
70	403215				0.3236
	451868	R85962	Hs.221926	ESTs, Weakly similar to I38022 hypothe	0.3236
	446901	AI347274		gb:tc05d02.x1 NCL_CGAP_Co16 Homo sapiens	0.3242
	430553	AW392821		gb:CM4-ST0275-021299-053-h09 ST0275 Homo	0.3254
	445848	AA774824	Hs.13377	Homo sapiens clone Z3649 and Z3755 unino	0.3257
75	441143	AI027604	Hs.159650	ESTs	0.3257
	405138				0.3262
	412888	M86151		gb:EST02679 Hippocampus, Stralagene (cat	0.3262
	409662	AW452320	Hs.279726	ESTs	0.3262
	425438	T62216	Hs.270840	ESTs	0.3263
80	416426	AA180256	Hs.210473	Homo sapiens cDNA FLJ14872 fis, clone PL	0.3263
	423512	AW844694	Hs.306752	Homo sapiens cDNA: FLJ21391 fis, clone C	0.3264
	436777	AA731199	Hs.293130	ESTs	0.3267
	431651	BE250915	Hs.266914	hypothetical protein FLJ10355	0.3267
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	0.3268
	426048	AI768853	Hs.134478	ESTs	0.3269
	451096	BE383234	Hs.25925	Homo sapiens, clone MGC:15393, mRNA, com	0.3270
	426942	AA393551	Hs.97450	ESTs	0.3271

454947	AW846590		gb:QV0-CT0180-011099-025-d07 CT0180 Homo	0.3275
413814	BE169692		gb:PM1-HT0527-290200-006-a05 HT0527 Homo	0.3275
422818	AA040290	Hs.97848	ESTs	0.3277
423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	0.3278
414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	0.3278
452164	AI853171		gb:tz44b02.x1 NCI_CGAP_Bm52 Homo sapien	0.3279
458477	NM_000314	Hs.10712	phosphatase and tensin homolog (mutated	0.3279
433197	AB040889	Hs.281022	KIAA1456 protein	0.3280
405701				0.3282
437782	AI370876	Hs.79090	exportin 1 (CRM1, yeast, homolog)	0.3284
459001	AI761313	Hs.204605	ESTs	0.3286
422783	AA598956	Hs.120439	ethanolamine kinase	0.3289
417036	AF039918	Hs.80975	ectonucleoside triphosphate diphosphohyd	0.3290
456041	BE270795	Hs.268864	ESTs	0.3295
423310	AA325225	Hs.124023	Homo sapiens cDNA FLJ14218 fis, clone NT	0.3296
427530	AA405093	Hs.126519	ESTs	0.3296
420172	AA601122	Hs.95655	secreted and transmembrane 1	0.3297
445610	AI831648	Hs.143993	ESTs	0.3297
411328	AW837063		gb:QV1-LT0037-150200-069-g08 LT0037 Homo	0.3300

Table 8B

Pkey:	Unique Eos probeset identifier number
CAT number:	Gene cluster number
Accession:	Genbank accession numbers

Pkey	CAT number	Accession
409921	1159516_1	AW600239 AW600255 AW505332
410626	1212621_1	BE407727
410845	1223881_1	AW807182 AW807328 AW807063 AW807183 AW807192 AW807033 AW807061 AW807286 AW807097 AW807270 AW807372 AW807280 AW807283
410950	1227728_1	AW811633 AW811652 AW811898
411288	1237709_1	AW835511 AW835517 AW835513
411319	1238595_1	BE537094 AW836542
411328	1238987_1	AW837063 AW935882 AW935957
411466	1246771_1	AW847669 AW847667 BE145799
411514	1248638_1	AW850178 AW850233 AW850445 AW850446
411620	1252014_1	AW854536 AW854417 AW854495 AW854355
411880	1263110_1	AW872477 BE088101 T05990
412474	129869_1	AI791451 AI791288 BE019234 BE296601 AA111939
412506	1301336_1	AW957159 H09937 T75143
412682	1321572_1	AW983772 AW983730 AW983769 AW983836 AW983835 AW983837
412888	1334784_1	M86151 BE061884 BE061883 BE061898 BE061882 BE061887 BE061891 BE061890 BE061896 BE061893 BE061895 BE061894 BE061885 BE007474
413056	1347545_1	BE007481 BE007553
413537	1375441_1	BE063031 BE063002 BE063008 BE063024 BE063040 BE063006 BE063072
413541	1375499_1	BE146866 BE146865 BE146867
413814	1391574_1	BE147036 BE146951 BE146958 BE146966 BE146976 BE146955
414026	1411109_1	BE169692 BE169421
414193	1424706_-2	BE241713 BE241912
414349	1437515_-1	BE260069
414484	1452830_-1	BE512968
414539	1460320_1	BE314385
415154	1525577_1	BE379046 BE395459
415160	1525766_1	D63175 D78984 D63269
416035	1567254_1	T82802 D78570 R08505
417945	1711126_1	H42314 H43080 H45217 H15384
419850	188485_1	R29072 R29717 R29699 R29709 R29751 R29609 R29060 R29718 R29057 R29591 R29683 R29575 R28913 R28910
422909	222858_1	F06844 F06845 Z45488 AW748501 AW748591 AW752021 AW748545 AW853362 AW853363 AW853427 AA251253
422954	223239_1	AA533356 AW468427 R67736 AA779031 AA614088 AI823404 AA318991 AA720986
423521	230314_1	AW998605 AW993131 BE514709 AA319445
424648	241947_1	BE002904 H64880 AA328679
426132	261431_1	AA344576 AA732430 AA344601
426497	268121_1	AA370501 AW962784 AA370727
430553	319868_1	AA379913 AA379981 AW963523
431822	338082_1	AW392821 AW392809 AW843258 AW843049 AW603156 BE165656 AW821728
434098	380006_1	AA516049 AW004922
437483	43756_1	AA625499 AA625269 AA625184
440507	495677_1	AL390174 AW898817
441042	50823_1	H06994 BE147898
441083	50904_1	AA077736 AA078505 BE562497 Z17859
445682	647580_1	BE562611 AA436054
446294	670076_1	AW378397 AW378390 AW378358 AI247957
446901	697809_1	AI284935 AW409822 BE408182
447787	73719_1	AI347274 AW844024
451385	86787_1	BE620108 BE312062 AW896316 BE262546
452164	902091_1	AA017658 AA017374 AA019761
454186	1049791_1	AI863171 BE047919
		BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581
		BE141477 BE141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460
		BE141749 AW177598

5 454790 1234752_1 AW820852 AW820773 AW821088
 454947 1245953_1 AW846590 AW846615 AW846584 AW846592 AW846621 AW846610
 455353 1284289_1 W25786 AW998612 AW902272
 457115 286601_1 AA420712 AA469165 AA420737
 459138 918860_1 AI903291 AI903455 AI903367 AI903403 AI903447 AI903405 AI903364 AI903229 AI903240 AI903346
 459233 944881_1 AI939966 AI939988 AI939951 AI939981 AI939976 AI939959

Table 8C

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Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

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Pkey	Ref	Strand	Nt_position
400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750-93891
400541	8117693	Plus	4785-4992
400672	8118724	Minus	148067-148503
400767	8131627	Minus	80531-80629,82169-82278
400865	1945037	Minus	44482-45526
401024	8117489	Plus	60551-60802
401042	8117611	Plus	151364-151606
401371	9650602	Plus	80901-81283
401381	8570226	Minus	118629-119146,119392-119657
401465	6682292	Plus	25676-25800
401521	7705251	Plus	9127-9234
401753	9838183	Minus	155287-155529,159719-159997
401776	9966323	Plus	115535-115743,117746-117839,120290-120455
401887	7229981	Plus	93973-94120
401974	3126777	Plus	85330-85683
402076	8117410	Plus	128316-128627
402182	8575917	Minus	98298-98439
402425	9796347	Minus	50224-50395
402610	9926549	Minus	22955-23124
402695	8569871	Minus	159927-160055
403047	3540153	Minus	59793-59968
403215	7630945	Minus	177270-177971
403418	6862692	Minus	176202-176395
403548	8081591	Minus	38760-39352
403957	8076835	Minus	81649-81754
404070	2996642	Plus	7210-7414,10043-10195
404246	7406725	Plus	82477-82628,82721-82817,82910-83071,83149-83387
404414	7382165	Plus	143127-143398
404605	8212566	Plus	125032-125291
404638	9796751	Minus	99433-99528,100035-100161
404696	9800109	Minus	60037-60144,62675-63081
404767	7882827	Minus	23244-23759
404769	8099713	Minus	175801-176823
404927	7342002	Plus	68680-69563
404958	7407941	Minus	2731-4531
405071	7708797	Minus	11115-11552
405073	7769921	Plus	31419-31774
405138	8576241	Plus	90303-90516
405277	3980473	Plus	23471-23572
405282	3810573	Minus	10482-10689
405334	3135285	Plus	139386-139856
405384	2281075	Minus	48325-48491,49136-49252
405385	6552772	Plus	48332-48454
405535	9796658	Plus	63364-63545
405610	5757553	Minus	71907-72080
405654	4896155	Minus	53624-53759
405691	4508112	Plus	171350-171739
405701	4263751	Plus	93243-93364
405880	6758747	Minus	55673-56287
405913	7712139	Minus	7484-7678
406140	9168231	Minus	49887-50219
406592	4567182	Plus	352560-352963

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Table 9A lists about 1,234 genes up-regulated in colon cancer compared to normal adult tissues and to non-malignant colon tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 2.5, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 70th percentile value amongst non-malignant tissues, the "average" colon value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of have an oncogenic function or of transducing an intracellular signal, or of being modifiable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion_transporter). In order to remove gene-specific

background levels of non-specific hybridization, the 15th percentile value amongst the over non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

5 TABLE 9A: 1,234 genes up-regulated in colon cancer compared to normal adult tissues and to non-malignant colon tissues

10 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of tumor samples divided by the 70th percentile of normal body tissue samples, where the 15th percentile of normal body tissues was subtracted from the numerator and denominator

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
15	436749	AA584890	Hs.5302	NM_005149:Homo sapiens lactin, galactosi	29.34
	406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carcin	25.56
	406667	M12523			20.28
	414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	18.84
20	428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	17.38
	416768	AA363733	Hs.1032	NM_005507:Homo sapiens regenerating isle	16.99
	446787	U57167	Hs.315	NM_002457:Homo sapiens mucin 2, intestin	16.61
	431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S384_H	16.42
	437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	15.92
	407242	M18728		(locuslink)NM_002483:Homo sapiens carcin	15.84
25	423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease I	15.59
	441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	15.02
	406885	M18728		(locuslink)NM_002483:Homo sapiens carcin	14.54
	422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	13.68
30	432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	13.23
	421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	13.21
	453863	X02544	Hs.572	Hs.572:orosomucoid 1	13.06
	421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefoil factor 1	12.35
	436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	12.11
35	422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	11.99
	418888	AU076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, LI c	11.87
	407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	11.81
	424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	11.27
	414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	11.18
40	407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	10.82
	413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	10.73
	450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	10.57
	418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.39
	423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	10.10
45	423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	9.91
	421964	X73079	Hs.288579	NM_002644:Homo sapiens polymetric immunog	9.68
	447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	9.44
	421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	9.38
	405741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	9.34
50	427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (9.18
	422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX),	9.08
	406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	9.02
	409153	W03754	Hs.50813	NM_017625:Homo sapiens interleukin (ITLN)	8.89
	424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	8.53
55	422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	8.23
	452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	8.10
	430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	8.05
	413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	7.96
	406399				7.73
60	422424	AI186431	Hs.296638	Hs.296638:prostate differentiation facto	7.71
	428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homol	7.43
	417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:225881	7.40
	435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	7.29
	430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	7.25
65	451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	7.21
	421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	7.19
	452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	7.18
	452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfa	7.03
	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysi	7.00
70	443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	6.92
	452194	AI694413	Hs.373599	Hs.373599:EST	6.88
	411975	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	6.76
	408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	6.59
	422310	AA316622	Hs.98370	(locuslink)NM_030522:Homo sapiens cytoch	6.55
75	431330	X69532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	6.53
	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protei	6.49
	422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	6.33
	412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	6.31
	451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (t iso)	6.30
80	428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	6.29
	430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	6.28
	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	6.27
	444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	6.26
	409632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cystei	6.23

5	417491	AW376842	Hs.1085	NM_004963: Homo sapiens guanylate cyclase	6.23
	413936	AF113676	Hs.297681	NM_000295: Homo sapiens serine (or cystei	6.23
	422627	BE336857	Hs.118787	Hs.118787: transforming growth factor, be	6.19
	411825	AK000334	Hs.352415	NM_017767: Homo sapiens solute carrier fa	6.17
	446921	AB012113	Hs.16530	NM_002988: Homo sapiens small inducible c	6.17
	415214	AJ445236	Hs.125124	NM_004442: Homo sapiens EphB2 (EPHB2), tr	6.17
	414816	Y13709	Hs.77399	NM_001265: Homo sapiens caudal type homeo	6.16
	422106	D94239	Hs.111732	NM_003890: Homo sapiens IgG Fc binding pr	6.14
10	423803	NM_005709	Hs.132945	(locuslink)NM_005709: Homo sapiens PDZ-73	6.13
	452281	T93500	Hs.28792	Hs.28792: Homo sapiens cDNA FLJ11041 fis,	6.09
	447342	AJ199268	Hs.19322	Hs.19322: Homo sapiens, Similar to RIKEN	6.02
	443957	AA521049	Hs.353013	Hs.353013: chromosome 20 open reading fra	5.95
	403220				5.90
15	408908	BE296227	Hs.250822	(locuslink)NM_003158: Homo sapiens serine	5.88
	449722	BE280074	Hs.23960	Hs.23960: cyclin B1	5.87
	425976	C75094	Hs.334514	NM_025257: Homo sapiens chromosome 6 open	5.79
	414617	AJ339520	Hs.288817	(locuslink)NM_025130: Homo sapiens hypoth	5.79
	408983	NM_000492	Hs.663	NM_000492: Homo sapiens cystic fibrosis 1	5.77
20	423445	NM_014324	Hs.128749	NM_014324: Homo sapiens alpha-methylacyl-	5.77
	421379	Y15221	Hs.103982	NM_005409: Homo sapiens small inducible c	5.76
	431301	AA502384	Hs.151529	Hs.151529: ESTs	5.71
	418318	U47732	Hs.84072	NM_004616: Homo sapiens transmembrane 4 s	5.71
	415992	C05837	Hs.145807	Hs.145807: hypothetical protein FLJ13593	5.68
	436972	AA284679	Hs.25640	Hs.25640: claudin 3	5.66
25	414987	AA524394	Hs.294022	NM_032865: Homo sapiens hypothetical prot	5.61
	431657	AJ345227	Hs.105448	Hs.105448: protein kinase, lysine deficie	5.57
	424273	W40460	Hs.144442	NM_003561: Homo sapiens phospholipase A2,	5.55
	413916	N49813	Hs.75615	NM_000483: Homo sapiens apolipoprotein C-	5.54
	409757	NM_001898	Hs.123114	NM_001898: Homo sapiens cystatin SN (CST1	5.53
30	430204	AA618335	Hs.356664	Hs.356664: hypothetical protein FLJ32334	5.50
	426227	U67059	Hs.154299	(locuslink)NM_005242: Homo sapiens coagul	5.38
	420542	NM_000505	Hs.1321	NM_000505: Homo sapiens coagulation facto	5.33
	414809	AJ434699	Hs.77356	Hs.77356: transferrin receptor (p90, CD71	5.32
	414639	X67055	Hs.76716	NM_002217: Homo sapiens pre-alpha (globul	5.32
35	410418	D31382	Hs.63325	NM_019894: Homo sapiens transmembrane pro	5.28
	414590	NM_000506	Hs.76530	NM_000506: Homo sapiens coagulation facto	5.28
	444151	AW972917	Hs.128749	(locuslink)NM_014324: Homo sapiens alpha-	5.27
	438746	AJ885815	Hs.184727	Hs.184727: ESTs, Weakly similar to T45738	5.26
40	408704	AA056635	Hs.5366	NM_139053: Homo sapiens epidermal growth	5.25
	414798	AJ285323	Hs.97411	Hs.97411: hypothetical protein MGC12335	5.25
	436251	BE151065	Hs.296585	(locuslink)NM_006392: Homo sapiens nuclea	5.25
	414753	AF158255	Hs.77225	NM_006437: Homo sapiens ADP-ribosyltransf	5.23
	428970	BE276881	Hs.194691	NM_003979: Homo sapiens retinoic acid ind	5.22
45	443991	NM_002250	Hs.10082	NM_002250: Homo sapiens potassium intama	5.20
	432978	AF126743	Hs.279884	NM_013238: Homo sapiens DNAB domain-conta	5.18
	425834	NM_001639	Hs.1957	Hs.1957: amyloid P component, serum	5.13
	432179	X75208	Hs.2913	NM_004443: Homo sapiens EphB3 (EPHB3), mR	5.12
	408482	NM_000676	Hs.45743	NM_000676: Homo sapiens adenosine A2b rec	5.11
50	430135	NM_000035	Hs.234234	NM_000035: Homo sapiens aldolase B, fruct	5.08
	426174	AA547959	Hs.115838	Hs.115838: ESTs	5.07
	403218				5.07
	411142	NM_014256	Hs.69009	NM_014256: Homo sapiens UDP-GlcNAc:betaGa	5.00
55	449027	AJ271216	Hs.22880	NM_005700: Homo sapiens dipeptidylpeptida	4.98
	433083	AL042759	Hs.191762	Hs.191762: hypothetical protein MGC20258	4.96
	431779	AW971178	Hs.268571	(locuslink)NM_001645: Homo sapiens apolip	4.92
	421408	AJ688223	Hs.91096	NM_052816: Homo sapiens tripartite motif-	4.91
	430603	AA148164	Hs.247280	Hs.247280: chromosome 20 open reading fra	4.91
	422867	L32137	Hs.1584	Hs.1584: cartilage oligomeric matrix prot	4.90
60	422539	AJ009936	Hs.118138	NM_033013: Homo sapiens nuclear receptor	4.89
	424010	AL080188	Hs.137556	NM_033100: Homo sapiens MT-protocadherin	4.86
	428953	AA306610	Hs.348183	NM_003823: Homo sapiens tumor necrosis fa	4.86
	457001	J03258	Hs.2062	Hs.2062: vitamin D (1,25- dihydroxyvitami	4.83
	425883	AK000226	Hs.165619	NM_031265: Homo sapiens mucin and cadheri	4.81
65	428289	M26301	Hs.2253	Hs.2253: complement component 2	4.79
	418322	AA284166	Hs.84113	NM_005192: Homo sapiens cyclin-dependent	4.78
	409889	AW630041	Hs.56937	NM_021978: Homo sapiens suppression of tu	4.77
	447472	AW207347	Hs.211101	Hs.211101: ESTs	4.74
	423164	AK000232	Hs.124835	NM_019062: Homo sapiens hypothetical prot	4.72
70	429345	R11141	Hs.199695	Hs.199695: hypothetical protein MAC30	4.72
	430680	AW138724	Hs.168974	Hs.168974: ESTs	4.69
	414998	NM_002543	Hs.77729	NM_002543: Homo sapiens oxidised low dens	4.69
	417165	R80137	Hs.302738	Hs.302738: Homo sapiens cDNA: FLJ21425 fi	4.67
	403221				4.65
75	415000	AW025529	Hs.239812	Hs.239812: serologically defined breast c	4.65
	433437	U20536	Hs.3280	NM_001226: Homo sapiens caspase 6, apopto	4.64
	414052	AW578849	Hs.283552	Hs.283552: hypothetical protein BC016153	4.64
	406673	M34996	Hs.198253	Hs.198253: major histocompatibility compl	4.64
	418203	X54942	Hs.83758	NM_001827: Homo sapiens CDC28 protein kin	4.60
80	422714	AB018335	Hs.119387	NM_014698: Homo sapiens KIAA0792 gene pro	4.60
	410639	BE269047	Hs.65234	(locuslink)NM_017895: Homo sapiens DEAD/H	4.60
	411393	AW797437	Hs.69771	NM_001710: Homo sapiens B-factor, propend	4.59
	431193	AW749505	Hs.296770	Hs.296770: KIAA1719 protein	4.57
	428450	NM_014791	Hs.184339	NM_014791: Homo sapiens maternal embryoni	4.56

	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	4.56
	422765	AW409701	Hs.1578	NM_001158:Homo sapiens baculoviral IAP r	4.55
	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	4.55
5	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	4.55
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens sialidase 1 (lyso	4.54
	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	4.53
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	4.53
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	4.53
10	408194	AA601038	Hs.191797	Hs.191797:ESTs	4.52
	439580	AF085401	Hs.293847	Hs.293847:ESTs	4.50
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	4.49
	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome prolif	4.48
	432378	AI493046	Hs.146133	Hs.146133:ESTs	4.48
15	431958	X63629	Hs.2877	NM_001793:Homo sapiens cadherin 3, type	4.47
	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	4.47
	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	4.47
	422511	AU076442	Hs.117938	NM_000494:Homo sapiens collagen, type XV	4.46
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	4.46
20	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis,	4.44
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	4.44
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	4.43
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	4.43
	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	4.40
25	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	4.38
	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	4.37
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23656	4.36
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	4.36
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	4.35
30	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	4.33
	432575	AA553722	Hs.194346	Hs.194346:Spir-2 protein	4.33
	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	4.33
	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	4.32
	418245	AA088767	Hs.83683	NM_020182:Homo sapiens transmembrane, pr	4.32
35	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	4.30
	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	4.30
	429933	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	4.30
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	4.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	4.29
40	408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	4.29
	422163	AF027208	Hs.112360	Hs.112360:promitin-like 1 (mouse)	4.28
	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	4.28
	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	4.27
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	4.27
45	414361	AI086138	Hs.204044	Hs.204044:ESTs	4.26
	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	4.26
	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	4.24
	409012	AL117435	Hs.49725	Hs.49725:DKFZP4341216 protein	4.22
	420039	NM_004605	Hs.376147	Hs.376147:Homo sapiens cDNA FLJ39099 fis	4.20
50	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	4.19
	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	4.18
	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	4.18
	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-lik	4.18
	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	4.18
55	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	4.17
	426761	AI015709	Hs.172089	Hs.172089:pro-oncogene receptor inducing	4.17
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	4.16
	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	4.15
	453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	4.15
60	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3)-glycoprote	4.14
	403219				4.14
	407103	AA424881	Hs.255301	Hs.255301:hypothetical protein MGC13170	4.14
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	4.14
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	4.13
65	409956	AW103364	Hs.727	NM_002192:Homo sapiens Inhibin, beta A (4.12
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	4.12
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	4.12
	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (4.11
	428698	AA852773	Hs.334838	Hs.334838:KIAA1866 protein	4.10
70	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	4.09
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	4.07
	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	4.07
	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	4.06
	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	4.06
75	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	4.05
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (4.04
	425280	U31519	Hs.1872	NM_002591:Homo sapiens phosphoenolpyruva	4.03
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	4.03
	452017	AF109302	Hs.27495	Hs.27495:prostate cancer associated prot	4.03
80	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	4.02
	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	4.01
	450906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	4.01
	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	4.01
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	4.01

	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	3.99
	403739				3.99
	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	3.98
	405484				3.98
5	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	3.98
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antigen	3.97
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	3.97
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	3.97
	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	3.96
10	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	3.96
	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	3.96
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	3.95
	413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	3.95
	400130		Hs.155560	NM_001746:Homo sapiens calnexin (CANX),	3.93
15	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	3.93
	443802	AW504924	Hs.9805	Hs.9805:exportin 5	3.93
	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	3.92
	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	3.92
	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	3.91
20	422293	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synthe	3.90
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	3.89
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomuta	3.89
	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	3.88
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	3.88
25	413950	AA249096	Hs.32793	Hs.32793:Homo sapiens cDNA FLJ31108 fis,	3.88
	409453	AI885516	Hs.95612	Hs.95612:ESTs	3.87
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	3.86
	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	3.86
	434263	N34895	Hs.79187	Hs.79187:coxsa-like virus and adenovirus	3.85
30	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	3.85
	433662	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	3.84
	418526	BE019020	Hs.85638	NM_004207:Homo sapiens solute carrier fa	3.84
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	3.84
	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.83
35	408056	AA312329	Hs.42331	Hs.42331:ephrin-A4	3.83
	407233	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	3.83
	426514	BE616633	Hs.170195	Hs.170195:bone morphogenetic protein 7 (3.82
	451541	BE279383	Hs.26557	NM_007183:Homo sapiens plakophilin 3 (PK	3.82
	424441	X14850	Hs.147097	Hs.147097:H2A, histone family, member X	3.81
40	426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	3.81
	409636	AA305729	Hs.18272	(locuslink)NM_030574:Homo sapiens solute	3.81
	407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	3.80
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	3.79
	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	3.79
45	405556				3.79
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	3.79
	400529				3.79
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.78
	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	3.78
50	429638	AI916662	Hs.211577	(locuslink)NM_004986:Homo sapiens kinect	3.77
	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	3.77
	415003	M11437	Hs.77741	Hs.77741:kinninogen	3.77
	443639	BE269042	Hs.9661	Hs.9661:proteasome (prosome, macropain)	3.76
	400290	H18836	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	3.76
55	431350	AI192528	Hs.164537	Hs.164537:ESTs	3.76
	430154	AW583058	Hs.234726	NM_001085:Homo sapiens serine (or cyste	3.75
	435099	AC004770	Hs.4756	NM_004111:Homo sapiens flap structure-sp	3.75
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	3.74
	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	3.74
60	413063	AL035737	Hs.75184	Hs.75184:chitinase 3-like 1 (cartilage g	3.73
	420665	AW469240	Hs.371581	Hs.371581:ESTs	3.73
	452299	AW206330	Hs.355663	Hs.355663:ESTs	3.72
	444664	N26362	Hs.11615	NM_016086:Homo sapiens map kinase phosph	3.72
	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	3.72
65	444006	BE395085	Hs.334762	(locuslink)NM_032832:Homo sapiens hypoth	3.72
	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	3.71
	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	3.71
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	3.71
	427333	AF067797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	3.70
70	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	3.70
	414806	D14694	Hs.77329	(locuslink)NM_014754:Homo sapiens phosph	3.70
	456362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nuclea	3.69
	409093	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.69
	437016	AU076916	Hs.5398	Hs.5398:guanine monophosphate synthetase	3.69
75	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	3.69
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	3.69
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	3.68
	413813	M96956	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	3.68
	428376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	3.67
80	431890	X17033	Hs.271986	NM_002203:Homo sapiens Integrin, alpha 2	3.67
	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	3.67
	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	3.67
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acf	3.67

5	452679	Z42387	Hs.83883	(locuslink)NM_020182:Homo sapiens transm	3.66
	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	3.66
	433020	AJ375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	3.66
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	3.66
	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	3.66
10	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	3.65
	409152	AA176585	Hs.194346	Hs.194346:Spr-2 protein	3.64
	404826				3.63
	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	3.63
	409964	AW368226	Hs.67928	Hs.67928:ESTs	3.63
15	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	3.63
	452098	AJ858183		BF755039:QV0-CT0583-181000-428-f07 CT058	3.62
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protei	3.61
	439223	AW238289	Hs.250618	NM_025217:Homo sapiens UL16 binding prot	3.60
	408137	AJ694131	Hs.29002	Hs.29002:KIAA1706 protein	3.59
20	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	3.59
	436856	AJ469355	Hs.127310	(locuslink)NM_144624:Homo sapiens kinase	3.59
	449667	AB023227	Hs.23860	Hs.23860:KIAA1010 protein	3.59
	406684	X16354	Hs.50954	(locuslink)NM_001712:Homo sapiens carcin	3.58
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	3.58
25	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens cispla	3.58
	417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	3.57
	443044	N28522	Hs.8935	NM_014298:Homo sapiens quinolinate phosp	3.57
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	3.57
	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	3.56
30	413880	AJ660842	Hs.110915	NM_021258:Homo sapiens interleukin 22 re	3.55
	421357	AK000609	Hs.103808	NM_017896:Homo sapiens chromosome 20 ope	3.55
	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanin	3.55
	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	3.55
	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.55
35	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	3.55
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	3.55
	413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine mono	3.54
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	3.54
	435777	AW419202	Hs.286192	NM_032182:Homo sapiens protein phosphata	3.54
40	431211	M86849	Hs.323733	Hs.323733:gap junction protein, beta 2,	3.54
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prote	3.53
	414812	X72755	Hs.77367	NM_002416:Homo sapiens monodine induced	3.53
	423068	M25629	Hs.123107	NM_002257:Homo sapiens kalikrein 1, ren	3.53
	443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN1	3.53
45	425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation facto	3.53
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	3.52
	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	3.52
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	3.51
	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	3.51
50	409213	U61412	Hs.51133	NM_005975:Homo sapiens PTK6 protein tyro	3.51
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell d	3.51
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.51
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	3.51
	431842	NM_005764	Hs.271473	Hs.271473:epithelial protein up-regulate	3.51
55	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisi	3.51
	411678	AJ907114	Hs.71465	NM_003128:Homo sapiens squalene epoxidase	3.51
	437704	AA766142	Hs.131810	Hs.131810:Homo sapiens cDNA FLJ35976 fis	3.51
	418693	AA133749	Hs.301350	Hs.301350:FXD domain-containing ion tra	3.51
	407971	AA691117	Hs.62918	Hs.62918:CDC91 cell division cycle 91-f	3.50
60	424865	AF011333	Hs.153663	NM_002349:Homo sapiens lymphocyte antige	3.50
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	3.50
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	3.50
	436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	3.50
	440334	BE276112	Hs.7165	NM_003904:Homo sapiens zinc finger prote	3.50
65	428788	AF082283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lympho	3.50
	424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	3.50
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyrido	3.49
	417129	AJ381800	Hs.300684	Hs.300684:calcitonin gene-related peptid	3.49
	409463	AJ458165	Hs.17296	NM_023930:Homo sapiens hypothetical prot	3.48
70	407137	T97307			3.48
	454390	AB020713	Hs.56966	(locuslink)NM_024923:Homo sapiens hypoth	3.48
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433 fis	3.48
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	3.47
	446946	AJ878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	3.47
75	413380	AJ904232	Hs.75323	Hs.75323:prohibitin	3.46
	430237	AJ272144	Hs.236522	Hs.236522:DKFZP434P106 protein	3.46
	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 ope	3.45
	407770	AW607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1	3.45
	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	3.44
80	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	3.44
	420319	AW406289	Hs.95593	NM_019034:Homo sapiens ras homolog gene	3.44
	425209	ALD49761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	3.44
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	3.43
	429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inacti	3.43
	426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically def	3.43
	437967	BE277414	Hs.5947	NM_005370:Homo sapiens mel transforming	3.43
	428093	AW594506	Hs.104830	Hs.104830:ESTs	3.43

	414862	BE621310	Hs.923	Hs.923: single-stranded DNA binding prote	3.43
	400750				3.42
	413186	AU077141	Hs.374548	Hs.374548: solute carrier family 16 (mono	3.41
5	425263	NM_001197	Hs.155419	NM_001197: Homo sapiens BCL2-interacting	3.40
	453857	AL080235	Hs.35861	Hs.35861: Ras-induced senescence 1	3.40
	428474	AB023182	Hs.184523	Hs.184523: serine/threonine kinase 38 lik	3.39
	410315	AI638871	Hs.378965	Hs.378965: Homo sapiens cDNA FLJ37658 fis	3.39
	428205	AB020643	Hs.183006	Hs.183006: likely homolog of mouse hepari	3.39
10	450506	NM_004460	Hs.418	(locuslink)NM_004460: Homo sapiens fibrob	3.39
	413179	N99692	Hs.75227	NM_005002: Homo sapiens NADH dehydrogenas	3.38
	440676	NM_004987	Hs.112378	(locuslink)NM_004987: Homo sapiens LIM an	3.38
	400847				3.37
	431685	AW296135	Hs.267659	NM_006113: Homo sapiens vav 3 oncogene (V	3.37
	410199	AW377424	Hs.205126	Hs.205126: Homo sapiens cDNA: FLJ22667 fi	3.37
15	432633	AI796390	Hs.210667	Hs.210667: ESTs	3.36
	429344	R34038	Hs.374664	NM_005538: Homo sapiens Inhibin, beta C (3.36
	424685	W21223	Hs.151734	Hs.151734: nuclear transport factor 2	3.36
	456950	AF111170	Hs.306165	Hs.306165: ESTs, Highly similar to unknow	3.35
20	418313	BE244231	Hs.84038	NM_015937: Homo sapiens CGI-06 protein (L	3.35
	453454	AW052006	Hs.374973	NM_004697: Homo sapiens PRP4 pre-mRNA pro	3.35
	400448				3.35
	424142	AI678727	Hs.378970	Hs.378970: Homo sapiens cDNA FLJ35102 fis	3.35
	430720	U85768	Hs.247838	NM_002991: Homo sapiens small inducible c	3.35
25	416412	NM_014742	Hs.79305	Hs.79305: KIAA0255 gene product	3.35
	429824	AA286363	Hs.121520	Hs.121520: Homo sapiens cDNA FLJ35792 fis	3.35
	412948	BE243313	Hs.334851	Hs.334851: LIM and SH3 protein 1	3.34
	451129	BE072881		BE072881: RC2-BT0548-200300-012-e09 BT054	3.34
	425322	U63630	Hs.155637	NM_006904: Homo sapiens protein kinase, D	3.34
30	446291	BE397753	Hs.14623	Hs.14623: interferon, gamma-inducible pro	3.34
	431731	BE266322	Hs.211374	(locuslink)NM_145051: Homo sapiens hypoth	3.34
	423198	M81933	Hs.1634	Hs.1634: cell division cycle 25A	3.34
	448093	AW977382	Hs.15898	Hs.15898: 2,4-dienoyl CoA reductase 2, pe	3.34
35	414045	NM_002951	Hs.75722	NM_002951: Homo sapiens ribophorin II (RP	3.34
	421190	U95031	Hs.102482	Hs.102482: mucin 5, subtype B, tracheobro	3.34
	419607	R52557	Hs.91579	NM_033416: Homo sapiens similar to HYPOTH	3.33
	435975	AL118990	Hs.373554	(locuslink)NM_130786: Homo sapiens alpha-	3.33
	418416	U11700	Hs.84999	NM_000053: Homo sapiens ATPase, Cu++ tran	3.33
	433570	AI580053	Hs.109007	Hs.109007: Homo sapiens, Similar to LOC16	3.33
40	441128	AA570258	Hs.348504	Hs.348504: hypothetical protein BC014072	3.33
	432320	AW411066	Hs.274351	NM_016032: Homo sapiens zinc finger, DHHC	3.33
	444019	BE173977	Hs.10098	NM_019082: Homo sapiens putative nucleola	3.32
	432680	T47364	Hs.278613	(locuslink)NM_005532: Homo sapiens Interf	3.32
	410219	T98226	Hs.171952	Hs.171952: occludin	3.32
45	410563	AA194952	Hs.36093	Hs.36093: Homo sapiens cDNA FLJ12885 fis,	3.32
	402829				3.32
	445921	AW015211	Hs.153799	Hs.153799: Homo sapiens cDNA FLJ38333 fis	3.32
	414188	AW505308	Hs.75812	NM_004563: Homo sapiens phosphoenolpyruva	3.32
	443425	AI056776	Hs.133397	Hs.133397: ESTs	3.32
50	438485	X59135	Hs.156110	Hs.156110: immunoglobulin kappa constant	3.31
	410268	AA316181	Hs.61635	NM_012449: Homo sapiens six transmembrane	3.30
	425159	NM_004341	Hs.154868	NM_004341: Homo sapiens carbamoyl-phospha	3.30
	420614	AL110291	Hs.99364	Hs.99364: abhydrolase domain containing 1	3.30
	421814	L12350	Hs.108623	NM_003247: Homo sapiens thrombospondin 2	3.30
55	432215	AU076609	Hs.2934	NM_001033: Homo sapiens ribonucleotide re	3.30
	409402	AF028234	Hs.695	Hs.695: cystatin B (steifin B)	3.30
	421038	AL080192	Hs.101282	Hs.101282: Homo sapiens mRNA; cDNA DKFZp4	3.29
	424408	AI754813	Hs.146428	Hs.146428: collagen, type V, alpha 1	3.29
	448775	AB025237	Hs.388	NM_002452: Homo sapiens nudix (nucleoside	3.29
60	442821	BE391929	Hs.8752	Hs.8752: transmembrane protein 4	3.29
	458306	AW578452		AW578452: RC1-CT0252-030100-023-b07 CT025	3.28
	400846				3.28
	422256	M64673	Hs.1499	NM_005526: Homo sapiens heat shock transc	3.28
	408089	H59789	Hs.42644	Hs.42644: thioredoxin-like 2	3.28
65	432078	BE314877	Hs.24553	(locuslink)NM_022369: Homo sapiens hypoth	3.27
	435575	AF213457	Hs.44234	NM_018965: Homo sapiens triggering recept	3.27
	456534	X91195	Hs.100623	NM_138689: Homo sapiens protein phosphata	3.27
	447335	BE617695	Hs.286192	NM_032192: Homo sapiens protein phosphata	3.27
	414368	W70171	Hs.75939	NM_012474: Homo sapiens uridine monophosp	3.27
70	422599	BE387202	Hs.118638	Hs.118638: non-metastatic cells 1, protei	3.26
	437897	AA770561	Hs.146170	Hs.146170: hypothetical protein FLJ22969	3.26
	431183	NM_006855	Hs.250696	NM_006855: Homo sapiens KDEL (Lys-Asp-Glu	3.26
	457635	AV660976	Hs.3569	Hs.3569: chromosome 20 open reading frame	3.26
	432391	AI732374	Hs.339827	Hs.339827: ESTs, Weakly similar to protea	3.25
75	417640	D30857	Hs.82353	NM_006404: Homo sapiens protein C recepto	3.25
	440086	NM_005402	Hs.6906	NM_005402: Homo sapiens v-ral simian leuk	3.25
	401179				3.25
	411125	AA151647	Hs.68877	Hs.68877: cytochrome b-245, alpha polypep	3.25
80	453323	AF034102	Hs.32951	NM_001532: Homo sapiens solute carrier fa	3.25
	407236	W79485	Hs.173980	Hs.173980: nuclear matrix protein NMP200	3.25
	447250	AI878909	Hs.17883	NM_002707: Homo sapiens protein phosphata	3.25
	452875	BE275760	Hs.30928	NM_006114: Homo sapiens translocase of ou	3.24
	428390	AI640377	Hs.350077	NM_000982: Homo sapiens ribosomal protein	3.24
	425811	AL039104	Hs.159557	NM_002266: Homo sapiens karyopherin alpha	3.24

5	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	3.24
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	3.24
	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	3.23
	418558	AW082265	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	3.23
	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	3.23
	444734	NM_001360	Hs.11806	NM_001360:Homo sapiens 7-dehydrocholeste	3.23
	424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	3.23
	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-1	3.23
10	409686	AK000002	Hs.55879	(locuslink)NM_033450:Homo sapiens multi	3.23
	418681	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	3.23
	419705	AW368634	Hs.154331	Hs.154331:ESTs	3.22
	420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	3.22
	413835	AI272727	Hs.249163	NM_024306:Homo sapiens fatty acid hydrox	3.22
15	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	3.22
	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	3.21
	435472	AW972330	Hs.283022	NM_018643:Homo sapiens triggering recept	3.21
	451932	AA360954	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.21
	420085	AF1741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	3.21
20	412006	AW451618	Hs.290216	Hs.290216:ESTs	3.21
	424954	NM_000546	Hs.1846	NM_000546:Homo sapiens tumor protein p53	3.21
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	3.21
	414602	AW630088	Hs.76550	NM_052886:Homo sapiens mal, T-cell diffe	3.20
	400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.20
25	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	3.20
	452203	X57522	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.20
	413431	AW246428	Hs.75355	NM_003348:Homo sapiens ubiquitin-conjuga	3.19
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	3.19
	408716	AI567839	Hs.151714	(locuslink)NM_033405:Homo sapiens peroxi	3.19
30	433627	AF078866	Hs.284296	NM_033161:Homo sapiens surfact 4 (SURF4)	3.19
	430393	BE185030	Hs.241305	(locuslink)NM_006470:Homo sapiens tripar	3.19
	417286	AA122237	Hs.81874	NM_002413:Homo sapiens microsomal glutat	3.18
	434224	AA380731	Hs.84	NM_000206:Homo sapiens interleukin 2 rec	3.18
	428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associa	3.18
35	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	3.18
	420531	AI652069	Hs.98614	NM_004587:Homo sapiens ribosome binding	3.18
	417389	BE260964	Hs.82045	Hs.82045:midkine (neurite growth-promoti	3.18
	412276	BE262621	Hs.73798	Hs.73798:macrophage migration inhibitory	3.18
	452700	AI859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	3.18
40	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	3.18
	414883	AA926960	Hs.348669	Hs.348669:CDK28 protein kinase 1	3.18
	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	3.18
	447698	AI420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	3.17
	424089	AL036662	Hs.144949	Hs.144949:ESTs	3.17
45	414788	X78342	Hs.77313	Hs.77313:cyclin-dependent kinase (CDC2)	3.17
	442315	AA173992	Hs.79556	Hs.79556:ESTs	3.17
	449944	AF290512	Hs.58215	(locuslink)NM_033046:Homo sapiens rhotek	3.17
	425244	AK002127	Hs.155313	NM_022105:Homo sapiens death associated	3.16
50	428484	AF104032	Hs.184601	(locuslink)NM_003486:Homo sapiens solute	3.16
	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	3.16
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	3.15
	447151	AI022813	Hs.92679	(locuslink)NM_145754:Homo sapiens kines	3.15
	418862	BE550964	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	3.15
	410636	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.15
55	423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	3.15
	435886	BE265839	Hs.12126	NM_018487:Homo sapiens hepatocellular ca	3.15
	458778	AW451034	Hs.326525	NM_001659:Homo sapiens arylsulfatase D (3.14
	420190	AI816209	Hs.95867	(locuslink)NM_024112:Homo sapiens chromo	3.14
	428371	AB012193	Hs.183874	NM_003589:Homo sapiens cullin 4A (CUL4A)	3.14
60	450690	AA296696	Hs.333418	(locuslink)NM_014164:Homo sapiens FXYD d	3.14
	413900	AW409747	Hs.75612	NM_006819:Homo sapiens stress-induced-ph	3.13
	406698	X03068	Hs.73931	Hs.73931:major histocompatibility comple	3.13
	407797	AK000524	Hs.39850	Hs.39850:uridine kinase-like 1	3.13
	447321	AW271217	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.13
65	426841	AI052358	Hs.131741	Hs.131741:ESTs	3.13
	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	3.12
	420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mRNA, comple	3.12
	438444	AI064707	Hs.301226	Hs.301226:Homo sapiens, clone IMAGE:3456	3.12
	439778	AL109729	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.12
70	412326	R07566	Hs.73817	NM_002983:Homo sapiens small inducible c	3.12
	447656	NM_003726	Hs.19126	NM_003726:Homo sapiens src family associ	3.12
	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	3.11
	421779	AI879159	Hs.108219	NM_004626:Homo sapiens wingless-type MMT	3.11
	400262		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.11
75	418803	U50079	Hs.88556	NM_004864:Homo sapiens histone deacetyla	3.11
	449230	BE613348	Hs.356392	Hs.356392:ESTs, Highly similar to S-phas	3.11
	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	3.11
	432026	AA524545	Hs.224630	Hs.224630:Homo sapiens cDNA FLJ33318 fis	3.11
	433179	AW362945	Hs.162459	Hs.162459:ESTs	3.11
80	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	3.11
	418641	BE243136	Hs.86947	NM_001109:Homo sapiens a disintegrin and	3.10
	421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens 8D6 an	3.10
	427349	AA360154	Hs.177415	(locuslink)NM_001997:Homo sapiens Finkel	3.10
	457670	AF119666	Hs.23449	NM_018842:Homo sapiens insulin receptor	3.10

5	438407	AI457122	Hs.129673	Hs.129673:eukaryotic translation initiat	3.10
	428293	BE250944	Hs.183556	Hs.183556:solute carrier family 1 (neutr	3.10
	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 264	3.10
	418181	U37012	Hs.83727	NM_013291:Homo sapiens cleavage and poly	3.10
	434826	AF155661	Hs.22265	Hs.22265:pyruvate dehydrogenase phosphat	3.10
	428734	BE303044	Hs.192023	NM_003757:Homo sapiens eukaryotic transl	3.09
	423022	AA320525	Hs.201076	Hs.201076:ESTs	3.09
	427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	3.08
10	404240				3.08
	408989	AW361866	Hs.49500	Hs.49500:KIAA0746 protein	3.08
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	3.08
	446506	AI123118	Hs.15159	(locuslink)NM_016326:Homo sapiens chemok	3.08
	402260				3.08
15	429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	3.08
	409267	NM_012453	Hs.52515	NM_012453:Homo sapiens transducin (beta)	3.08
	445937	AI452943	Hs.321231	(locuslink)NM_003779:Homo sapiens UDP-Ga	3.07
	431243	U46455	Hs.252189	NM_002999:Homo sapiens syndecan 4 (amphi	3.07
	422611	AA158177	Hs.118722	(locuslink)NM_004480:Homo sapiens fucosy	3.07
20	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.07
	449644	AW960707	Hs.148324	Hs.148324:ESTs	3.07
	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteinase	3.07
	417457	AA378907	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.07
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	3.07
25	424927	AW973666	Hs.153850	Hs.153850:hypothetical protein C32102.4	3.07
	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	3.07
	426440	BE382756	Hs.169902	NM_006516:Homo sapiens solute carrier fa	3.06
	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	3.06
	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	3.06
30	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	3.06
	421802	BE261458	Hs.108408	(locuslink)NM_016022:Homo sapiens CGI-78	3.06
	421905	AI660247	Hs.32699	Hs.32699:Homo sapiens, Similar to RIKEN	3.06
	430542	AI557486	Hs.119122	Hs.119122:ribosomal protein L13a	3.06
	427268	X78520	Hs.174139	NM_001829:Homo sapiens chloride channel	3.06
35	412525	AA581439	Hs.152328	Hs.152328:ESTs	3.06
	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	3.05
	441406	Z45957	Hs.7837	Hs.7837:phosphoprotein regulated by mito	3.05
	408806	AW847814	Hs.75608	Hs.75608:tight junction protein 2 (zona	3.05
	435730	AB020635	Hs.4984	Hs.4984:KIAA0828 protein	3.05
40	432871	NM_016142	Hs.279617	Hs.279617:hydroxysteroid (17-beta) dehyd	3.05
	447783	AF054178	Hs.19561	NM_005001:Homo sapiens NADH dehydrogenas	3.05
	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	3.05
	450447	AF212223	Hs.25010	NM_018698:Homo sapiens hypothetical prot	3.05
	427337	Z46223	Hs.176663	NM_000569:Homo sapiens Fc fragment of Ig	3.05
	406363				3.05
45	438841	AF038961	Hs.6710	NM_004870:Homo sapiens mannosyl-P-dolicho	3.05
	431738	AW237726	Hs.288549	NM_032828:Homo sapiens ubiquitin UBF-1	3.04
	447966	AA340605	Hs.105887	(locuslink)NM_145252:Homo sapiens simila	3.04
	439246	AM98072	Hs.351474	Hs.351474:Homo sapiens cDNA FLJ30002 fis	3.04
50	419493	AF001212	Hs.90744	Hs.90744:proteasome (prosome, macropain)	3.04
	427597	D15049	Hs.179770	NM_002842:Homo sapiens protein tyrosine	3.04
	430281	AI878842	Hs.237924	NM_016016:Homo sapiens CGI-69 protein (L	3.04
	446620	AA128808	Hs.179902	(locuslink)NM_022109:Homo sapiens CDw92	3.04
	452865	AI924046	Hs.119567	Hs.119567:ESTs, Weakly similar to ALU1_H	3.04
55	422164	NM_014312	Hs.112377	Hs.112377:cortical thymocyte receptor (X	3.04
	444301	AK000136	Hs.10760	NM_017680:Homo sapiens asporin (LRR clas	3.04
	451455	AI937227	Hs.8821	NM_021175:Homo sapiens hepcidin antihist	3.03
	417777	AI823763	Hs.7055	Hs.7055:Homo sapiens cDNA FLJ33420 fis,	3.03
	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	3.03
60	450825	AC005954	Hs.25527	(locuslink)NM_014428:Homo sapiens tight	3.03
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	3.03
	409430	R21945	Hs.346735	Hs.346735:Homo sapiens, clone IMAGE:3881	3.03
	440659	AF134160	Hs.7327	NM_021101:Homo sapiens claudin 1 (CLDN1)	3.03
	432268	BE311856	Hs.274230	Hs.274230:3'-phosphoadenosine 5'-phospho	3.03
65	438930	AW843633	Hs.343261	Hs.343261:histocompatibility (minor) 13	3.02
	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	3.02
	426788	U66615	Hs.172280	NM_003074:Homo sapiens SWI/SNF related,	3.02
	425866	NM_001761	Hs.1973	NM_001761:Homo sapiens cyclin F (CCNF),	3.02
	448847	AI587180	Hs.110905	Hs.110905:hypothetical protein BC004501	3.02
70	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	3.02
	414702	L22005	Hs.76932	NM_004359:Homo sapiens cell division cyc	3.02
	430024	AI808780	Hs.227730	NM_000210:Homo sapiens Integrin, alpha 6	3.02
	424394	BE277024	Hs.146381	Hs.146381:RNA binding motif protein, X c	3.01
	442993	BE018682	Hs.166196	Hs.166196:ATPase, Class I, type 8B, memb	3.01
75	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	3.01
	410293	AK000047	Hs.61950	NM_018992:Homo sapiens hypothetical prot	3.01
	454358	AW792876	Hs.288936	NM_031420:Homo sapiens mitochondrial rib	3.01
	411531	AB014511	Hs.70604	Hs.70604:ATPase, Class II, type 9A	3.00
	447032	AK000310	Hs.17138	(locuslink)NM_017755:Homo sapiens hypoth	3.00
	414249	AI797994	Hs.279929	(locuslink)NM_017510:Homo sapiens gp25L2	3.00
80	448440	AA173467	Hs.62402	Hs.62402:p21/Cdc42/Rac1-activated kinase	3.00
	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EFNA1)	3.00
	419452	U33635	Hs.90572	Hs.90572:PTK7 protein tyrosine kinase 7	3.00
	417878	U90916	Hs.82845	Hs.82845:Homo sapiens cDNA: FLJ21930 fis	3.00

5	431884	AA521246	Hs.210792	Hs.210792:Homo sapiens cDNA FLJ36691 fis	3.00
	425261	BE385099	Hs.355814	Hs.355814:Homo sapiens clone IMAGE:29333	3.00
	445229	BE276013	Hs.343828	Hs.343828:Homo sapiens mRNA; cDNA DKFZp7	3.00
	412146	M92444	Hs.73722	Hs.73722:APEX nuclease (multifunctional)	2.99
	437763	AA469369	Hs.5831	Hs.5831:tissue inhibitor of metalloprote	2.99
	405865	AI025931	Hs.181357	Hs.181357:laminin receptor 1 (67kD, ribo	2.99
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	2.99
	417259	AW903838	Hs.81800	Hs.81800:chondroitin sulfate proteoglyca	2.98
10	453902	BE502341	Hs.3402	NM_139177:Homo sapiens chromosome 17 ope	2.98
	432396	AW295956	Hs.11900	(locuslink)NM_032527:Homo sapiens hypoth	2.98
	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	2.98
	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	2.98
	446913	AA194422	Hs.22564	NM_004999:Homo sapiens myosin VI (MYO6),	2.98
	440943	AW082298	Hs.146161	NM_032331:Homo sapiens hypothetical prot	2.98
15	414013	AA766605	Hs.47099	NM_024642:Homo sapiens hypothetical prot	2.98
	452124	AA454220	Hs.61170	Hs.61170:ESTs	2.98
	416391	A878927	Hs.79284	NM_002402:Homo sapiens mesoderm specific	2.98
	419092	J05581	Hs.89603	NM_002456:Homo sapiens mucin 1, transmem	2.97
20	426375	AK000597	Hs.169549	NM_017893:Homo sapiens sema domain, immu	2.97
	437296	AA350994	Hs.20281	Hs.20281:MAPK phosphatase-7	2.97
	407736	N41744	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	2.97
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	2.97
	424756	AW504657	Hs.152931	(locuslink)NM_002296:Homo sapiens lamin	2.97
25	430354	AA954810	Hs.239784	Hs.239784:scribble	2.97
	417079	U65590	Hs.81134	(locuslink)NM_000577:Homo sapiens interl	2.97
	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	2.97
	414186	U33446	Hs.75799	Hs.75799:protease, serine, 8 (prostasin)	2.97
	432065	AA401039	Hs.2903	Hs.2903:protein phosphatase 4 (formerly	2.96
30	452012	AA307703	Hs.279766	(locuslink)NM_012310:Homo sapiens kines	2.96
	412429	AV650262	Hs.75765	NM_002089:Homo sapiens GRO2 oncogene (GR	2.96
	452714	AW770994	Hs.30340	Hs.30340:hypothetical protein KIAA1165	2.96
	429922	Z97630	Hs.226117	NM_005318:Homo sapiens H1 histone family	2.96
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	2.96
35	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	2.96
	428781	AF164799	Hs.193384	Hs.193384:putative 28 kDa protein	2.96
	445350	AF052112	Hs.12540	NM_006330:Homo sapiens lysophospholipase	2.96
	422396	W21872	Hs.7907	(locuslink)NM_145059:Homo sapiens L-fuco	2.96
	429597	NM_003816	Hs.2442	Hs.2442:alpha disintegrin and metalloprotein	2.95
40	421179	U72664	Hs.148495	NM_002810:Homo sapiens proteasome (proso	2.95
	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	2.95
	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	2.95
	430589	AJ002744	Hs.246315	NM_017423:Homo sapiens UDP-N-acetyl-eph	2.95
	409220	BE243323	Hs.51233	(locuslink)NM_003842:Homo sapiens tumor	2.95
45	443883	AA114212	Hs.9930	Hs.9930:serine (or cysteine) proteinase	2.95
	445720	AL040482	Hs.286173	Hs.286173:KIAA1595 protein	2.95
	429583	NM_006412	Hs.209119	NM_006412:Homo sapiens 1-acylglycerol-3-	2.95
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif	2.94
	419193	D26643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	2.94
50	419152	L12711	Hs.89643	(locuslink)NM_001064:Homo sapiens transk	2.94
	444824	AA843575	Hs.12056	NM_001671:Homo sapiens asialoglycoprotei	2.94
	431629	AU077025	Hs.265827	NM_022873:Homo sapiens interferon, alpha	2.94
	425118	AU076611	Hs.154672	Hs.154672:methylene tetrahydrofolate deh	2.94
	422010	AA302049	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	2.93
55	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	2.93
	412338	AA151527	Hs.69485	(locuslink)NM_024661:Homo sapiens hypoth	2.93
	413073	AL038165	Hs.75187	NM_014765:Homo sapiens translocase of ou	2.93
	412088	AI689496	Hs.108932	Hs.108932:ESTs	2.93
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	2.92
60	426746	J03626	Hs.2057	NM_000373:Homo sapiens uridine monophosp	2.92
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	2.92
	417944	AU077196	Hs.82985	NM_000393:Homo sapiens collagen, type V,	2.92
	428343	AL043021	Hs.12705	(locuslink)NM_145294:Homo sapiens simila	2.92
	435640	AF220053	Hs.54960	NM_018468:Homo sapiens uncharacterized h	2.92
65	451608	AA384525	Hs.26745	NM_016499:Homo sapiens HSPC244 (MGC:1337	2.92
	434608	AA805443	Hs.179909	NM_024831:Homo sapiens nuclear receptor	2.92
	437186	AA338305	Hs.377816	Hs.377816:Homo sapiens cDNA FLJ36808 fis	2.91
	429574	BE268321	Hs.208912	Hs.208912:hypothetical protein MGC861	2.91
	438549	BE386801	Hs.21858	Hs.21858:serine (or cysteine) proteinase	2.91
70	440246	W52010	Hs.191379	Hs.191379:ESTs	2.91
	426924	BE222542	Hs.126782	Hs.126782:Homo sapiens cDNA FLJ31512 fis	2.91
	444193	Y17801	Hs.10574	Hs.10574:solute carrier family 2, (facil	2.91
	422030	X51416	Hs.110849	(locuslink)NM_004451:Homo sapiens estrog	2.91
	415938	BE383507	Hs.78921	NM_003488:Homo sapiens A kinase (PRKA) a	2.91
75	450167	AA446404	Hs.24563	NM_013248:Homo sapiens NTF2-like export	2.91
	408815	AW957974	Hs.25485	(locuslink)NM_024599:Homo sapiens hypoth	2.91
	414820	AA371931	Hs.77422	Hs.77422:proteolipid protein 2 (colonic	2.91
	410013	AF067173	Hs.57904	Hs.57904:mago-nashi homolog, proliferati	2.91
	444823	BE262989	Hs.12045	Hs.12045:C2f protein	2.91
80	422197	AW974265	Hs.111632	Hs.111632:Lsm3 protein	2.90
	432710	AA609685	Hs.278672	NM_005898:Homo sapiens membrane compon	2.90
	405203				2.90
	432465	D56165	Hs.275163	NM_002512:Homo sapiens non-metastatic ce	2.90
	412926	AI879076	Hs.75061	Hs.75061:macrophage myristoylated alanin	2.90

	455967	L12535	Hs.75551	(locuslink)NM_012425: Homo sapiens Ras su	2.90
	402104				2.90
	414814	D14697	Hs.77393	(locuslink)NM_002004: Homo sapiens farnes	2.90
	442739	NM_007274	Hs.8679	(locuslink)NM_007274: Homo sapiens cyto	2.90
5	456157	AW979153	Hs.336881	Hs.336881: ESTs	2.90
	429505	AW820035	Hs.278679	NM_033274: Homo sapiens a disintegrin and	2.89
	430567	NM_003028	Hs.244542	Hs.244542: Homo sapiens cDNA FLJ38908 fis	2.89
	437822	AW450485	Hs.4437	NM_000991: Homo sapiens ribosomal protein	2.89
10	438543	AA810141	Hs.192182	Hs.192182: ESTs	2.89
	426158	NM_001982	Hs.199067	NM_001982: Homo sapiens v-erb-b2 erythro	2.89
	441455	AJ271671	Hs.7854	NM_014437: Homo sapiens soluble carrier fa	2.89
	420166	AW732276	Hs.95583	NM_012339: Homo sapiens transmembrane 4 s	2.89
	415674	BE394784	Hs.78596	NM_002797: Homo sapiens proteasome (proso	2.89
15	409591	AA532963	Hs.9100	Hs.9100: hypothetical gene supported by A	2.89
	418062	AW630656	Hs.83383	NM_005406: Homo sapiens peroxiredoxin 4 (2.89
	436540	BE397032	Hs.14468	NM_020230: Homo sapiens pater pan homolog	2.89
	426675	AW084791	Hs.133122	Hs.133122: hypothetical protein FLJ14524	2.89
	417018	M16038	Hs.80887	Hs.80887: v-yes-1 Yamaguchi sarcoma viral	2.89
	421684	BE281591	Hs.106768	NM_018120: Homo sapiens hypothetical prot	2.88
20	429404	NM_005738	Hs.10706	NM_005738: Homo sapiens ADP-ribosylation	2.88
	411030	BE387193	Hs.67896	(locuslink)NM_007346: Homo sapiens oipoid	2.88
	413822	R08950	Hs.272044	Hs.272044: ESTs, Weakly similar to hypoth	2.88
	438085	R52518	Hs.7967	Hs.7967: ESTs, Weakly similar to extensin	2.88
	409132	AJ224538	Hs.50732	NM_005399: Homo sapiens protein kinase, A	2.88
25	440490	AW513684	Hs.7218	Hs.7218: acetyl-Coenzyme A synthetase 2 (2.87
	431498	AK001777	Hs.258551	NM_012100: Homo sapiens aspartyl aminopep	2.87
	423570	AW838306	Hs.129819	NM_018344: Homo sapiens hypothetical prot	2.87
	448569	BE382657	Hs.21486	Hs.21486: signal transducer and activator	2.87
	451711	AK000461	Hs.26890	NM_017829: Homo sapiens cat eye syndrome	2.87
30	442643	U82756	Hs.374973	(locuslink)NM_004697: Homo sapiens PRP4 p	2.87
	447887	AA114050	Hs.211610	NM_001228: Homo sapiens caspase 8, apopto	2.87
	421178	BE267994	Hs.102419	Hs.102419: zinc finger protein	2.87
	443329	BE262943	Hs.9234	NM_032635: Homo sapiens seven transmembra	2.87
	416448	L13210	Hs.79339	NM_005567: Homo sapiens lectin, galactosi	2.87
35	453145	R63438	Hs.183454	Hs.183454: Homo sapiens cDNA FLJ14883 fis	2.86
	427775	R26944	Hs.180777	Hs.180777: Homo sapiens mRNA; cDNA DKFZp5	2.86
	424732	D80001	Hs.152629	Hs.152629: KIAA0179 protein	2.86
	426125	X87241	Hs.166994	Hs.166994: FAT tumor suppressor homolog 1	2.86
40	450273	AW296454	Hs.24743	Hs.24743: hypothetical protein FLJ20171	2.86
	407082	Z47055			2.86
	450038	AA005159	Hs.188489	Hs.188489: ESTs	2.86
	457274	AW674193	Hs.227152	NM_016391: Homo sapiens hypothetical prot	2.85
	417831	H16423	Hs.82685	Hs.82685: CD47 antigen (Rb-related antige	2.85
45	417824	AA084788	Hs.82646	NM_006145: Homo sapiens DnaJ (Hsp40) homo	2.85
	426989	AJ815206	Hs.100293	Hs.100293: O-linked N-acetylglucosamine (2.85
	434916	AF161383	Hs.284207	Hs.284207: hypothetical protein BC003515	2.85
	412664	AA421404	Hs.346868	NM_006824: Homo sapiens EBNA1 binding pro	2.85
	414172	AW954324	Hs.75790	(locuslink)NM_002642: Homo sapiens phosph	2.85
50	409504	AA304961	Hs.699	Hs.699: peptidylprolyl isomerase B (cyclo	2.84
	439920	H05430	Hs.288433	NM_016522: Homo sapiens neurotrimin (HNT)	2.84
	418462	BE001586	Hs.85266	Hs.85266: Integrin, beta 4	2.84
	442199	BE277633	Hs.372542	NM_004879: Homo sapiens etoposide-induced	2.84
	406710	AJ708347	Hs.184014	Hs.184014: ribosomal protein L31	2.84
	433435	BE545277	Hs.340959	NM_005726: Homo sapiens Ts translation el	2.84
55	415402	AA164587	Hs.177576	Hs.177576: mannosyl (alpha-1,3)-glycopro	2.84
	448730	AB032983	Hs.21894	Hs.21894: KIAA1157 protein	2.84
	433027	AF191018	Hs.279923	(locuslink)NM_014366: Homo sapiens putati	2.84
	449090	AK001735	Hs.22983	NM_020121: Homo sapiens UDP-glucose ceram	2.84
60	439737	AJ751438	Hs.41271	Hs.41271: Homo sapiens mRNA full length i	2.84
	403912				2.84
	423225	AA852604	Hs.125359	NM_006288: Homo sapiens Thy-1 cell surfac	2.84
	458376	AB023179	Hs.9059	Hs.9059: KIAA0962 protein	2.84
	429211	AF052683	Hs.198249	NM_005268: Homo sapiens gap junction prot	2.84
65	452518	AA280722	Hs.24758	Hs.24758: Homo sapiens cDNA FLJ32068 fis	2.84
	418127	BE243982	Hs.83532	(locuslink)NM_002389: Homo sapiens membra	2.83
	448489	AJ523875		R45782: Ha616-f Adult heart, Clontech Hom	2.83
	426194	T50872	Hs.2001	NM_001061: Homo sapiens thromboxane A syn	2.83
	422129	AU076635	Hs.1478	NM_000185: Homo sapiens serine (or cystei	2.83
70	437651	BE560672	Hs.13543	(locuslink)NM_145214: Homo sapiens tripar	2.83
	415173	AW501735	Hs.180059	Hs.180059: Homo sapiens cDNA FLJ31360 fis	2.83
	408201	AK000568	Hs.43654	NM_017882: Homo sapiens ceroid-lipofuscin	2.83
	444758	AL044878	Hs.11899	NM_000858: Homo sapiens 3-hydroxy-3-methyl	2.83
	423323	AJ951628	Hs.127007	NM_003740: Homo sapiens potassium channel	2.83
75	439720	AJ935202	Hs.31181	Hs.31181: Homo sapiens cDNA: FLJ23230 fis	2.83
	435550	AJ224456	Hs.324507	Hs.324507: hypothetical protein FLJ20986	2.83
	425907	AA365752	Hs.155955	Hs.155955: ESTs	2.83
	426234	BE314534	Hs.168159	Hs.168159: bifunctional apoptosis regulat	2.82
	427640	AF058293	Hs.180015	NM_001355: Homo sapiens D-dopachrome taut	2.82
	433233	AB040927	Hs.301804	Hs.301804: KIAA1494 protein	2.82
80	415697	AJ365603	Hs.279696	Hs.279696: DKFZP566I1024 protein	2.82
	441321	H17182	Hs.7771	NM_007273: Homo sapiens repressor of estr	2.82
	430040	AW503115	Hs.227823	NM_014287: Homo sapiens pM5 protein (PM5)	2.82
	449954	AA641636	Hs.37477	Hs.37477: ESTs, Weakly similar to T46220	2.82

	427022	AW245839	Hs.173255	NM_004596:Homo sapiens small nuclear rib	2.82
	410047	AI167810	Hs.379753	Hs.379753:Homo sapiens cDNA FLJ33176 fis	2.82
	400845				2.81
5	419501	AW843822	Hs.199961	Hs.199961:ESTs, Weakly similar to hypoth	2.81
	418140	BE613836	Hs.83551	(locuslink)NM_002403:Homo sapiens microf	2.81
	422032	AA476966	Hs.110857	NM_016310:Homo sapiens polymerase (RNA)	2.81
	419768	T72104	Hs.93194	Hs.93194:apolipoprotein A-I	2.81
	436673	AF201931	Hs.5268	Hs.5268:zinc finger, DHHC domain contain	2.81
10	421140	AA298741	Hs.102135	NM_006280:Homo sapiens signal sequence r	2.81
	450126	BE018138	Hs.24447	(locuslink)NM_005866:Homo sapiens type I	2.81
	439018	AW300887	Hs.26638	NM_031457:Homo sapiens membrane-spanning	2.81
	433061	AW068033	Hs.296422	(locuslink)NM_025233:Homo sapiens nucleo	2.81
	400278		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	2.81
15	407338	AA773213	Hs.91202	Hs.91202:Homo sapiens cDNA FLJ25946 fis,	2.81
	410240	AL157424	Hs.61289	Hs.61289:synaptotagmin 2	2.80
	423880	BE278111	Hs.134200	Hs.134200:DKFZP564C186 protein	2.80
	422098	H03117	Hs.111497	Hs.111497:neuronal protein 17.3	2.80
	426680	AA320160	Hs.171811	NM_001625:Homo sapiens adenylate kinase	2.80
20	437672	AW748265	Hs.5741	NM_016230:Homo sapiens flavohemoprotein	2.80
	456602	AA411607	Hs.118964	NM_017650:Homo sapiens hypothetical prot	2.80
	457329	AI634860	Hs.359682	(locuslink)NM_016442:Homo sapiens type 1	2.80
	426437	BE076537	Hs.169895	Hs.169895:ubiquitin-conjugating enzyme E	2.79
	412627	BE391959	Hs.74276	Hs.74276:chloride intracellular channel	2.79
25	452695	AW780199	Hs.30327	NM_003658:Homo sapiens mitogen-activated	2.79
	409531	BE384319	Hs.54702	(locuslink)NM_007255:Homo sapiens xylosy	2.79
	448988	Y09763	Hs.22785	NM_021987:Homo sapiens gamma-aminobutyri	2.79
	447627	AF090922	Hs.152738	NM_016050:Homo sapiens mitochondrial rib	2.79
30	419846	NM_015977	Hs.285681	NM_032951:Homo sapiens Williams Beuren s	2.79
	412969	AI373162	Hs.75103	NM_003406:Homo sapiens tyrosine 3-monoox	2.79
	424867	AI024860	Hs.153591	NM_005787:Homo sapiens Nsl56 (D. melanog	2.79
	410600	AW575742	Hs.351676	Hs.351676:Homo sapiens cDNA FLJ25921 fis	2.79
	451452	BE560065	Hs.26433	NM_001382:Homo sapiens dolichyl-phosphat	2.79
	407844	AW073716	Hs.8037	(locuslink)NM_005723:Homo sapiens tetras	2.79
35	448752	AA593867	Hs.300842	NM_024820:Homo sapiens KIAA1608 protein	2.79
	419235	AW470411	Hs.288433	NM_016522:Homo sapiens neurotrophin (HNT)	2.78
	407754	AA527348	Hs.288967	Hs.288967:Homo sapiens, similar to RIKEN	2.78
	422282	AF019225	Hs.114309	(locuslink)NM_003661:Homo sapiens apolip	2.78
	414181	AK000476	Hs.75798	NM_016470:Homo sapiens chromosome 20 ope	2.78
40	418869	AW516565		AA229762:nc49101.1 NCL CGAP_Pr3 Homo sa	2.78
	419444	NM_002496	Hs.90443	NM_002496:Homo sapiens NADH dehydrogenas	2.78
	430250	NM_016829	Hs.283021	NM_016829:Homo sapiens chloride intracel	2.78
	412760	AW379030	Hs.41324	Hs.41324:ESTs	2.78
	423013	AW875443	Hs.22209	Hs.22209:secreted modular calcium-bindin	2.78
45	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	2.78
	447402	H54520	Hs.351327	(locuslink)NM_017828:Homo sapiens hypoth	2.78
	417896	AA379770	Hs.82890	Hs.82890:defender against cell death 1	2.78
	422061	AW327546	Hs.111024	(locuslink)NM_005984:Homo sapiens solute	2.78
	450607	AL050373	Hs.25213	NM_015677:Homo sapiens hypothetical prot	2.78
50	419757	AA773820	Hs.63970	Hs.63970:ESTs	2.77
	409932	AI367750	Hs.57600	NM_001283:Homo sapiens adaptor-related p	2.77
	408044	BE206939	Hs.42287	NM_001952:Homo sapiens E2F transcription	2.77
	430014	H59354	Hs.374303	(locuslink)NM_144691:Homo sapiens hypoth	2.77
	451690	AW451469	Hs.209990	Hs.209990:ESTs	2.77
55	446950	AA305800	Hs.5672	(locuslink)NM_030799:Homo sapiens golgi	2.77
	444207	AI665004	Hs.374415	Hs.374415:ESTs	2.77
	417089	H52280	Hs.18612	Hs.18612:Homo sapiens cDNA: FLJ21909 fis	2.77
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	2.77
	425978	BE253927	Hs.24983	Hs.24983:hypothetical protein from EURCO	2.77
60	422753	AI928995	Hs.1575	Hs.1575:small nuclear ribonucleoprotein	2.77
	449051	AW961400	Hs.333526	NM_032339:Homo sapiens hypothetical prot	2.77
	450701	H39960	Hs.288467	Hs.288467:Homo sapiens cDNA FLJ12280 fis	2.77
	412890	T85247	Hs.351875	NM_004374:Homo sapiens cytochrome c oxid	2.77
	415752	BE314524	Hs.78776	NM_012342:Homo sapiens putative transmem	2.76
65	427609	AK000436	Hs.179791	NM_017817:Homo sapiens RAB20, member RAS	2.76
	450770	AA019924	Hs.28803	Hs.28803:ESTs	2.76
	419594	AA013061	Hs.91417	(locuslink)NM_007027:Homo sapiens topois	2.76
	450876	AF189062	Hs.285976	(locuslink)NM_013384:Homo sapiens LAG1 I	2.76
	417767	BE242241	Hs.82542	NM_001637:Homo sapiens acylglycyl hydro	2.76
70	439968	AA224760	Hs.153	NM_000971:Homo sapiens ribosomal protein	2.76
	426520	BE545584	Hs.343566	Hs.343566:KIAA0251 protein	2.75
	441028	AI333660	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	2.75
	445033	AV652402	Hs.72901	Hs.078487:Homo sapiens cyclin-dependent	2.75
	418478	U38945	Hs.1174	NM_000077:Homo sapiens cyclin-dependent	2.75
75	428157	AT738719	Hs.198427	NM_000189:Homo sapiens hexokinase 2 (HK2	2.75
	416178	AI808527	Hs.192822	NM_030949:Homo sapiens protein phosphata	2.75
	435025	T08990	Hs.4742	Hs.4742:GPAAP1 anchor attachment protein	2.75
	421917	AB028943	Hs.109445	Hs.109445:hypermethylated in cancer 2	2.75
	406621	X57809	Hs.181125	Hs.181125:immunoglobulin lambda locus	2.75
80	408196	AL034548	Hs.43627	NM_006943:Homo sapiens SRY (sex determin	2.75
	412600	L28824	Hs.74101	Hs.74101:spleen tyrosine kinase	2.75
	452806	AW014549	Hs.58373	Hs.58373:ESTs	2.75
	451356	AA748418	Hs.33368	Hs.33368:hypothetical protein FLJ11175	2.75
	421643	BE281170	Hs.106357	NM_007126:Homo sapiens valosin-containing	2.74

5	423527	AI206965	Hs.105861	(locustink)NM_024712:Homo sapiens engulf	2.74
	428000	R35145	Hs.291904	Hs.291904:accessory protein BAP31	2.74
	441565	AW953575	Hs.303125	Hs.303125:p53-induced protein FIGP1	2.74
	450247	AF123303	Hs.24713	NM_013386:Homo sapiens hypothetical prot	2.74
	422691	NM_003365	Hs.119251	NM_003365:Homo sapiens ubiquinol-cytochr	2.74
	440457	BE387593	Hs.21321	(locustink)NM_145808:Homo sapiens granul	2.74
	422675	BE018517	Hs.119140	NM_001970:Homo sapiens eukaryotic transl	2.74
	428428	AL037544	Hs.184298	NM_001799:Homo sapiens cyclin-dependent	2.73
10	423598	BE247600	Hs.377968	NM_020400:Homo sapiens G protein-coupled	2.73
	428297	AA236291	Hs.183583	NM_030666:Homo sapiens serine (or cystei	2.73
	421921	H83363	Hs.355993	NM_012456:Homo sapiens translocase of In	2.73
	403217				2.73
	423671	AW860155	Hs.234101	Hs.234101:Homo sapiens, similar to choli	2.73
15	418733	AA227714	Hs.374897	Hs.374897:Homo sapiens cDNA FLJ36874 fis	2.73
	400275		Hs.4888	NM_006513:Homo sapiens seryl-tRNA synthe	2.73
	445084	H38914	Hs.250848	Hs.250848:Homo sapiens cDNA FLJ14761 fis	2.73
	411872	AW327356	Hs.90918	Hs.90918:chromosome 11 open reading fram	2.73
	403483				2.73
20	438119	AW963217	Hs.203961	Hs.203961:ESTs, Weakly similar to hypoth	2.73
	422009	AF742845	Hs.110713	NM_003472:Homo sapiens DEK oncogene (DNA	2.73
	436995	AI160015	Hs.125489	Hs.125489:KIAA1951 protein	2.73
	400509				2.73
	429305	AF095727	Hs.287832	Hs.287832:myelin protein zero-like 1	2.73
25	445899	AI263736	Hs.145626	Hs.145626:Homo sapiens, Similar to hypot	2.72
	453557	AA522464	Hs.285996	NM_024956:Homo sapiens hypothetical prot	2.72
	446859	AA94299	Hs.16297	NM_005694:Homo sapiens COX17 homolog, cy	2.72
	424439	AA579635	Hs.1770	Hs.1770:ligase I, DNA, ATP-dependent	2.72
	437809	AL137723	Hs.5855	Hs.5855:Homo sapiens mRNA; cDNA DKFZp434	2.72
30	428466	AF151053	Hs.184456	NM_016486:Homo sapiens hypothetical prot	2.71
	445176	AI878907	Hs.12379	NM_001419:Homo sapiens ELAV (embryonic l	2.71
	438000	AI825880	Hs.5985	Hs.5985:non-kinase Cdc42 effector protel	2.71
	423359	W00482	Hs.2399	NM_004995:Homo sapiens matrix metallopro	2.71
	427782	AI956052	Hs.115960	NM_024036:Homo sapiens hypothetical prot	2.71
35	415169	W42913	Hs.78089	NM_004231:Homo sapiens ATPase, H+ transp	2.71
	400277		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	2.71
	426263	AI908774	Hs.259785	Hs.259785:camitine palmitoyltransferase	2.71
	445515	BE388665	Hs.179999	Hs.179999:Homo sapiens, clone IMAGE:3457	2.71
	416976	BE243985	Hs.80680	Hs.80680:major vault protein	2.71
40	441238	AI372565	Hs.322456	NM_032039:Homo sapiens hypothetical prot	2.71
	420511	AF052692	Hs.98485	NM_024009:Homo sapiens gap junction prot	2.71
	424965	AW956282	Hs.144609	NM_080652:Homo sapiens similar to RIKEN	2.71
	421808	AK000157	Hs.108502	NM_017688:Homo sapiens hypothetical prot	2.71
	412973	L37368	Hs.75104	Hs.75104:RNA binding protein S1, serine-	2.70
45	410113	AW995564	Hs.250824	Hs.250824:Homo sapiens cDNA: FLJ23435 fi	2.70
	413092	AA126856	Hs.118665	Hs.118665:ESTs	2.70
	447096	BE539199	Hs.62112	(locustink)NM_003457:Homo sapiens zinc f	2.70
	450493	M93718	Hs.166373	Hs.166373:nitric oxide synthase 3 (endot	2.70
50	413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	2.70
	450747	AI064821	Hs.129953	Hs.129953:Ewing sarcoma breakpoint regio	2.70
	436042	AF284422	Hs.119178	(locustink)NM_020246:Homo sapiens cation	2.70
	432981	NM_002733	Hs.3136	Hs.3136:protein kinase, AMP-activated, g	2.70
	413341	AA307211	Hs.251531	NM_002789:Homo sapiens proteasome (proso	2.70
	408204	AA454501	Hs.43666	NM_007079:Homo sapiens protein tyrosine	2.70
55	416770	AW163570	Hs.79768	NM_014740:Homo sapiens KIAA0111 gene pro	2.70
	447507	H59696	Hs.18747	NM_005837:Homo sapiens POP7 (processing	2.70
	424500	AF040704	Hs.149443	(locustink)NM_007022:Homo sapiens putad	2.69
	414237	BE536554	Hs.278270	Hs.278270:inactive progesterone receptor	2.69
	400231		Hs.169476	NM_002046:Homo sapiens glyceraldehyde-3-	2.69
60	431209	NM_001533	Hs.2730	Hs.2730:heterogeneous nuclear ribonucleo	2.69
	444118	AA458542	Hs.10326	NM_007263:Homo sapiens coatomer protein	2.69
	424608	X80695	Hs.151134	Hs.151134:oxidase (cytochrome c) assembl	2.69
	418546	AA224827		AA224827:nc32g04.s1 NCI_CGAP_Py2 Homo sa	2.69
	440002	AW769844	Hs.111222	Hs.111222:hypothetical protein FLJ22875	2.69
65	449957	D31365	Hs.24220	(locustink)NM_016479:Homo sapiens scotin	2.69
	432920	U37689	Hs.3128	NM_006232:Homo sapiens polymerase (RNA)	2.69
	450306	AL080080	Hs.24766	NM_030755:Homo sapiens thioredoxin domai	2.69
	429544	BE299343	Hs.2430	NM_005997:Homo sapiens transcription fac	2.68
	428582	BE336699	Hs.185055	Hs.185055:BENE protein	2.68
70	445139	AB037848	Hs.12365	Hs.12365:synaptotagmin XII	2.68
	453905	NM_002314	Hs.36566	NM_016735:Homo sapiens LIM domain kinase	2.68
	418883	BE387036	Hs.1211	NM_001611:Homo sapiens acid phosphatase	2.68
	420957	X98743	Hs.100555	Hs.100555:DEADH (Asp-Glu-Ala-Asp/His) b	2.68
	418187	NM_004604	Hs.83734	NM_004604:Homo sapiens syntxin 4A (plac	2.68
75	409533	AW969543	Hs.144609	NM_080652:Homo sapiens similar to RIKEN	2.68
	433184	AA147979	Hs.285006	NM_020243:Homo sapiens translocase of ou	2.68
	455303	AW892049		BE066891:PM3-BT0338-211299-002-e12 BT033	2.68
	452600	AI910842	Hs.103381	Hs.103381:ESTs, Weakly similar to hypoth	2.68
	415410	AF037332	Hs.278569	NM_014748:Homo sapiens KIAA0064 gene pro	2.67
80	426432	AF001601	Hs.169857	NM_000305:Homo sapiens paraoxonase 2 (PO	2.67
	435049	AL122087	Hs.4746	NM_021941:Homo sapiens hypothetical prot	2.67
	450528	NM_014072	Hs.25063	NM_031268:Homo sapiens PRO0461 protein (2.67
	433339	AF019226	Hs.8036	NM_004283:Homo sapiens RAB3D, member RAS	2.67
	408783	AF192522	Hs.47701	NM_013389:Homo sapiens NPC1 (Niemann-Pic	2.67

	451798	BE297567	Hs.27047	Hs.27047:hypothetical protein FLJ20392	2.67
	427716	L38951	Hs.180446	Hs.180446:karyopherin (importin) beta 1	2.67
	436319	H90727	Hs.5123	Hs.5123:hypothetical protein BC008246	2.67
5	415116	AA160363	Hs.269956	Hs.269956:ESTs	2.67
	425838	NM_014071	Hs.159613	NM_014071:Homo sapiens nuclear receptor	2.66
	418706	U73524	Hs.87465	NM_006831:Homo sapiens ATP/GTP-binding p	2.66
	410165	BE560228	Hs.71869	NM_013258:Homo sapiens apoptosis-associa	2.66
	410134	U68140	Hs.58927	(locuslink)NM_002533:Homo sapiens nuclea	2.66
10	430066	AI929659	Hs.237825	Hs.237825:signal recognition particle 72	2.66
	425910	AA830797	Hs.184760	NM_005760:Homo sapiens CCAAT-box-binding	2.66
	427954	J03060	Hs.247551	NM_002455:Homo sapiens melanin 1 (MTX1).	2.66
	439971	W32474	Hs.301746	Hs.301746:Homo sapiens cDNA FLJ37267 fis	2.66
	438449	AK001333	Hs.6216	Hs.6216:DnaJ (Hsp40) homolog, subfamily	2.66
15	435906	AI686379	Hs.110796	(locuslink)NM_020150:Homo sapiens SAR1 p	2.66
	433387	L76528	Hs.3260	NM_000021:Homo sapiens presenilin 1 (Alz	2.66
	447191	NM_014521	Hs.17667	(locuslink)NM_014521:Homo sapiens SH3-do	2.66
	444099	D87432	Hs.10315	NM_003983:Homo sapiens solute carrier fa	2.66
	417821	BE245149	Hs.82643	NM_002822:Homo sapiens protein tyrosine	2.66
20	418529	AW006695	Hs.250897	Hs.250897:TRK-fused gene	2.65
	426025	AW138330	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	2.65
	420187	AK001714	Hs.95744	NM_019028:Homo sapiens hypothetical prot	2.65
	408150	BE620274	Hs.43112	Hs.43112:Homo sapiens mRNA; cDNA DKFZp43	2.65
	444395	N66148	Hs.11125	(locuslink)NM_014041:Homo sapiens signal	2.65
25	431222	X56777	Hs.273790	NM_007155:Homo sapiens zona pellucida gl	2.65
	406790	AA293303	Hs.356342	Hs.356342:ESTs, Highly similar to 211320	2.65
	440708	AF038962	Hs.7381	Hs.7381:voltage-dependent anion channel	2.65
	416526	H61082	Hs.14743	Hs.14743:ESTs	2.65
30	413995	BE048146	Hs.75671	NM_004603:Homo sapiens syntaxin 1A (brai	2.65
	424908	AW513963	Hs.39143	Hs.39143:hypothetical protein MGC13125	2.65
	442110	AF113008	Hs.8102	NM_001023:Homo sapiens ribosomal protein	2.65
	452882	AW972990	Hs.196270	NM_030780:Homo sapiens folate transporte	2.65
	406862	AW150807	Hs.356262	Hs.356262:ESTs, Highly similar to A31233	2.64
	451295	AI557212	Hs.17132	Hs.17132:ESTs	2.64
35	448428	AF282874	Hs.21201	NM_015480:Homo sapiens necdin 3 (DKFZP56	2.64
	426611	BE178050	Hs.171271	NM_001904:Homo sapiens catenin (cadherin	2.64
	426216	N77630	Hs.13895	Hs.13895:Homo sapiens cDNA FLJ11654 fis,	2.64
	407223	H96850		H96850:yrw03b12.s1 Soares melanocyte 2NbH	2.64
	427725	U66839	Hs.180633	NM_002756:Homo sapiens mitogen-activated	2.64
40	420157	AA857991	Hs.123106	Hs.123106:ESTs	2.64
	428471	X57348	Hs.184510	Hs.184510:stratillin	2.64
	451544	AK000429	Hs.26570	NM_017814:Homo sapiens hypothetical prot	2.64
	413245	BE244334	Hs.75249	Hs.75249:ADP-ribosylation factor-like 6	2.64
	415020	BE249915	Hs.293533	Hs.293533:Homo sapiens cDNA FLJ37093 fis	2.64
45	437193	BE259190	Hs.289721	Hs.289721:growth arrest-specific 5	2.64
	418684	H82987	Hs.87246	NM_014417:Homo sapiens BCL2 binding comp	2.64
	410668	BE379794	Hs.159651	NM_014452:Homo sapiens tumor necrosis fa	2.64
	438183	AI146327	Hs.334802	(locuslink)NM_024718:Homo sapiens hypoth	2.64
	441225	BE563042	Hs.118820	Hs.118820:hypothetical protein BC007882	2.64
50	432788	AA521091	Hs.178499	Hs.178499:HSPC063 protein	2.64
	432746	AA545412	Hs.372775	Hs.372775:Homo sapiens, clone IMAGE:3946	2.64
	450377	AB033091	Hs.355925	Hs.355925:KIAA1265 protein	2.64
	434633	AI189587	Hs.120915	Hs.120915:ESTs	2.64
	424707	BE061914	Hs.10844	Hs.10844:leucine-rich alpha-2-glycoprote	2.64
55	427600	AW630918	Hs.179774	Hs.179774:proteasome (prosome, macropain	2.63
	446522	NM_003876	Hs.15196	NM_003876:Homo sapiens putative receptor	2.63
	436906	H95990	Hs.181244	Hs.181244:major histocompatibility compl	2.63
	410701	AF198620	Hs.10283	NM_005105:Homo sapiens RNA binding motif	2.63
	410182	NM_001983	Hs.59544	NM_001983:Homo sapiens excision repair c	2.63
60	406716	AW148546	Hs.169476	Hs.169476:glyceraldehyde-3-phosphate deh	2.63
	430308	BE540865	Hs.238990	NM_004064:Homo sapiens cyclin-dependent	2.63
	431074	BE072772	Hs.8997	Hs.8997:Sad1 unc-84 domain protein 1	2.63
	412867	AU076861	Hs.74637	Hs.74637:testis enhanced gene transcript	2.63
	440524	R71264	Hs.16798	Hs.16798:Homo sapiens mRNA; cDNA DKFZp56	2.63
65	435968	AW161481	Hs.111577	(locuslink)NM_030926:Homo sapiens integr	2.63
	422672	X12784	Hs.119129	NM_001845:Homo sapiens collagen, type IV	2.63
	447528	AI612027	Hs.76277	NM_138393:Homo sapiens hypothetical prot	2.63
	406774	AW518383	Hs.177592	Hs.177592:ribosomal protein, large, P1	2.63
	439755	AW748482	Hs.77873	Hs.77873:B7 homolog 3	2.63
70	435311	W86610	Hs.185736	Hs.185736:ESTs	2.63
	426699	AW578252	Hs.190161	Hs.190161:LR8 protein	2.62
	410678	BE540516	Hs.378825	Hs.378825:Homo sapiens cDNA FLJ37850 fis	2.62
	414839	X63692	Hs.77462	(locuslink)NM_001379:Homo sapiens DNA (c	2.62
	443217	NM_001545	Hs.9078	Hs.9078:immature colon carcinoma transcr	2.62
75	448749	AW859679	Hs.21902	Hs.21902:Homo sapiens clone 25237 mRNA s	2.62
	450009	AI399947	Hs.166486	Hs.166486:Homo sapiens cDNA FLJ11432 fis	2.62
	407687	AK002011	Hs.37558	NM_018339:Homo sapiens hypothetical prot	2.62
	442232	AI357813	Hs.337460	Hs.337460:ESTs, Highly similar to HYEP_H	2.62
	419625	U91616	Hs.182885	NM_004556:Homo sapiens nuclear factor of	2.62
80	416114	AI695549	Hs.183868	Hs.183868:glucuronidase, beta	2.62
	439437	AI207788	Hs.343628	Hs.343628:sialyltransferase 4B (beta-gal	2.61
	408452	AA054683	Hs.222728	Hs.222728:Homo sapiens cDNA FLJ39004 fis	2.61
	443142	AI696513	Hs.108705	Hs.108705:protein phosphatase 2 (former	2.61
	426152	BE299190	Hs.167246	Hs.167246:P450 (cytochrome) oxidoreducta	2.61

	419667	AU077005	Hs.92208	NM_003815:Homo sapiens a disintegrin and	2.61
	415072	BE253687	Hs.77876	Hs.77876:hypothetical gene MGC19595	2.61
	406670	W79632	Hs.256301	Hs.256301:hypothetical protein MGC13170	2.61
5	403399				2.61
	419579	W49529	Hs.296200	NM_023948:Homo sapiens hypothetical prot	2.61
	437202	AA326110	Hs.374481	Hs.374481:ESTs, Weakly similar to T34549	2.61
	414020	NM_002984	Hs.75703	NM_002984:Homo sapiens small inducible c	2.61
	421295	AW081061	Hs.103180	Hs.103180:DC2 protein	2.61
10	446488	AB037782	Hs.15119	Hs.15119:KIAA1361 protein	2.61
	442504	BE503373	Hs.334335	NM_022484:Homo sapiens hypothetical prot	2.60
	448204	AA75124	Hs.170561	Hs.170561:ESTs	2.60
	449175	AJ005892	Hs.23170	(locuslink)NM_012280:Homo sapiens FtsJ h	2.60
	411201	T74588	Hs.8509	Hs.8509:ESTs, Weakly similar to C3HU com	2.60
	424805	AF230904	Hs.153260	NM_031892:Homo sapiens SH3-domain kinase	2.60
15	425421	L11669	Hs.157145	Hs.157145:tetracycline transporter-like	2.60
	422739	H20106	Hs.119591	(locuslink)NM_004069:Homo sapiens adapto	2.60
	450858	C18458	Hs.25597	Hs.25597:elongation of very long chain f	2.59
	443195	BE148235	Hs.193063	Hs.193063:Homo sapiens cDNA FLJ14201 fis	2.59
	430504	H52761	Hs.44095	Hs.44095:scyclin M3	2.59
20	439578	AW263124	Hs.350547	NM_024665:Homo sapiens nuclear receptor	2.59
	416041	AA345547	Hs.53263	(locuslink)NM_024647:Homo sapiens nucleo	2.59
	451920	AA224483	Hs.27239	Hs.27239:zinc finger, DHHC domain contai	2.59
	414163	BE262310	Hs.75782	NM_001621:Homo sapiens general transcrip	2.59
25	422140	BE295918	Hs.112193	(locuslink)NM_025259:Homo sapiens chromo	2.59
	452817	AA322859	Hs.284275	Hs.284275:p21 (CDKN1A)-activated kinase	2.59
	413353	AW293542	Hs.75309	Hs.75309:eukaryotic translation elongati	2.59
	421700	BE515018	Hs.107014	NM_016641:Homo sapiens membrane interact	2.59
	410801	BE275469	Hs.66493	NM_016430:Homo sapiens Down syndrome cri	2.59
30	440511	AF132959	Hs.7236	NM_015953:Homo sapiens eNOS interacting	2.59
	407887	AA579668	Hs.41072	(locuslink)NM_004568:Homo sapiens serine	2.59
	425356	BE244879	Hs.155939	NM_005541:Homo sapiens inositol polyphos	2.59
	408102	U46351	Hs.621	Hs.621:lectin, galactoside-binding, solu	2.59
	417952	AI192838	Hs.173135	Hs.173135:dual-specificity tyrosine-(Y)-	2.59
35	433053	BE301909	Hs.279952	NM_015917:Homo sapiens glutathione S-tra	2.59
	450935	BE514743	Hs.379039	NM_005851:Homo sapiens tumor suppressor	2.59
	417891	W79410	Hs.82887	(locuslink)NM_021959:Homo sapiens protei	2.59
	438364	AK000860	Hs.6191	NM_020441:Homo sapiens coronin, actin-bi	2.59
	430976	AA505112	Hs.282990	NM_033550:Homo sapiens chromosome 20 ope	2.58
40	444838	AV651680	Hs.208558	Hs.208558:ESTs	2.58
	416435	AA31301	Hs.374897	Hs.374897:Homo sapiens cDNA FLJ36874 fis	2.58
	415444	BE247295	Hs.78452	Hs.78452:solute carrier family 20 (phosp	2.58
	452222	AW806287	Hs.21432	Hs.21432:SEX gene	2.58
	400541				2.58
45	444309	U83236	Hs.10803	Hs.10803:calcium and integrin binding 1	2.58
	416116	H51847	Hs.99858	Hs.99858:ribosomal protein L7a	2.58
	418629	BE247550	Hs.86859	(locuslink)NM_005310:Homo sapiens growth	2.58
	432996	AF105025	Hs.279901	Hs.279901:PTD009 protein	2.57
	426781	AL048967	Hs.172207	(locuslink)NM_007363:Homo sapiens non-PO	2.57
50	452636	BE615074	Hs.145279	Hs.145279:SET translocation (myeloid leu	2.57
	406851	AA609784	Hs.352392	Hs.352392:major histocompatibility compl	2.57
	447674	BE270640	Hs.19192	NM_001798:Homo sapiens cyclin-dependent	2.57
	445647	AV654627	Hs.271808	Hs.271808:Homo sapiens cDNA FLJ38018 fis	2.57
	444736	AA533491	Hs.23317	NM_032824:Homo sapiens hypothetical prot	2.57
	402861				2.57
55	450069	AI698139	Hs.202093	Hs.202093:ESTs	2.57
	414029	BE297731	Hs.75709	NM_002355:Homo sapiens mannose-6-phospha	2.57
	427700	AA262294	Hs.180383	NM_001946:Homo sapiens dual specificity	2.57
	449961	AW265634	Hs.133100	Hs.133100:ESTs	2.56
60	449378	AW664026	Hs.59892	Hs.59892:ESTs, Weakly similar to alpha 5	2.56
	442599	AF078037	Hs.324051	(locuslink)NM_006663:Homo sapiens RelA-a	2.56
	448633	AA311426	Hs.21635	NM_001070:Homo sapiens tubulin, gamma 1	2.56
	416078	AL034349	Hs.79005	NM_002844:Homo sapiens protein tyrosine	2.56
	428044	AA093322	Hs.301404	NM_006743:Homo sapiens RNA binding motif	2.56
65	451564	AU076698	Hs.132760	(locuslink)NM_001487:Homo sapiens glucos	2.56
	457601	AF041429	Hs.284265	(locuslink)NM_145169:Homo sapiens simila	2.56
	439630	AA313607	Hs.58633	Hs.58633:Homo sapiens cDNA: FLJ22145 fis	2.55
	419587	S62907	Hs.91343	NM_000807:Homo sapiens gamma-aminobutyl	2.55
	448279	BE250564	Hs.283655	Hs.283655:lysophospholipase II	2.55
70	453350	AI917771	Hs.61790	(locuslink)NM_024668:Homo sapiens Import	2.55
	423720	AL044191	Hs.23388	NM_030817:Homo sapiens hypothetical prot	2.55
	400237		Hs.83347	NM_001087:Homo sapiens angio-associated,	2.55
	420856	BE513294	Hs.205736	Hs.205736:KIAA1978 protein	2.55
	421541	NM_003942	Hs.105584	Hs.105584:ribosomal protein S6 kinase, 9	2.55
75	434848	BE256304	Hs.32148	NM_018445:Homo sapiens AD-015 protein (L	2.55
	424488	AK000413	Hs.149227	(locuslink)NM_017806:Homo sapiens hypoth	2.55
	449089	D78850	Hs.250465	Hs.250465:Homo sapiens mRNA; cDNA DKFZp4	2.55
	430053	AF052155	Hs.227949	NM_030673:Homo sapiens SEC13-like 1 (S.	2.55
	437469	AW753112	Hs.15514	Hs.15514:hypothetical protein MGC3260	2.55
	407755	AI151353	Hs.29742	Hs.29742:Homo sapiens cDNA FLJ32147 fis	2.55
80	446673	NM_016361	Hs.15871	NM_016361:Homo sapiens LPAP for lysophos	2.55
	411766	AA399671	Hs.71969	Hs.71969:Homo sapiens mRNA; cDNA DKFZp66	2.55
	415198	AW009480	Hs.943	Hs.943:natural killer cell transcript 4	2.55
	436495	BE258948	Hs.290874	Hs.290874:Homo sapiens, clone MGC:31984	2.55

5	417785	X59812	Hs.82568	NM_000784:Homo sapiens cytochrome P450,	2.55
	443358	H65417	Hs.17757	(locuslink)NM_021622:Homo sapiens plects	2.55
	452349	AB028944	Hs.29189	Hs.29189:ATPase, Class VI, type 11A	2.55
	427721	A1582843	Hs.180455	NM_005053:Homo sapiens RAD23 homolog A (2.54
	407559	AA313352	Hs.280858	Hs.280858:Homo sapiens cDNA FLJ32370 fis	2.54
	413426	U88637	Hs.75354	Hs.75354:GCN1 general control of amino-a	2.54
	425465	L18964	Hs.1904	Hs.1904:protein kinase C, iota	2.54
	444152	A125594	Hs.149305	Hs.149305:hypothetical protein MGC2603	2.54
10	451820	AW058357	Hs.199248	NM_000958:Homo sapiens prostaglandin E r	2.54
	414356	BE384361	Hs.182885	(locuslink)NM_004556:Homo sapiens nuclea	2.54
	444410	BE387360	Hs.33719	Hs.33719:Homo sapiens, similar to data s	2.54
	415200	AL040328	Hs.78202	NM_003072:Homo sapiens SW/SNF related,	2.54
	403955				2.54
15	430361	A1033965	Hs.239926	Hs.239926:sterol-C4-methyl oxidase-like	2.54
	432401	NM_013330	Hs.274479	NM_013330:Homo sapiens NME7 (NME7), mRNA	2.54
	446719	W39500	Hs.301872	Hs.301872:hypothetical protein MGC4840	2.54
	439941	AJ392640	Hs.18272	NM_030674:Homo sapiens solute carrier fa	2.54
	436885	W28661	Hs.5288	Hs.5288:Homo sapiens mRNA; cDNA DKFZp434	2.54
20	424522	AL134847	Hs.149957	Hs.149957:ribosomal protein S6 kinase, 9	2.54
	442904	AW575008	Hs.11355	Hs.11355:thymopietin	2.54
	422605	H16646	Hs.118666	Hs.118666:hypothetical protein PP591	2.54
	442069	AW664144	Hs.297007	Hs.297007:Homo sapiens cDNA FLJ32174 fis	2.54
	447362	AW176120	Hs.9061	NM_024099:Homo sapiens hypothetical prot	2.53
25	416305	AU076628	Hs.79187	NM_001338:Homo sapiens coxsackie virus a	2.53
	422624	BE616678	Hs.76152	NM_006854:Homo sapiens KDEL (Lys-Asp-Glu	2.53
	447298	BE617527	Hs.239818	NM_006219:Homo sapiens phosphoinositide-	2.53
	412833	AW960547	Hs.298262	Hs.298262:ribosomal protein S19	2.53
	404854				2.53
30	415761	AA132666	Hs.78802	(locuslink)NM_002093:Homo sapiens glyco	2.53
	431104	AW970859	Hs.313503	Hs.313503:ESTs	2.53
	439180	AJ393742	Hs.199067	Hs.199067:v-erb-b2 erythroblastic leukem	2.53
	424250	AF073310	Hs.143648	NM_003749:Homo sapiens insulin receptor	2.53
	452878	AW081128	Hs.246374	Hs.246374:Homo sapiens cDNA FLJ31250 fis	2.53
35	415742	BE410243	Hs.78769	NM_003249:Homo sapiens thimet oligopepti	2.53
	404140				2.53
	407255	AA012992	Hs.256301	Hs.256301:hypothetical protein MGC13170	2.53
	422509	AA258513	Hs.117865	Hs.117865:solute carrier family 17 (anio	2.53
	434866	AW002565	Hs.355460	Hs.355460:Homo sapiens cDNA: FLJ21763 fi	2.53
40	429743	AA804398	Hs.288995	(locuslink)NM_017951:Homo sapiens hypoth	2.53
	433047	M86135	Hs.279946	NM_004990:Homo sapiens methionine-tRNA s	2.53
	418945	BE246762	Hs.89499	Hs.89499:arachidonate 5-Epoxygenase	2.52
	445926	AF054284	Hs.334826	NM_012433:Homo sapiens splicing factor 3	2.52
	411353	BE383533	Hs.279784	Hs.279784:prolactin regulatory element b	2.52
45	448252	BE622791	Hs.12199	NM_030577:Homo sapiens hypothetical prot	2.52
	447365	BE383676	Hs.334	(locuslink)NM_005435:Homo sapiens Rho gu	2.52
	414844	AA296874	Hs.77494	NM_080916:Homo sapiens deoxyguanosine ki	2.52
	444025	AA578364	Hs.349093	NM_015945:Homo sapiens ovarian cancer ov	2.52
	416149	AA311965	Hs.79058	NM_003168:Homo sapiens suppressor of Ty	2.52
50	418741	H83265	Hs.8881	Hs.8881:Homo sapiens cDNA FLJ32163 fis	2.52
	437952	D63209	Hs.5944	NM_014585:Homo sapiens solute carrier fa	2.52
	445625	BE246743	Hs.353181	(locuslink)NM_025092:Homo sapiens hypoth	2.52
	431565	AF161470	Hs.260622	Hs.260622:butyrate-induced transcript 1	2.52
	410179	W27723	Hs.59498	(locuslink)NM_003718:Homo sapiens cell d	2.52
55	431476	BE612705	Hs.256697	(locuslink)NM_005340:Homo sapiens histid	2.52
	406672	M26041	Hs.198253	(locuslink)NM_002122:Homo sapiens major	2.52
	418180	BE618087	Hs.83724	Hs.83724:hypothetical protein MGC5466	2.52
	428248	A126772	Hs.40479	Hs.40479:Homo sapiens cDNA FLJ25802 fis,	2.52
	419935	AB020980	Hs.93832	Hs.93832:putative membrane protein	2.52
60	446143	BE245342	Hs.306079	NM_013336:Homo sapiens protein transport	2.52
	426691	NM_006201	Hs.171834	(locuslink)NM_006201:Homo sapiens PCTAIR	2.51
	408124	U89337	Hs.42853	NM_004381:Homo sapiens cAMP responsive e	2.51
	456266	L29073	Hs.198726	NM_003651:Homo sapiens cold shock domain	2.51
	428921	Z43809	Hs.194638	Hs.194638:polymerase (RNA) II (DNA direc	2.51
65	414721	X90392	Hs.77091	NM_006730:Homo sapiens deoxyribonuclease	2.51
	422607	Z45471	Hs.118684	NM_006923:Homo sapiens stromal cell-deri	2.51
	421846	AA017707	Hs.1432	NM_002743:Homo sapiens protein kinase C	2.51
	414874	D26351	Hs.77515	NM_002224:Homo sapiens inositol 1,4,5-tr	2.51
	432956	AL037895	Hs.279861	NM_015959:Homo sapiens CGI-31 protein (L	2.51
70	438393	AA351815	Hs.50740	Hs.50740:Homo sapiens mRNA; cDNA DKFZp76	2.51
	418360	AW296974	Hs.84264	NM_006401:Homo sapiens acidic (leucine-r	2.50
	401061				2.50
	426559	AB001914	Hs.170414	Hs.170414:paired basic amino acid cleavi	2.50
	412204	A125507	Hs.24937	Hs.24937:transformer-2 alpha (tra-2 alp	2.50
75	448950	AF288687	Hs.9275	NM_020410:Homo sapiens CGI-152 protein (2.50
	409936	AK001691	Hs.57655	(locuslink)NM_018234:Homo sapiens dudui	2.50
	414675	R79015	Hs.288958	Hs.288958:RAB22A, member RAS oncogene fa	2.50
	409983	D50922	Hs.57729	(locuslink)NM_012289:Homo sapiens Kelch-	2.50
	450914	A1743761	Hs.142528	Hs.142528:ESTs	2.50
80	444630	A1753230	Hs.323562	(locuslink)NM_032121:Homo sapiens hypoth	2.50
	401353				2.50
	441680	AW444598	Hs.7940	(locuslink)NM_021159:Homo sapiens RAP1,	2.50
	406860	AA876469		AA876469:oe48b04.s1 NCI_CGAP_Pr25 Homo s	2.50
	449163	AW161356	Hs.23119	NM_003492:Homo sapiens chromosome X open	2.50

432975	AA331517	Hs.286055	Hs.286055:chimera (chimera) 2	2.50
430600	AW950967	Hs.274348	NM_004639: Homo sapiens HLA-B associated	2.50
407584	W25945	Hs.8173	Hs.8173: hypothetical protein FLJ10803	2.50

5 TABLE 9B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

10	Pkey	CAT Number	Accession
	406685	0_0	M18728
	452098	161393_1	BG028348 BF772844 H83066 AW817969 H90985 BF755039 A1858183
	451129	1495511_1	BE072881 A1762181 BE072946
15	459306	223120_4	AW578452
	448489	2189115_1	R45782 R45781
	418869	12789_14	AA229762 AA230035
	418546	242836_1	T59708 AA224827 T59843 BE156903
20	455303	1152492_1	BE066891 BE066895 AW892049 BE066897 BE903884
	406860	0_0	AA876469

TABLE 9C

25 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

30	Pkey	Ref	Strand	NL_position
	406399	9256288	Minus	63448-63554
	403220	7630969	Plus	64338-64517
	403218	7630969	Plus	58039-58149
35	403221	7630969	Plus	66294-66438,66936-67124
	403219	7630969	Plus	61858-61995
	403739	7630882	Plus	44563-44766,48209-48483,52255-52495
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
40	405556	1552511	Plus	163497-163623,164715-164958,165389-16550
	400529	9796988	Plus	138232-138423
	404826	6572184	Plus	47726-48046
	400750	8119067	Plus	198991-199168,199316-199548
	400847	9188605	Plus	44643-44835
45	400448	9887687	Minus	177372-177674
	402829	8918414	Plus	101532-101852,102008-102263
	400846	9188605	Plus	39310-39474
	401179	9438647	Plus	113477-113893
	404240	5002624	Minus	116132-116407,116653-116922
50	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	406363	9256114	Plus	14403-14602,17000-17147,17241-17368
	405203	7230116	Plus	125295-125463
	402104	8119072	Plus	122409-122600
	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
55	400845	9188605	Plus	34428-34612
	403217	7630969	Plus	54089-54163,55427-55623
	403483	9966188	Minus	144546-144854
	400509	9796539	Minus	157909-158430
	403399	6684178	Plus	61841-62145,62367-62756
60	400541	7574902	Plus	126235-126380,126478-126597
	402861	2814366	Minus	14933-15231,15387-15627
	403955	7770475	Minus	54527-54740
	404854	7143420	Plus	14260-14537
	404140	9843520	Plus	37761-38147
65	401061	3242744	Minus	99468-99549,100707-100848,100918-101107,
	401353	9931296	Minus	50831-51352

70 Table 10A lists about 1,103 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium). These were selected from the starting collection of 59580 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 2.5, the "average" colon level was set to the 80th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 85th percentile value amongst non-malignant tissues minus the colonic derived samples, the "average" colon value was greater than or equal to 50 units. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the over non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

75 TABLE 10A: 1,103 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium)

80 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

	Pkey	ExAcon	UnigeneID	Unigene Title	R1
5	436749	AA584890	Hs.5302	NM_006149:Homo sapiens lectin, galactosi	15.54
	428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	14.52
	446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intestin	14.04
	431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S3B4_H	14.02
	423541	AA286922	Hs.129778	NM_014471:Homo sapiens serine protease i	13.72
10	406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carcin	13.44
	418406	X73501	Hs.84905	Hs.84905:cytokeratin 20	12.70
	406667	M12523			12.42
	416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating isla	11.98
	437935	AW939591	Hs.5940	NM_033049:Homo sapiens mucin 13, epithel	11.58
15	422578	AF239566	Hs.1545	NM_001804:Homo sapiens caudal type homeo	11.50
	418898	AU076801	Hs.89436	NM_004053:Homo sapiens cadherin 17, Ll c	10.16
	418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.11
	422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	10.01
	421582	AI910275	Hs.350470	NM_003225:Homo sapiens trefol factor 1	9.77
20	441031	AI110584	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	9.69
	424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	9.48
	453863	X02544	Hs.572	Hs.572:corosomucoid 1	9.20
	407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	9.18
	436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	9.04
25	423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	8.69
	430178	AW449612	Hs.152475	Hs.152475:ESTs	8.51
	423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	8.43
	447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	8.17
	409683	U33317	Hs.711	NM_001926:Homo sapiens defensin, alpha 6	8.12
30	431777	AA570296	Hs.307047	NM_032579:Homo sapiens colon and small i	8.08
	450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	8.06
	427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (7.95
	436624	T64297	Hs.351719	NM_001443:Homo sapiens fatty acid bindin	7.74
	410407	X66839	Hs.63287	NM_001216:Homo sapiens carbonic anhydras	7.46
35	413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	7.41
	407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	7.40
	412374	X01388	Hs.73849	NM_000040:Homo sapiens apolipoprotein C-	7.34
	407244	M10014			7.31
	419741	NM_007019	Hs.93002	Hs.93002:ubiquitin-conjugating enzyme E2	7.31
40	405741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	7.26
	414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	7.21
	404519				7.18
	413585	AI133452	Hs.75431	NM_000509:Homo sapiens fibrinogen, gamma	7.13
	422281	M36803	Hs.346335	NM_000613:Homo sapiens hemopexin (HPX),	7.10
45	414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	7.02
	430828	AI763257	Hs.86327	Hs.86327:homeo box B9	6.83
	433927	AI557019	Hs.116467	NM_032391:Homo sapiens small nuclear pro	6.81
	406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	6.78
	423538	AW603823	Hs.146268	Hs.146268:ESTs, Weakly similar to C71400	6.53
50	434206	AW136973	Hs.362915	Hs.362915:Homo sapiens cDNA FLJ34876 fis	6.37
	409041	AB033025	Hs.50081	Hs.50081:KIAA1199 protein	6.33
	432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	6.19
	422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	6.19
	436330	NM_004413	Hs.109	NM_004413:Homo sapiens dipeptidase 1 (re	6.01
55	421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	6.00
	430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	5.97
	413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	5.94
	420923	AF097021	Hs.273321	NM_006418:Homo sapiens differentially ex	5.94
	428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homol	5.90
60	420802	U22376	Hs.1334	NM_005375:Homo sapiens v-myb myeloblasto	5.89
	452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10690	5.89
	431727	AW293464	Hs.162031	Hs.162031:ESTs	5.85
	421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	5.84
	432023	AW273128	Hs.300268	Hs.300268:EST	5.75
65	447033	AI357412	Hs.157601	Hs.157601:ESTs	5.69
	411734	AW374954	Hs.71779	Hs.71779:ESTs, Weakly similar to S24C_AR	5.69
	406685	M18728		(locuslink)NM_002483:Homo sapiens carcin	5.55
	428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	5.48
	443247	BE614387	Hs.333893	Hs.333893:cell division cycle associated	5.45
70	409153	W03754	Hs.50813	NM_017625:Homo sapiens intelectin (ITLN)	5.44
	449388	H53191	Hs.36723	Hs.36723:ESTs, Weakly similar to C05G5.5	5.38
	428046	AW812795	Hs.337534	Hs.337534:Homo sapiens cDNA FLJ25241 fis	5.38
	433013	AI697890	Hs.127337	(locuslink)NM_004655:Homo sapiens axn 2	5.38
	419079	AW014839	Hs.18844	Hs.18844:ESTs	5.37
75	428355	BE256452	Hs.22257	NM_000638:Homo sapiens vitronectin (seru	5.35
	422956	BE545072	Hs.122579	(locuslink)NM_018098:Homo sapiens epithe	5.34
	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysi	5.30
	450543	AI394037	Hs.170296	Hs.170296:Homo sapiens cDNA: FLJ22090 fi	5.30
	428187	AI687303	Hs.285529	Hs.285529:G protein-coupled receptor 49	5.30
80	435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	5.28
	411825	AK000334	Hs.352415	NM_017677:Homo sapiens solute carrier fa	5.28
	427722	AK000123	Hs.180479	NM_017671:Homo sapiens chromosome 20 ope	5.26
	430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	5.26
	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	5.21
	430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	5.16

5	447208	BE315291	Hs.237971	NM_024096:Homo sapiens hypothetical prot	5.14
	430207	AW079559	Hs.152258	Hs.152258:ESTs	5.12
	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	5.12
	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.07
	447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RUKEN	5.06
10	452194	AI694413	Hs.373599	Hs.373599:EST	5.01
	421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	4.99
	406399				4.98
	403220				4.94
	408380	AF123050	Hs.44532	NM_006398:Homo sapiens ubiquitin D (UBD)	4.92
15	415214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPH82), tr	4.92
	431330	X89532	Hs.2777	NM_002215:Homo sapiens Inter-alpha (glob	4.85
	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protei	4.84
	452594	AIJ076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfa	4.81
	441377	BE218239	Hs.202656	Hs.202656:ESTs	4.81
20	444566	BE293347	Hs.11638	(locuslink)NM_016234:Homo sapiens fatty-	4.80
	415701	NM_003878	Hs.78619	(locuslink)NM_003878:Homo sapiens gamma-	4.80
	419354	M62839	Hs.1252	NM_000042:Homo sapiens apolipoprotein H	4.80
	455630	AV655701	Hs.75183	NM_000773:Homo sapiens cytochrome P450,	4.78
	422310	AA316622	Hs.98370	(locuslink)NM_030622:Homo sapiens cytoch	4.78
25	423337	NM_004655	Hs.127337	NM_004655:Homo sapiens adn 2 (conductin	4.75
	422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	4.73
	408908	BE296227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	4.70
	423936	U77629	Hs.135639	NM_005170:Homo sapiens achaete-scute com	4.70
	404661				4.68
30	408704	AA056635	Hs.5366	NM_139053:Homo sapiens epidermal growth	4.67
	420005	AW271106	Hs.133294	Hs.133294:ESTs	4.66
	451035	AU076785	Hs.430	NM_002670:Homo sapiens plasmin 1 (I) iso	4.61
	427506	AK000134	Hs.179100	NM_017678:Homo sapiens hypothetical prot	4.60
	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	4.59
35	453884	AA355925	Hs.36232	NM_021067:Homo sapiens KIAA0186 gene pro	4.55
	431301	AA502384	Hs.151529	Hs.151529:ESTs	4.54
	408983	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	4.54
	449032	AA045573	Hs.22900	NM_004289:Homo sapiens nuclear factor (e	4.54
	434540	NM_016045	Hs.3945	NM_016045:Homo sapiens chromosome 20 ope	4.54
40	407242	M18728		(locuslink)NM_002483:Homo sapiens carcin	4.53
	458748	AI381530	Hs.371132	Hs.371132:ESTs	4.53
	408298	AI745325	Hs.271923	Hs.271923:Homo sapiens cDNA: FLJ22785 fi	4.51
	424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	4.50
	411975	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	4.49
45	425371	D49441	Hs.155981	NM_005823:Homo sapiens mesothelin (MSLN)	4.49
	451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	4.46
	432867	AW016936	Hs.233364	Hs.233364:ESTs	4.44
	419559	Y07828	Hs.91096	NM_007028:Homo sapiens tripartite motif-	4.44
	430294	AI538226	Hs.32976	(locuslink)NM_004485:Homo sapiens guanin	4.42
50	411248	AA551538	Hs.69321	Hs.69321:KIAA1359 protein	4.39
	402496				4.38
	430937	X53463	Hs.2704	NM_002083:Homo sapiens glutathione perox	4.37
	434414	AI798376		AF134163:Homo sapiens Human endogenous r	4.36
	443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	4.35
55	422539	AJ009938	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.33
	436972	AA284679	Hs.25640	Hs.25640:claudin 3	4.33
	450531	AW301032	Hs.203800	Hs.203800:ESTs	4.33
	403055				4.31
	414809	AI434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	4.31
60	400965				4.30
	430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	4.29
	432978	AF126743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-conta	4.29
	417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:22588 I	4.28
	430832	AI073913	Hs.100686	Hs.100686:anterior gradient protein 3	4.28
65	409482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	4.28
	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	4.27
	414617	AI339520	Hs.288817	(locuslink)NM_025130:Homo sapiens hypoth	4.27
	452940	AA029722	Hs.2173	NM_002033:Homo sapiens fucosyltransferas	4.27
	439211	AI890347	Hs.271923	Hs.271923:Homo sapiens cDNA: FLJ22785 fi	4.27
70	459299	BE094291	Hs.155651	NM_021784:Homo sapiens hepatocyte nuclea	4.25
	449720	AA311152	Hs.288708	(locuslink)NM_025113:Homo sapiens hypoth	4.24
	411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc:betaGa	4.24
	421777	BE562088	Hs.108195	NM_016095:Homo sapiens HSPC037 protein (4.21
	419395	BE268326	Hs.90280	Hs.90280:5-aminimidazole-4-carboxamide	4.20
75	443211	AI128388	Hs.143655	Hs.143655:ESTs	4.20
	403218				4.20
	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	4.19
	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	4.19
	426227	U67058	Hs.154299	(locuslink)NM_005242:Homo sapiens coagul	4.19
80	421408	AI688223	Hs.91096	NM_052816:Homo sapiens tripartite motif-	4.18
	421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	4.18
	440869	NM_014297	Hs.7486	NM_014297:Homo sapiens protein expressed	4.17
	414075	U11862	Hs.75741	NM_001091:Homo sapiens amiloride binding	4.17
	444151	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-	4.16
	440409	AW294316	Hs.125608	Hs.125608:ESTs	4.16
	445564	AB028957	Hs.12896	Hs.12896:KIAA1034 protein	4.16
	424687	JO5070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	4.12

	401866				4.11
	431611	U58766	Hs.264428	Hs.264428:tissue specific transplanta	4.10
	430187	AJ799909	Hs.158989	Hs.158989:Homo sapiens cDNA FLJ37936 fis	4.10
5	414590	NM_000506	Hs.76530	NM_000505:Homo sapiens coagulation facto	4.08
	449281	AJ808699	Hs.162717	NM_032756:Homo sapiens hypothetical prot	4.08
	449722	BE280074	Hs.23960	Hs.23960:cyclin B1	4.08
	418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	4.06
	435066	BE261750	Hs.4747	NM_001363:Homo sapiens dyskeratosis cong	4.05
10	414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	4.04
	403221				4.04
	409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	4.03
	449027	AJ271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	4.03
	431657	AJ345227	Hs.105448	Hs.105448:protein kinase, lysine defic	4.01
15	439759	AL359055	Hs.67709	Hs.67709:Homo sapiens mRNA full length l	4.00
	441362	BE614410	Hs.23044	NM_080668:Homo sapiens similar to RIKEN	3.99
	417900	BE250127	Hs.82906	Hs.82906:CD20 cell division cycle 20 ho	3.99
	428987	NM_004751	Hs.194710	NM_004751:Homo sapiens glucosaminyl (N-a	3.99
	456977	AK000252	Hs.169758	NM_017723:Homo sapiens hypothetical prot	3.99
20	445919	T53519	Hs.334692	Hs.334692:hypothetical protein MGC14141	3.98
	423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	3.98
	422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	3.97
	422363	T55979	Hs.115474	NM_002915:Homo sapiens replication facto	3.97
	433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	3.97
25	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	3.96
	425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	3.96
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	3.95
	432407	AA221036		AF134164:Homo sapiens Human endogenous r	3.95
	408243	Y00787	Hs.524	NM_000584:Homo sapiens interleukin 8 (IL	3.94
30	408494	AA554714	Hs.187578	Hs.187578:Homo sapiens cDNA FLJ11639 fis	3.94
	412610	X90908	Hs.74126	NM_001445:Homo sapiens fatty acid bindin	3.94
	433323	AA805132	Hs.159142	Hs.159142:unatic fringe homolog (Drosop	3.94
	422515	AW500470	Hs.117950	Hs.117950:phosphoribosylaminimidazole c	3.92
	436543	NM_002212	Hs.5215	Hs.5215:integrin beta 4 binding protein	3.91
35	418113	AJ272141	Hs.83484	Hs.83484:SRY (sex determining region Y)-	3.91
	433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	3.90
	431939	AW008061	Hs.231994	Hs.231994:Homo sapiens, clone IMAGE:4341	3.90
	453439	AJ572438	Hs.32976	NM_004485:Homo sapiens guanine nucleotid	3.89
	441888	AJ733306	Hs.128071	NM_022901:Homo sapiens hypothetical prot	3.89
40	432150	AK000224	Hs.272789	NM_017716:Homo sapiens membrane-spanning	3.89
	425234	AW152225	Hs.165909	Hs.165909:ESTs, Weakly similar to hypoth	3.89
	423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	3.87
	410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	3.85
	436251	BE515065	Hs.296585	(locuslink)NM_006392:Homo sapiens nucleo	3.85
45	422424	AI186431	Hs.296638	Hs.296638:prostate differentiation facto	3.84
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	3.84
	424905	NM_002497	Hs.153704	NM_002497:Homo sapiens NIMA (never in mi	3.84
	416209	AA236776	Hs.79078	NM_002358:Homo sapiens MAD2 mitotic arre	3.83
	430680	AW138724	Hs.168974	Hs.168974:ESTs	3.83
50	434370	AF130988	Hs.58346	NM_022336:Homo sapiens ectodysplasin 1,	3.82
	436481	AA379597	Hs.5199	NM_014176:Homo sapiens HSPC150 protein s	3.82
	453700	AB009426	Hs.5560	NM_001644:Homo sapiens apolipoprotein B	3.81
	410619	BE512730	Hs.65114	Hs.65114:keratin 18	3.81
	409420	Z15008	Hs.54451	NM_005562:Homo sapiens laminin, gamma 2	3.79
55	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	3.79
	432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPH3), mR	3.78
	453957	AW009077	Hs.232947	Hs.232947:ESTs	3.78
	426108	AI678765	Hs.21812	Hs.21812:ESTs	3.78
	434170	AA626509	Hs.159542	(locuslink)NM_001490:Homo sapiens glucos	3.78
60	418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	3.78
	444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	3.74
	419229	AI872737	Hs.362919	Hs.362919:ESTs	3.74
	437158	AI916600	Hs.121194	Hs.121194:Homo sapiens cDNA: FLJ21569 fi	3.74
	452833	BE556681	Hs.30736	(locuslink)NM_015201:Homo sapiens block	3.73
65	426831	BE295216	Hs.172673	NM_000687:Homo sapiens S-adenosylthiomocys	3.73
	428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid ind	3.72
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading tra	3.71
	408832	AW085690	Hs.63428	Hs.63428:Homo sapiens cDNA FLJ34457 fis,	3.71
	440300	N39760	Hs.8859	NM_138793:Homo sapiens apyrase (SHAPY),	3.71
70	425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	3.71
	432575	AA553722	Hs.194346	Hs.194346:Spir-2 protein	3.71
	412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	3.71
	417001	AU076648	Hs.80741	NM_000282:Homo sapiens propionyl Coenzym	3.69
	421225	AA463798	Hs.102696	Hs.102696:MCT-1 protein	3.69
75	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectonucleoside tr	3.69
	428330	L22524	Hs.12256	NM_002423:Homo sapiens matrix metallopro	3.67
	447472	AW207347	Hs.211101	Hs.211101:ESTs	3.67
	423349	AF010258	Hs.127428	NM_002142:Homo sapiens homeo box A9 (HOX	3.67
	422026	U80736	Hs.110826	Hs.110826:trinucleotide repeat containin	3.66
80	419574	AK001989	Hs.91165	Hs.91165:hypothetical protein FLJ11127	3.66
	417720	AA205625	Hs.208067	Hs.208067:ESTs	3.66
	411257	AA628957	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	3.66
	421515	Y11339	Hs.105352	(locuslink)NM_018414:Homo sapiens GalNAc	3.65
	433675	AW977653	Hs.75319	Hs.75319:ribonucleotide reductase M2 pol	3.65

5	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	3.65
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis,	3.64
	412140	AA219891	Hs.73625	NM_005733:Homo sapiens RAB6 interacting,	3.64
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	3.63
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	3.63
	414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	3.62
	428862	NM_000346	Hs.2316	Hs.2316:SRF (sex determining region Y)-b	3.62
	414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	3.62
10	412056	T28160	Hs.778	Hs.778:guanylate cyclase activator 2A (g	3.61
	401519				3.60
	428011	BE387514	Hs.181418	NM_014730:Homo sapiens KIAA0152 gene pro	3.60
	450505	NM_004572	Hs.25051	NM_004572:Homo sapiens plakophilin 2 (PK	3.60
	421903	AW079940	Hs.15951	(locuslink)NM_145202:Homo sapiens prol	3.58
15	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystei	3.58
	424544	M88700	Hs.150403	NM_000790:Homo sapiens dopa decarboxylas	3.58
	431563	AI027643	Hs.120912	Hs.120912:ESTs	3.57
	435602	AF217515	Hs.283532	NM_018455:Homo sapiens uncharacterized b	3.57
	434369	AI650363	Hs.116462	Hs.116462:ESTs	3.57
20	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acety	3.56
	447334	AA515032	Hs.91109	Hs.91109:ESTs, Weakly similar to putativ	3.56
	422150	AI867118	Hs.279607	Hs.279607:Homo sapiens cDNA FLJ34399 fis	3.56
	450663	H43540	Hs.25292	Hs.25292:ribonuclease H2, large subunit	3.56
	428225	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	3.56
25	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	3.55
	422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	3.55
	422532	AL008726	Hs.118126	(locuslink)NM_000308:Homo sapiens protec	3.55
	425860	L29339	Hs.1964	NM_000343:Homo sapiens solute carrier fa	3.55
	442053	R35343	Hs.24968	Hs.24968:hypothetical protein BC016683	3.55
30	437386	W52452	Hs.356766	Hs.356766:Homo sapiens mRNA; cDNA DKFZp7	3.54
	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	3.53
	446372	AB020644	Hs.14945	Hs.14945:fatty-acid-Coenzyme A ligase, I	3.53
	432378	AI93046	Hs.146133	Hs.146133:ESTs	3.53
	434171	BE247688	Hs.347349	(locuslink)NM_004749:Homo sapiens cell c	3.52
35	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	3.52
	415099	AI492170	Hs.77917	NM_005002:Homo sapiens ubiquitin carboxy	3.51
	414918	AI219207	Hs.72222	Hs.72222:fer-1-like 4 (C. elegans)	3.51
	440340	AW895503	Hs.125276	Hs.125276:Homo sapiens cDNA FLJ25833 fis	3.51
	418384	AW149266	Hs.25130	Hs.25130:Homo sapiens cDNA FLJ14923 fis,	3.51
40	418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kin	3.51
	425833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	3.51
	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	3.50
	431567	N51357	Hs.260855	(locuslink)NM_145175:Homo sapiens NSE1 (3.50
	453883	AI638516	Hs.347524	Hs.347524:Homo sapiens, clone MGC24665	3.50
45	442700	AA377618	Hs.103834	NM_024056:Homo sapiens hypothetical prot	3.50
	410237	AI750589	Hs.61258	Hs.61258:argininosuccinate lyase	3.50
	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	3.49
	436213	AA325512	Hs.71472	NM_024662:Homo sapiens hypothetical prot	3.49
	442923	AW248322	Hs.95835		3.49
50	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	3.48
	452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	3.48
	448993	AI471630	Hs.355952	Hs.355952:ESTs, Weakly similar to 090320	3.48
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC23656	3.48
	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	3.47
55	420996	AK001927	Hs.100895	(locuslink)NM_018099:Homo sapiens hypoh	3.47
	439580	AF086401	Hs.293847	Hs.293847:ESTs	3.46
	422158	L10343	Hs.112341	NM_002638:Homo sapiens protease inhibito	3.46
	418256	AW845318	Hs.12271	(locuslink)NM_012162:Homo sapiens F-box	3.46
	400157		Hs.356473	NM_006713:Homo sapiens activated RNA pol	3.46
60	406709	AI355761	Hs.242463	Hs.242463:keratin 8	3.46
	453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.46
	421526	AL080121	Hs.105460	NM_015393:Homo sapiens DKFZP564O0823 pro	3.45
	415164	AW084352	Hs.157123	Hs.157123:ESTs	3.45
	405451				3.44
65	414361	AI086138	Hs.204044	Hs.204044:ESTs	3.44
	422237	M13149	Hs.1498	NM_000412:Homo sapiens histidine-rich gl	3.44
	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	3.44
	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25-dihydroxyvitami	3.43
	450983	AA305384	Hs.25740	NM_014584:Homo sapiens ERO1-like (S. cer	3.43
70	421828	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE/4701	3.42
	418588	BE397040	Hs.182476	NM_031295:Homo sapiens Williams Beuren s	3.42
	417348	AI940507	Hs.318526	NM_025138:Homo sapiens hypothetical prot	3.42
	423554	M90516	Hs.1674	NM_002056:Homo sapiens glutamine-fructos	3.42
	451310	AW250651	Hs.26213	NM_052951:Homo sapiens chromosome 20 ope	3.41
75	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	3.41
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	3.40
	437575	AW954355	Hs.36529	NM_024320:Homo sapiens hypothetical prot	3.40
	432677	NM_004482	Hs.278611	NM_004482:Homo sapiens UDP-N-acetyl-alph	3.40
	439955	AW203959	Hs.149532	Hs.149532:ESTs	3.40
80	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interne	3.40
	435745	AW967059	Hs.374342	Hs.374342:Homo sapiens clone 24711 mRNA	3.40
	403532				3.39
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	3.39
	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	3.39

	424996	AF006005	Hs.154104	NM_002657:Homo sapiens pleiomorphic aden	3.38
	402944				3.37
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	3.37
5	427528	AU077143	Hs.179565	NM_002388:Homo sapiens MCM3 minichromoso	3.37
	426711	AA383471	Hs.343800	(locuslink)NM_033255:Homo sapiens epitha	3.37
	439186	AI697274	Hs.105435	Hs.105435:GDP-mannose 4,6-dehydratase	3.36
	444763	AK001468	Hs.62180	NM_018685:Homo sapiens anillin, actin bi	3.36
	426174	AA547959	Hs.115838	Hs.115838:ESTs	3.36
10	421585	U95626	Hs.302043	NM_003965:Homo sapiens chemokine (C-C mo	3.36
	421605	BE440108	Hs.106127	NM_015972:Homo sapiens RNA polymerase I	3.36
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	3.36
	438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	3.36
	403219				3.36
15	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome profil	3.34
	456946	T29678	Hs.166068	Hs.166068:villin 1	3.33
	425580	L11144	Hs.1907	Hs.1907:galanin	3.33
	412605	AW410734	Hs.74111	Hs.74111:RNA binding protein (autoantige	3.33
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	3.33
20	416782	L35035	Hs.79886	(locuslink)NM_144563:Homo sapiens ribose	3.33
	426761	AI015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	3.33
	441633	AW958544	Hs.112242	NM_032413:Homo sapiens normal mucosa of	3.32
	416975	NM_004131	Hs.1051	NM_004131:Homo sapiens granzyme B (granz	3.31
	428874	W32133	Hs.194366	Hs.194366:transferrin (prealbumin, amy	3.31
25	431192	AI670056	Hs.137274	Hs.137274:ESTs, Weakly similar to hypoth	3.30
	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP-cle	3.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	3.30
	410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H	3.29
	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	3.29
30	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	3.29
	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	3.29
	437810	BE246399	Hs.367646	NM_016617:Homo sapiens hypothetical prot	3.29
	403381				3.28
	434031	BE384165	Hs.23723	(locuslink)NM_025215:Homo sapiens pseudo	3.28
35	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	3.28
	452299	AW206330	Hs.355663	Hs.355663:ESTs	3.28
	428024	Z29067	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	3.28
	412994	D32257	Hs.75113	Hs.75113:general transcription factor II	3.28
	443162	T49951	Hs.9029	(locuslink)NM_015515:Homo sapiens type I	3.28
40	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3)-glycoprote	3.28
	424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	3.28
	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	3.27
	419359	AL043202	Hs.90073	Hs.90073:CSE1 chromosome segregation 1-4	3.27
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	3.27
	444371	BE540274	Hs.239	Hs.239:forkhead box M1	3.27
45	450221	AA328102	Hs.24641	NM_018204:Homo sapiens cytoskeleton asso	3.27
	449207	AL044222	Hs.23255	NM_004298:Homo sapiens nucleoporin 155kD	3.27
	422609	Z46023	Hs.118721	NM_000434:Homo sapiens stathase 1 (tyso	3.27
	403485				3.27
50	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	3.26
	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	3.26
	405484				3.26
	435849	BE305242	Hs.16098	Hs.16098:claudin 2	3.26
	449139	BE268315	Hs.23111	NM_004461:Homo sapiens phenylalanine-TRN	3.26
	404684				3.25
55	447188	H65423	Hs.17631	NM_030804:Homo sapiens hypothetical prot	3.25
	423226	AA323414	Hs.146109	Hs.146109:ESTs, Weakly similar to T28937	3.24
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	3.24
	424243	AI949359	Hs.143600	Hs.143600:golgi phosphoprotein 4	3.24
60	435014	BE560898	Hs.10026	NM_022061:Homo sapiens ribosomal protein	3.24
	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fis	3.24
	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	3.23
	427333	AF067797	Hs.176558	NM_001169:Homo sapiens aquaporin 8 (AQP8	3.23
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	3.23
65	432035	AA524725	Hs.162108	Hs.162108:ESTs	3.23
	408868	AW292286	Hs.255058	Hs.255058:ESTs	3.23
	429504	X99133	Hs.204238	Hs.204238:fipocatin 2 (oncogene 24p3)	3.22
	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	3.22
	426991	AK001536	Hs.214410	Hs.214410:Homo sapiens cDNA FLJ31573 fis	3.22
70	408901	AK001330	Hs.48855	(locuslink)NM_018101:Homo sapiens hypoth	3.22
	439979	AW600291	Hs.6823	NM_018092:Homo sapiens neuropilin (NRP)	3.22
	453968	AA847843	Hs.62711	Hs.62711:Homo sapiens, clone IMAGE:33512	3.22
	457465	AW301344	Hs.122908	NM_030928:Homo sapiens DNA replication f	3.22
	426317	AA312350	Hs.169294	NM_003202:Homo sapiens transcription fac	3.21
	414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	3.21
75	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	3.20
	444261	AA298958	Hs.10724	Hs.10724:mitochondrial ribosomal protein	3.20
	454033	AF107457	Hs.37035	NM_005515:Homo sapiens homeo box HB9 (HL	3.20
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	3.20
80	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	3.20
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	3.19
	400130		Hs.155560	NM_001746:Homo sapiens calnexin (CANX),	3.19
	422293	X94453	Hs.114366	Hs.114366:pyrroline-5-carboxylate synth	3.19
	400290	H18836	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	3.18

5	419239	AA468183	Hs.335798	(locustink)NM_033103:Homo sapiens rhophi	3.18
	426215	AW963419	Hs.155223	NM_003714:Homo sapiens slanniocalcin 2 (3.18
	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	3.17
	413313	NM_002047	Hs.293885	NM_002047:Homo sapiens glycyl-tRNA synth	3.17
	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	3.17
	408353	BE439838	Hs.44298	NM_015969:Homo sapiens mitochondrial rib	3.17
	400203		Hs.1390	NM_002794:Homo sapiens proteasome (proso	3.16
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	3.16
10	426088	AF038007	Hs.166196	NM_005603:Homo sapiens ATPase, Class I,	3.16
	416984	H38765	Hs.80706	NM_000903:Homo sapiens NAD(P)H dehydroge	3.16
	450635	AW403954	Hs.25237	NM_016647:Homo sapiens mesenchymal stem	3.16
	406708	AI282759		AI282759:qt84a01.x1 NCL_CGAP_Co14 Homo s	3.16
	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EFNB2)	3.16
	430127	AA219498	Hs.233952	Hs.233952:proteasome (prosome, macropain	3.16
15	417308	H60720	Hs.81892	NM_014736:Homo sapiens KIAA0101 gene pro	3.15
	408116	AA251393	Hs.289052	NM_052842:Homo sapiens BCL2-like 12 (pro	3.15
	402474				3.15
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	3.15
20	446595	T57448	Hs.15467	NM_017943:Homo sapiens hypothetical prot	3.15
	444954	AW247076	Hs.12163	NM_003908:Homo sapiens eukaryotic transl	3.15
	434263	N34895	Hs.79187	Hs.79187:cox sackie virus and adenovirus	3.15
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	3.15
	430696	AA531276	Hs.69509	Hs.69509:ESTs, Weakly similar to similar	3.15
	436391	AJ227892	Hs.146274	Hs.146274:ESTs	3.15
25	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	3.14
	445873	AA250970	Hs.251946	Hs.251946:Homo sapiens cDNA FLJ11840 fis	3.14
	432370	AA308334	Hs.274424	NM_018946:Homo sapiens N-acetylnearumini	3.14
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte anti	3.14
	417791	AW965339	Hs.44269	Hs.44269:Homo sapiens cDNA FLJ37972 fis,	3.14
30	417115	AW952792	Hs.334612	NM_003094:Homo sapiens small nuclear rib	3.13
	411126	NM_001202	Hs.68879	(locustink)NM_001202:Homo sapiens bone m	3.13
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	3.13
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomutas	3.13
35	408056	AA312329	Hs.42331	Hs.42331:ephrin-A4	3.13
	446386	AI032108	Hs.54424	Hs.54424:hepatocyte nuclear factor 4, al	3.12
	407804	AF228603	Hs.39957	NM_016445:Homo sapiens pleckstrin 2 (mou	3.12
	412723	AA648459	Hs.335951	Hs.335951:hypothetical protein AF301222	3.12
	407233	X16354	Hs.50984	(locustink)NM_001712:Homo sapiens carcin	3.11
40	407168	R45175	Hs.117183	Hs.117183:Homo sapiens mRNA: cDNA DKFZp5	3.11
	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	3.11
	426427	MB6699	Hs.169840	Hs.169840:TTK protein kinase	3.11
	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	3.10
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (3.10
45	434861	AA206153	Hs.4209	NM_016491:Homo sapiens mitochondrial rib	3.10
	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	3.10
	414805	D14694	Hs.77329	(locustink)NM_014754:Homo sapiens phosph	3.09
	454464	AW811606	Hs.271819	Hs.271819:mucin 17	3.09
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	3.09
50	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	3.09
	421470	R27496	Hs.1378	NM_005139:Homo sapiens annexin A3 (ANXA3	3.09
	419551	AW582256	Hs.91011	NM_006408:Homo sapiens anterior gradient	3.09
	418691	AW752389	Hs.87296	Hs.87296:Homo sapiens cDNA FLJ20269 fis,	3.08
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	3.08
55	447760	AI431328	Hs.348605	NM_052963:Homo sapiens mitochondrial top	3.08
	405506				3.08
	429957	AW204530	Hs.99500	Hs.99500:ESTs	3.08
	410166	AK001376	Hs.59346	NM_018122:Homo sapiens hypothetical prot	3.08
60	422880	AF228704	Hs.193974	Hs.193974:glutathione reductase	3.08
	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA: cDNA DKFZp6	3.08
	431722	AF161528	Hs.268049	(locustink)NM_016101:Homo sapiens hypoth	3.08
	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	3.08
	433659	AK001301	Hs.3487	NM_018093:Homo sapiens hypothetical prot	3.07
	439492	AF086310	Hs.103159	Hs.103159:ESTs, Weakly similar to T06291	3.07
65	417865	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	3.07
	412530	AA766268	Hs.266273	(locustink)NM_024918:Homo sapiens chromo	3.07
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	3.06
	453132	AW961952	Hs.293724	Hs.293724:Homo sapiens cDNA FLJ12683 fis	3.06
	424971	AA479005	Hs.154036	NM_003311:Homo sapiens tumor suppressing	3.06
70	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	3.05
	439273	AW139099	Hs.367692	Hs.367692:Homo sapiens cDNA FLJ25668 fis	3.05
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	3.05
	435703	AW630133	Hs.83313	(locustink)NM_020192:Homo sapiens GK003	3.05
	407289	AA135159	Hs.203349	Hs.203349:Homo sapiens cDNA FLJ12149 fis	3.04
	403739				3.04
75	444664	N26362	Hs.11615	NM_016086:Homo sapiens map kinase phosph	3.04
	409152	AA176585	Hs.194346	Hs.194346:Spr-2 protein	3.04
	409093	BE243834	Hs.50441	NM_015938:Homo sapiens CGI-04 protein (L	3.04
	406545				3.03
80	450553	AW850613	Hs.8715	Hs.8715:hypothetical protein MGC3232	3.03
	418867	D31771	Hs.89404	NM_002449:Homo sapiens msh homeo box hom	3.03
	422976	AU076657	Hs.1600	Hs.1600:chaperonin containing TCP1, subu	3.03
	434523	AA703709	Hs.23410	(locustink)NM_016539:Homo sapiens sirtui	3.03
	440088	BE559877	Hs.183232	NM_024839:Homo sapiens hypothetical prot	3.02

5	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	3.02
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	3.02
	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	3.02
	422283	AW411307	Hs.114311	NM_003504:Homo sapiens CDC45 cell divisi	3.02
	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	3.02
10	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase t	3.02
	417975	AA641836	Hs.30085	NM_024616:Homo sapiens hypothetical prot	3.02
	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.01
	436561	BE560135	Hs.5232	NM_014165:Homo sapiens HSPC125 protein (3.01
	426031	AA295251	Hs.166066	(locuslink)NM_006697:Homo sapiens dspla	3.01
15	417678	X06560	Hs.82395	(locuslink)NM_002534:Homo sapiens 2',5-	3.01
	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec61 alpha form	3.00
	429983	W92620	Hs.260855	(locuslink)NM_145175:Homo sapiens NSE1 (3.00
	417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	3.00
	414732	AW410976	Hs.77152	Hs.77152:MCM7 minichromosome maintenance	3.00
20	409614	BE297412	Hs.55189	NM_016489:Homo sapiens 5'-nucleotidase,	3.00
	439053	BE244588	Hs.6456	Hs.6456:chaperonin containing TCP1, subu	3.00
	411096	U80034	Hs.68583	NM_005932:Homo sapiens mitochondrial int	2.99
	433312	AI241331	Hs.131765	Hs.131765:ESTs, Moderately similar to l3	2.99
	420767	AF072711	Hs.99918	Hs.99918:carboxyl ester lipase (bile sal	2.99
25	429523	AK000788	Hs.205280	Hs.205280:Homo sapiens cDNA FLJ20781 fis	2.99
	423242	AL039402	Hs.125783	Hs.125783:chromosome 1 open reading fram	2.99
	420552	AK000492	Hs.98806	Hs.98806:hypothetical protein FLJ20485	2.99
	413380	AI904232	Hs.75323	Hs.75323:prohibitin	2.99
	421533	N71826	Hs.105465	NM_003095:Homo sapiens small nuclear rib	2.99
30	439352	BE614347	Hs.169615	NM_023080:Homo sapiens hypothetical prot	2.98
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23602 fi	2.98
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	2.98
	457211	AW972565	Hs.323399	(locuslink)NM_145240:Homo sapiens simila	2.98
	410467	AF102546	Hs.63931	NM_080759:Homo sapiens dachshund homolog	2.97
35	422066	AW249275	Hs.343521	Hs.343521:malate dehydrogenase 2, NAD (m	2.97
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	2.97
	453012	T95804	Hs.31334	NM_012469:Homo sapiens chromosome 20 ope	2.97
	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	2.97
	413813	M96956	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	2.97
40	418362	AL031714	Hs.84285	NM_003345:Homo sapiens ubiquitin-conjuga	2.97
	431350	AI192528	Hs.164537	Hs.164537:ESTs	2.96
	417911	AA333387	Hs.82916	Hs.82916:chaperonin containing TCP1, sub	2.96
	413597	AW302885	Hs.117183	Hs.117183:Homo sapiens mRNA; cDNA DKFZp5	2.96
	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (2.96
45	445462	AA378776	Hs.288649	(locuslink)NM_024051:Homo sapiens hypoth	2.96
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	2.96
	408194	AA601038	Hs.191797	Hs.191797:ESTs	2.96
	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	2.96
	458306	AW578452		AW578452:RC1-CT0252-030100-023-b07 CT025	2.96
50	425209	AL049761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	2.96
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	2.95
	408683	R56665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	2.95
	432843	BE250865	Hs.279529	NM_013237:Homo sapiens p19-like protein	2.95
	406684	X16354	Hs.50984	(locuslink)NM_001712:Homo sapiens carcin	2.95
55	410006	AW732308	Hs.57783	NM_003751:Homo sapiens eukaryotic transl	2.94
	442577	AA292998	Hs.163900	Hs.163900:ESTs, Highly similar to winged	2.94
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	2.94
	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	2.94
	427779	AA906997	Hs.180780	NM_021238:Homo sapiens TERA protein (TER	2.94
60	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	2.94
	414549	BE393069	Hs.183506	NM_024841:Homo sapiens hypothetical prot	2.93
	410817	AI262789	Hs.93659	(locuslink)NM_004911:Homo sapiens protei	2.93
	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	2.93
	428376	AF119655	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	2.93
65	414416	AW409985	Hs.76084	(locuslink)NM_032737:Homo sapiens hypoth	2.93
	434094	AA305599	Hs.238205	Hs.238205:hypothetical protein PRO2013	2.93
	409012	AL117435	Hs.49725	Hs.49725:DKFZP434I216 protein	2.93
	429048	AI372949	Hs.44241	Hs.44241:Homo sapiens cDNA: FLJ21447 fis	2.93
	426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	2.92
70	422397	AJ223366	Hs.116051	(locuslink)NM_138768:Homo sapiens myelom	2.92
	426715	AB037855	Hs.171917	Hs.171917:hypothetical protein FLJ11085	2.92
	429539	AK001839	Hs.206501	(locuslink)NM_020467:Homo sapiens hypoth	2.92
	443715	AI583187	Hs.9700	NM_001238:Homo sapiens cyclin E1 (CCNE1)	2.92
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	2.92
75	433888	BE176078	Hs.30819	Hs.30819:hypothetical protein C40	2.92
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	2.92
	422558	NM_006420	Hs.118249	Hs.118249:ADP-ribosylation factor guanin	2.92
	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	2.92
	429626	U36787	Hs.211571	NM_005333:Homo sapiens holocytochrome c	2.92
80	413374	NM_001034	Hs.75319	NM_001034:Homo sapiens ribonucleotide re	2.92
	442159	AW163390	Hs.278554	NM_007276:Homo sapiens chromobox homolog	2.92
	400133		Hs.184693	NM_005648:Homo sapiens transcription elo	2.91
	419381	AB023420	Hs.90093	Hs.90093:heat shock 70kD protein 4	2.91
	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanin	2.91
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	2.91
	436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	2.91
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	2.91

5	433487	U31814	Hs.3352	NM_001527:Homo sapiens histone deacetylase	2.91
	416933	BE561850	Hs.80506	NM_003090:Homo sapiens small nuclear rib	2.90
	430287	AW182459	Hs.125759	Hs.125759:likely ortholog of mouse RING	2.90
	434026	R15486	Hs.285218	(locuslink)NM_021213:Homo sapiens phosph	2.90
	447698	AJ420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	2.90
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	2.90
	432754	BE241691	Hs.3100	Hs.3100:cylsyl-URNA synthetase	2.90
	437016	AU076916	Hs.5398	Hs.5398:guanine monophosphate synthetase	2.90
10	446228	NM_016046	Hs.14415	NM_016046:Homo sapiens exosomal core pro	2.90
	420421	AF281133	Hs.343589	Hs.343589:exosome component Rrp41	2.89
	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	2.89
	414420	AA043424	Hs.76095	NM_052815:Homo sapiens immediate early r	2.89
	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisi	2.89
	401405				2.89
15	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	2.89
	400247		Hs.356473	NM_006713:Homo sapiens activated RNA pol	2.89
	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	2.89
	413610	AL117554	Hs.119908	NM_015934:Homo sapiens nucleolar protein	2.89
20	413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine mono	2.89
	418651	NM_001949	Hs.1189	NM_001949:Homo sapiens E2F transcription	2.88
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	2.88
	417634	W27202	Hs.82327	NM_000178:Homo sapiens glutathione synth	2.88
	435099	AC004770	Hs.4756	NM_004111:Homo sapiens flap structure-sp	2.88
25	425811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	2.88
	446849	AU076617	Hs.16251	(locuslink)NM_016207:Homo sapiens cleava	2.88
	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	2.88
	413179	N99692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenas	2.88
	407770	AW607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1	2.88
30	408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	2.87
	448250	NM_016034	Hs.20776	(locuslink)NM_016034:Homo sapiens mitoch	2.87
	428810	AF058236	Hs.193788	NM_000625:Homo sapiens nitric oxide synl	2.87
	427505	AA361562	Hs.178761	Hs.178761:26S proteasome-associated pad1	2.87
	418443	NM_005239	Hs.85146	Hs.85146:v-ets erythroblastosis virus E2	2.87
35	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	2.87
	409262	AK000631	Hs.52256	Hs.52256:hypothetical protein FLJ20624	2.87
	443323	BE560621	Hs.9222	Hs.9222:estrogen receptor binding site a	2.87
	450378	AW249181	Hs.154796	Hs.154796:Homo sapiens cDNA FLJ37976 fis	2.86
	411761	AI733848	Hs.71935	NM_021220:Homo sapiens zinc finger prote	2.86
40	415691	AW963979	Hs.24723	Hs.24723:ESTs	2.86
	417715	AW969587	Hs.86366	Hs.86366:ESTs	2.86
	452099	BE612992	Hs.27931	Hs.27931:hypothetical protein FLJ10507 s	2.86
	436138	H53323	Hs.25717	Hs.25717:Homo sapiens cDNA: FLJ23454 fis	2.86
	432858	BE618609	Hs.279591	Hs.279591:Homo sapiens, Similar to RNA p	2.86
45	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	2.86
	444237	AA336878	Hs.9842	Hs.9842:ESTs	2.85
	456362	AW973003	Hs.179909	(locuslink)NM_024831:Homo sapiens nuclea	2.85
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	2.85
	424270	AK001818	Hs.144407	NM_018283:Homo sapiens hypothetical prot	2.85
50	414396	BE548266	Hs.76057	(locuslink)NM_000403:Homo sapiens galact	2.85
	426120	AA325243	Hs.166887	Hs.166887:ocpline I	2.85
	448663	BE614599	Hs.356501	(locuslink)NM_032335:Homo sapiens hypoth	2.85
	443802	AW504924	Hs.9805	Hs.9805:exportin 5	2.85
	445863	R12234	Hs.13396	Hs.13396:Homo sapiens clone 25028 mRNA s	2.85
55	434808	AF155108	Hs.256150	Hs.256150:NY-REN-41 antigen	2.85
	440334	BE276112	Hs.7165	NM_003904:Homo sapiens zinc finger prote	2.85
	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	2.85
	432680	T47364	Hs.278613	(locuslink)NM_005532:Homo sapiens Interf	2.84
60	446421	BE297434	Hs.15071	Hs.15071:chaperonin containing TCP1, sub	2.84
	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	2.84
	425649	U30930	Hs.158540	(locuslink)NM_003360:Homo sapiens UDP gl	2.84
	429638	AI916662	Hs.211577	(locuslink)NM_004986:Homo sapiens kinect	2.84
	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphata	2.84
65	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	2.84
	407833	AW955632	Hs.66666	Hs.66666:chromosome 7 open reading frame	2.84
	415083	AI632683	Hs.27179	Hs.27179:Homo sapiens cDNA FLJ12933 fis	2.83
	421462	AF016495	Hs.104624	NM_020980:Homo sapiens aquaporin 9 (AQP9	2.83
	443572	AA025610	Hs.9605	Hs.9605:cleavage and polyadenylation spe	2.83
70	443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN1	2.83
	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (2.83
	453028	AB006532	Hs.31442	NM_004260:Homo sapiens RecQ protein-like	2.83
	425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation facto	2.83
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	2.83
	410197	NM_005518	Hs.59889	(locuslink)NM_005518:Homo sapiens 3-hydr	2.83
75	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	2.83
	417677	NM_016055	Hs.82389	NM_016055:Homo sapiens mitochondrial rib	2.83
	425263	NM_001197	Hs.155419	NM_001197:Homo sapiens BCL2-interacting	2.82
	437430	W44671	Hs.124	NM_014628:Homo sapiens gene predicted fr	2.82
	428289	M26301	Hs.2253	Hs.2253:complement component 2	2.82
80	407137	T97307			2.82
	400750				2.82
	428788	AF082283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lympho	2.82
	432633	AI796390	Hs.210667	Hs.210667:ESTs	2.82
	432816	N38913	Hs.221575	Hs.221575:ESTs	2.82

5	410045	AA806930	Hs.58189	Hs.58189:eukaryotic translation initiati	2.82
	454144	BE280478	Hs.182695	NM_024026:Homo sapiens mitochondrial rib	2.82
	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	2.81
	434583	AA095761	Hs.349092	Hs.349092:ESTs, Weakly similar to A42442	2.81
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	2.81
10	428093	AW594506	Hs.104830	Hs.104830:ESTs	2.81
	416047	BE438894	Hs.78991	NM_012080:Homo sapiens DNA segment, nume	2.81
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell d	2.81
	452199	BE255643	Hs.110695	Hs.110695:hypothetical protein MGC3133	2.81
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	2.80
15	445921	AW015211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fis	2.80
	422809	AK001379	Hs.121028	NM_018136:Homo sapiens hypothetical prot	2.80
	417869	BE076254	Hs.82793	Hs.82793:proteasome (prosome, macropain)	2.80
	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 ope	2.80
	418731	AI264688	Hs.1197	NM_002157:Homo sapiens heat shock 10kD p	2.80
20	432840	AK001403	Hs.279521	Hs.279521:hypothetical protein FLJ20530	2.80
	428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associa	2.80
	441181	AA416925	Hs.374811	Hs.374811:Homo sapiens, similar to 4-1BB	2.80
	409463	AI458165	Hs.17286	NM_023930:Homo sapiens hypothetical prot	2.79
	450010	AW293801	Hs.255052	Hs.255052:ESTs	2.79
25	418960	NM_004494	Hs.89525	(locuslink)NM_004494:Homo sapiens hepato	2.79
	401179				2.79
	419252	AW138434	Hs.129805	Hs.129805:ESTs	2.79
	434750	BE019254	Hs.4112	Hs.4112:complex 1	2.79
	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	2.79
30	400529				2.79
	438414	BE264633	Hs.143638	NM_033661:Homo sapiens WD repeat domain	2.79
	436291	BE568452	Hs.344037	(locuslink)NM_003981:Homo sapiens protei	2.79
	427963	AI042582	Hs.181271	NM_016057:Homo sapiens CGI-120 protein (2.79
	426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically def	2.79
35	413880	AI660842	Hs.110915	NM_021258:Homo sapiens Interleukin 22 re	2.79
	442468	N77737	Hs.8349	NM_138933:Homo sapiens apobec-1 compleme	2.79
	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	2.79
	413278	BE563085	Hs.833	Hs.833:Interferon-stimulated protein, 15	2.79
	430120	AW675298	Hs.233694	(locuslink)NM_018396:Homo sapiens putati	2.79
40	452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	2.79
	417164	AA338283	Hs.81361	Hs.81361:heterogeneous nuclear ribonucle	2.79
	407811	AW190902	Hs.40098	Hs.40098:cysteine knot superfamily 1, BM	2.79
	409536	AA305729	Hs.18272	(locuslink)NM_030674:Homo sapiens solute	2.78
	447619	AI174800	Hs.19054	(locuslink)NM_018530:Homo sapiens hypoth	2.78
45	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	2.78
	414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	2.78
	443639	BE269042	Hs.9661	Hs.9661:proteasome (prosome, macropain)	2.78
	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophorin II (RP	2.78
	430612	AF182284	Hs.241578	NM_016200:Homo sapiens U6 snRNA-associat	2.78
50	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	2.78
	414697	BE266134	Hs.76927	Hs.76927:translocase of outer mitochondr	2.78
	420665	AW469240	Hs.371581	Hs.371581:ESTs	2.78
	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	2.78
	448093	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	2.77
55	443343	BE409809	Hs.301005	Hs.301005:histone H2A.F/Z variant	2.77
	418313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	2.77
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	2.77
	456950	AF111170	Hs.308165	Hs.308165:ESTs, Highly similar to unknown	2.77
	432543	AA552690	Hs.152423	Hs.152423:Homo sapiens cDNA: FLJ21274 fi	2.77
60	423271	W47225	Hs.126256	NM_000576:Homo sapiens Interleukin 1, be	2.77
	410595	AW629223	Hs.64794	NM_006978:Homo sapiens zinc finger prote	2.77
	448140	AF146761	Hs.20450	NM_020125:Homo sapiens B lymphocyte acti	2.77
	457757	AA434109	Hs.12271	NM_012162:Homo sapiens F-box and leucine	2.77
	420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	2.77
65	410094	BE147897	Hs.58593	NM_004128:Homo sapiens general transcrip	2.77
	403817				2.77
	459125	AA811363	Hs.29464	Hs.29464:Homo sapiens cDNA: FLJ23460 fis	2.77
	432705	AI879473	Hs.157123	Hs.157123:ESTs	2.77
	446658	AI440137	Hs.164989	NM_138492:Homo sapiens hypothetical prot	2.76
70	419485	AA489023	Hs.99807	Hs.99807:Homo sapiens mRNA: cDNA DKFZp31	2.76
	432886	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	2.76
	428438	NM_001955	Hs.2271	NM_001955:Homo sapiens endothelin 1 (EDN	2.76
	414767	BE541381	Hs.178705	NM_033515:Homo sapiens MacGAP protein (M	2.76
	405830	AI829848	Hs.342389	Hs.342389:peptidylprolyl isomerase A (cy	2.76
75	432320	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	2.76
	430450	R23553	Hs.241489	(locuslink)NM_015913:Homo sapiens hypoth	2.76
	433808	NM_014062	Hs.3566	Hs.3566:ART-4 protein	2.75
	431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	2.75
	433369	Z49254	Hs.3254	NM_021134:Homo sapiens mitochondrial rib	2.75
80	446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	2.75
	432204	AI916132	Hs.121593	Hs.121593:Homo sapiens cDNA FLJ13123 fis	2.75
	424438	AA340724	Hs.271912	Hs.271912:Homo sapiens cDNA FLJ38690 fis	2.75
	433862	D86960	Hs.3610	NM_014873:Homo sapiens KIAA0205 gene pro	2.75
	417080	BE392846	Hs.1063	Hs.1063:small nuclear ribonucleoprotein	2.75
	428242	H55709	Hs.2250	Hs.2250:leukemia inhibitory factor (chol	2.75
	416188	BE157260	Hs.79070	NM_002467:Homo sapiens v-myc myelocytoma	2.75
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	2.75

	419489	AW411280	Hs.90693	NM_013400:Homo sapiens replication init	2.75
	407971	A469117	Hs.62918	Hs.62918:CDK91 cell division cycle 91-f	2.75
	432403	AA50815	Hs.124840	(locuslink)NM_138456:Homo sapiens hypoth	2.75
5	410775	AB014460	Hs.66196	NM_002528:Homo sapiens rnh endonuclease	2.75
	444197	BE266947	Hs.10590	NM_018683:Homo sapiens zinc finger prote	2.75
	447250	AI878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	2.75
	406806	AW086535	Hs.350108	Hs.350108:ribosomal protein, large, P0	2.75
	411580	AL080088	Hs.70877	NM_015421:Homo sapiens DKFZP564K2062 pro	2.75
10	433652	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	2.74
	426235	AI631964	Hs.34447	Hs.34447:Homo sapiens cDNA FLJ38512 fis,	2.74
	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	2.74
	419713	AW968058	Hs.92381	NM_019094:Homo sapiens nudix (nucleoside	2.74
	410174	AA306007	Hs.59461	Hs.59461:DKFZP434C245 protein	2.74
	430720	U85768	Hs.247838	NM_002991:Homo sapiens small inducible c	2.74
15	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	2.74
	452767	AW014195	Hs.61472	Hs.61472:Homo sapiens, clone IMAGE:51841	2.74
	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	2.73
	423198	M81933	Hs.1634	Hs.1634:cell division cycle 25A	2.73
	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	2.73
20	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	2.73
	423908	AJ006422	Hs.135183	NM_006869:Homo sapiens centaurin, alpha	2.73
	433412	AV653729	Hs.8185	NM_021199:Homo sapiens sulfide dehydroge	2.73
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433 fis	2.73
25	452461	N78223	Hs.108106	Hs.108106:ubiquitin-like, containing PHD	2.73
	407699	AA825974	Hs.32646	NM_024622:Homo sapiens hypothetical prot	2.73
	412258	AA376768	Hs.96125	(locuslink)NM_025151:Homo sapiens Rab co	2.73
	450256	AA286887	Hs.24724	Hs.24724:Homo sapiens cDNA FLJ39185 fis,	2.72
	443905	AI215948	Hs.143969	Hs.143969:ESTs	2.72
30	413274	NM_004893	Hs.75258	NM_004893:Homo sapiens H2A histone famil	2.72
	408885	C02741	Hs.48712	NM_017948:Homo sapiens hypothetical prot	2.72
	424585	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	2.72
	424692	AA429834	Hs.151791	NM_014679:Homo sapiens KIAA0092 gene pro	2.72
	413762	AW411479	Hs.848	NM_002014:Homo sapiens FK506 binding pro	2.72
35	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-like	2.72
	450164	AI239923	Hs.63931	NM_080759:Homo sapiens dachshund homolog	2.71
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	2.71
	450897	W16741	Hs.351629	NM_014017:Homo sapiens HSPC003 protein (2.71
40	447349	AI375546		BE743847:601577765F1 NIH_MGC_9 Homo sapi	2.71
	445413	AA151342	Hs.12677	(locuslink)NM_016077:Homo sapiens CGI-14	2.71
	448826	AI580252	Hs.255565	Hs.255565:Homo sapiens cDNA FLJ33892 fis	2.71
	406671	AA129547	Hs.285754	NM_000245:Homo sapiens met proto-oncogen	2.71
	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	2.71
45	441020	W79283	Hs.35962	Hs.35962:Homo sapiens mRNA; cDNA DKFZp68	2.70
	458933	AI638429	Hs.24763	NM_002882:Homo sapiens RAN binding prote	2.70
	423787	AJ295745	Hs.236204	Hs.236204:nuclear pore complex protein	2.70
	430462	AI584156	Hs.105640	Hs.105640:hypothetical protein BC007772	2.70
	439656	AW138241	Hs.160602	Hs.160602:Homo sapiens cDNA FLJ36008 fis	2.70
	425236	AW067800	Hs.155223	NM_003714:Homo sapiens stannocalcin 2 (2.70
50	420085	AJ741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	2.70
	448296	BE622756	Hs.10949	Hs.10949:Homo sapiens cDNA FLJ14162 fis,	2.70
	430200	BE613337	Hs.234896	Hs.234896:geminin	2.70
	424308	AW975531	Hs.154443	Hs.154443:MCM4 minichromosome maintenanc	2.70
	423453	AW450737	Hs.128791	NM_015939:Homo sapiens CGI-09 protein (L	2.70
55	421344	AW631030	Hs.103665	(locuslink)NM_015873:Homo sapiens villin	2.70
	446607	AI691065	Hs.155780	Hs.155780:ESTs	2.70
	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	2.70
	443835	AF016371	Hs.9680	NM_006347:Homo sapiens peptidyl prolyl	2.70
	413794	AF234532	Hs.61638	NM_012334:Homo sapiens myosin X (MYO10),	2.70
60	451481	AA300228	Hs.295866	(locuslink)NM_030974:Homo sapiens hypoth	2.70
	458820	BE552151	Hs.108118	Hs.108118:hypothetical protein FLJ22474	2.70
	425905	AB032959	Hs.318584	NM_032173:Homo sapiens hypothetical prot	2.69
	408089	H59799	Hs.42644	Hs.42644:thioredoxin-like 2	2.69
	431201	AA578405	Hs.8854	Hs.8854:Pvt1 oncogene homolog, MYC activ	2.69
65	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	2.69
	441703	AW390054	Hs.192843	NM_022145:Homo sapiens leucine zipper pr	2.69
	433916	AW732839	Hs.3631	NM_001551:Homo sapiens immunoglobulin (C	2.69
	422516	BE258862	Hs.117950	NM_006452:Homo sapiens phosphoribosylam	2.69
	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	2.69
70	427464	BE262956	Hs.178292	Hs.178292:protein O-fucosyltransferase 1	2.69
	453876	AW021748	Hs.110406	Hs.110406:ESTs	2.69
	424373	AJ133798	Hs.146219	NM_014427:Homo sapiens copine VII (CPNE7	2.69
	411619	AI418609	Hs.71040	NM_017816:Homo sapiens hypothetical prot	2.69
	413004	T35901	Hs.75117	Hs.75117:interleukin enhancer binding fa	2.69
75	420062	AW411096	Hs.94785	(locuslink)NM_021809:Homo sapiens TGF-beta	2.69
	446077	BE251048	Hs.22579	Hs.22579:Homo sapiens clone CDABP0036 mR	2.68
	446269	AW263155	Hs.14559	NM_018131:Homo sapiens hypothetical prot	2.68
	428728	NM_016625	Hs.191381	Hs.191381:hypothetical protein LOC51319	2.68
	400263		Hs.75309	NM_001861:Homo sapiens eukaryotic transl	2.68
80	421933	R88881	Hs.109655	NM_006746:Homo sapiens sex comb on middle	2.68
	417750	AI267720	Hs.260523	Hs.260523:neuroblastoma RAS viral (v-ras	2.68
	429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	2.68
	421720	AF155096	Hs.107213	Hs.107213:formin binding protein 3	2.68
	425601	AW629485	Hs.140720	NM_012083:Homo sapiens frequently rearra	2.68

5	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintainanc	2.68
	433159	AB035898	Hs.150587	NM_020242:Homo sapiens kinesin-like 7 (K	2.68
	406673	M34996	Hs.198253	Hs.198253:major histocompatibility compl	2.68
	428206	AB020643	Hs.183006	Hs.183006:likely homolog of mouse hepar	2.68
	429344	R94038	Hs.374664	NM_005538:Homo sapiens inhibin, beta C (2.68
	427719	AI393122	Hs.134726	(locustink)NM_145060:Homo sapiens hypoth	2.68
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	2.68
	457313	AF047002	Hs.241520	NM_005782:Homo sapiens transcriptional c	2.67
10	413142	M81740	Hs.75212	(locustink)NM_002539:Homo sapiens ornith	2.67
	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	2.67
	432391	AI732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	2.67
	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA: cDNA DKFZp56	2.67
	447913	AW438602	Hs.191179	Hs.191179:ESTs	2.67
15	418738	AW388633	Hs.6682	Hs.6682:solute carrier family 7, (cation	2.67
	439586	AA922936	Hs.110039	Hs.110039:ESTs	2.67
	427477	AW973119	Hs.178391	NM_021029:Homo sapiens ribosomal protein	2.67
	421839	BE258778	Hs.108809	NM_006429:Homo sapiens chaperonin contai	2.67
	400448				2.67
20	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu+++ tran	2.67
	445304	BE613206	Hs.279607	Hs.279607:Homo sapiens cDNA FLJ34399 fis	2.67
	417601	NM_014735	Hs.82292	NM_014735:Homo sapiens KIAA0215 gene pro	2.66
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	2.66
	431021	AI859664	Hs.351863	(locustink)NM_003312:Homo sapiens thiosu	2.66
25	453157	AF077036	Hs.31989	NM_015449:Homo sapiens NICE-3 protein (N	2.66
	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	2.66
	422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, protei	2.66
	456248	AL035786	Hs.82425	NM_005717:Homo sapiens actin related pro	2.66
	427691	AW194426	Hs.20726	Hs.20726:ESTs, Moderately similar to hyp	2.66
30	419705	AW368634	Hs.154331	Hs.154331:ESTs	2.66
	421254	AK001724	Hs.102950	NM_016128:Homo sapiens coal protein gamm	2.66
	422719	BE017985	Hs.102558	Hs.102558:Homo sapiens cDNA FLJ40369 fis	2.66
	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	2.66
	432435	BE218886	Hs.282070	Hs.282070:ESTs	2.66
35	433020	AI375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	2.65
	436106	AI050715	Hs.2331	Hs.2331:E2F transcription factor 5, p130	2.65
	431127	U66618	Hs.250581	Hs.250581:SWI/SNF related, matrix associ	2.65
	425568	AW963118	Hs.161784	Hs.161784:ESTs	2.65
	430508	AI015435	Hs.104637	Hs.104637:solute carrier family 1 (gluta	2.65
40	414761	AU077228	Hs.77256	NM_004456:Homo sapiens enhancer of zeste	2.65
	412738	N34731	Hs.74562	NM_078480:Homo sapiens fuse-binding prot	2.65
	409893	AW247090	Hs.57101	Hs.57101:MCM2 minichromosome maintenanc	2.65
	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	2.64
	428072	BE258602	Hs.182366	NM_016292:Homo sapiens heat shock protel	2.64
45	417957	H53497	Hs.83006	NM_016071:Homo sapiens mitochondrial rib	2.64
	409119	AA531133	Hs.4253	Hs.4253:hypothetical protein MGC2574	2.64
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	2.64
	409214	AW405967	Hs.333388	Hs.333388:similar to CG3714 gene product	2.64
50	414883	AA926860	Hs.348669	Hs.348669:CDK28 protein kinase 1	2.64
	433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	2.64
	408633	AW963372	Hs.222088	NM_014109:Homo sapiens PRO2000 protein (2.64
	447769	AW873704	Hs.320831	Hs.320831:chromosome 20 open reading fra	2.64
	432964	AF118395	Hs.279865	NM_014317:Homo sapiens trans-prenyltrans	2.63
55	444855	BE409261	Hs.12084	Hs.12084:Tu translation elongation facto	2.63
	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	2.63
	408137	AI694131	Hs.29002	Hs.29002:KIAA1706 protein	2.63
	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	2.63
	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	2.63
	430024	AI808760	Hs.227730	NM_000210:Homo sapiens Integrin, alpha 6	2.63
60	406122				2.63
	420988	AW006352	Hs.159643	Hs.159643:ESTs, Weakly similar to putati	2.63
	436433	AW631437	Hs.5184	(locustink)NM_016397:Homo sapiens TH1-fi	2.63
	417129	AI381800	Hs.300684	Hs.300684:calcitonin gene-related peptid	2.63
	410397	AF217517	Hs.63042	NM_018457:Homo sapiens DKFZp564J157 prot	2.63
65	419420	AA355435	Hs.30724	(locustink)NM_001516:Homo sapiens genera	2.63
	400298	AA032279	Hs.61635	Hs.61635:six transmembrane epithelial an	2.63
	412599	AU076782	Hs.248267	(locustink)NM_021126:Homo sapiens mercap	2.63
	436199	R38946	Hs.127951	Hs.127951:Homo sapiens cDNA FLJ14503 fis	2.63
	425081	X74794	Hs.154443	Hs.154443:MCM4 minichromosome maintenanc	2.63
70	442025	AW887434	Hs.11810	NM_032026:Homo sapiens CDA11 protein (CD	2.62
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	2.62
	409703	NM_006187	Hs.56009	Hs.56009:2'-5'-oligoadenylate synthetase	2.62
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens Integral membrane	2.62
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	2.62
75	451926	AW134519	Hs.96125	(locustink)NM_025151:Homo sapiens Rab co	2.62
	413781	J05272	Hs.850	(locustink)NM_000883:Homo sapiens IMP (i	2.62
	407236	W79485	Hs.173980	Hs.173980:nuclear matrix protein NMP200	2.62
	421405	AA251944	Hs.104058	NM_015957:Homo sapiens CGI-29 protein (L	2.62
	429491	NM_012111	Hs.204041	NM_012111:Homo sapiens chromosome 14 ope	2.62
80	453335	AW857376	Hs.169238	NM_000149:Homo sapiens fucosyltransferas	2.62
	441126	NM_000429	Hs.323715	(locustink)NM_000428:Homo sapiens methio	2.62
	417404	NM_007350	Hs.82101	(locustink)NM_007350:Homo sapiens plecks	2.62
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	2.62
	446766	AF083208	Hs.16178	NM_012138:Homo sapiens apoptosis antagon	2.62

	437033	AW248364	Hs.5409	(locuslink)NM_004875:Homo sapiens RNA po	2.62
	412123	BE251328	Hs.73291	NM_018256:Homo sapiens WD repeat domain	2.62
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	2.61
5	433037	NM_014158	Hs.279938	NM_014158:Homo sapiens HSPC067 protein (2.61
	414438	AI879277	Hs.76136	(locuslink)NM_003329:Homo sapiens titore	2.61
	416221	BE513171	Hs.79086	(locuslink)NM_007208:Homo sapiens mitoch	2.61
	443898	AW804296	Hs.9950	NM_014302:Homo sapiens Sec61 gamma (SEC6	2.61
	410007	AW950887	Hs.57813	NM_014596:Homo sapiens zinc ribbon domai	2.61
10	412715	NM_000947	Hs.74519	NM_000947:Homo sapiens primase, polypept	2.61
	449864	BE276386	Hs.111429	NM_032486:Homo sapiens dynactin 4 (MGC32	2.61
	448625	AW970786	Hs.178470	NM_024829:Homo sapiens hypothetical prot	2.61
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	2.61
	410686	AI733735	Hs.114905	NM_033266:Homo sapiens ER to nucleus sig	2.60
15	411400	AA311919	Hs.69851	NM_018983:Homo sapiens nucleolar protein	2.60
	429770	AI766047	Hs.99736	Hs.99736:hypothetical protein MGC3350	2.60
	425983	AK000226	Hs.165619	NM_031265:Homo sapiens mucin and cadheri	2.60
	430237	AI272144	Hs.236522	Hs.236522:DKFZP434P106 protein	2.60
	419607	R52557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	2.60
20	419508	AW997938	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	2.60
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prole	2.60
	457234	AW968360	Hs.14355	Hs.14355:Homo sapiens cDNA FLJ13207 fis,	2.60
	420911	U77413	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (2.60
	418478	U38945	Hs.1174	NM_000077:Homo sapiens cyclin-dependent	2.60
25	438533	AI440266	Hs.170673	NM_138959:Homo sapiens retinal short cha	2.60
	421699	AL161994	Hs.107003	NM_021178:Homo sapiens enhancer of invas	2.60
	452220	BE158006	Hs.212296	Hs.212296:ESTs	2.60
	439148	AA372280	Hs.178576	(locuslink)NM_030877:Homo sapiens cateni	2.60
30	453949	AU077146	Hs.36927	(locuslink)NM_006644:Homo sapiens heat s	2.59
	451110	AI955040	Hs.265398	Hs.265398:ESTs, Moderately similar to hy	2.59
	446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	2.59
	411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypep	2.59
	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	2.59
	442990	AA197226	Hs.19347	NM_032351:Homo sapiens mitochondrial rib	2.59
35	424197	AF095834	Hs.142989	NM_015982:Homo sapiens germ cell specifi	2.59
	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	2.59
	410219	T98226	Hs.171952	Hs.171952:occludin	2.59
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	2.59
40	441153	BE562828		BE562828:601336534F1 NIH_MGC_44 Homo sap	2.59
	410570	AI133096	Hs.64593	NM_006356:Homo sapiens ATP synthase, H+	2.58
	430594	AK000790	Hs.246885	NM_017958:Homo sapiens hypothetical prot	2.58
	410315	AI638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	2.58
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	2.58
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	2.58
45	449019	AI949085	Hs.67776	Hs.67776:Homo sapiens, clone IMAGE:54556	2.58
	410442	X73424	Hs.63788	Hs.63788:propionyl Coenzyme A carboxylas	2.58
	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	2.58
	454417	AI244459	Hs.110826	Hs.110826:trinucleotide repeat containin	2.58
	416330	AU077101	Hs.79222	Hs.79222:galactosidase, beta 1	2.58
50	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	2.58
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFDN	2.58
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	2.58
	406180				2.58
55	416297	AA157634	Hs.79172	Hs.79172:solute carrier family 25 (mitoc	2.58
	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	2.58
	447532	AK000614	Hs.18791	NM_017899:Homo sapiens hypothetical prot	2.57
	420309	AW043637	Hs.21766	Hs.21766:ESTs, Weakly similar to hypothe	2.57
	447418	AA063074	Hs.18552	Hs.18552:E2IG2 protein	2.57
60	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	2.57
	428342	AI739168	Hs.349283	Hs.349283:Homo sapiens cDNA FLJ31753 fis	2.57
	427254	AL121523	Hs.97774	Hs.97774:ESTs	2.57
	458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (2.57
	425689	W16480	Hs.24283	Hs.24283:Homo sapiens cDNA FLJ25952 fis,	2.57
	452700	AI859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	2.57
65	427678	BE267756	Hs.180312	NM_016065:Homo sapiens mitochondrial rib	2.57
	444656	AI277924	Hs.145199	Hs.145199:ESTs, Weakly similar to hypoth	2.57
	425206	NM_002153	Hs.155109	NM_002153:Homo sapiens hydroxysteroid (1	2.57
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	2.56
70	427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	2.56
	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	2.56
	409964	AW358226	Hs.67928	Hs.67928:ESTs	2.56
	431910	AK000142	Hs.101774	Hs.101774:hypothetical protein FLJ23045	2.56
	413010	AA393273	Hs.75133	NM_003201:Homo sapiens transcription fac	2.56
75	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	2.56
	419423	D26488	Hs.90315	Hs.90315:KIAA0007 protein	2.56
	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	2.56
	437623	D63880	Hs.5719	NM_014865:Homo sapiens chromosome conden	2.56
	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	2.56
80	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	2.56
	425369	AB014595	Hs.155976	(locuslink)NM_003588:Homo sapiens cullin	2.56
	420614	AL110291	Hs.99364	Hs.99364:abhydrolase domain containing 1	2.56
	427876	AI944291	Hs.369171	Hs.369171:ESTs	2.56
	418862	BE550864	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	2.56
	416432	BE391767	Hs.79322	(locuslink)NM_005051:Homo sapiens glutam	2.55

5	458814	AI498957	Hs.351937	Hs.351937:ribosomal protein, large P2	2.55
	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	2.55
	454003	AA058944	Hs.116602	Hs.116602:hypothetical protein BC009115	2.55
	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	2.55
	457400	AF032906	Hs.252549	NM_001336:Homo sapiens cathepsin Z (CTSZ)	2.55
10	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2)	2.55
	402829				2.55
	425843	BE313280	Hs.159627	NM_004632:Homo sapiens death associated	2.55
	400995				2.55
	452945	AW978187	Hs.79103	NM_030579:Homo sapiens cytochrome b5 out	2.55
15	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	2.55
	422192	AA305159	Hs.113019	NM_015931:Homo sapiens fls485 (LOC51066)	2.55
	424755	AB033094	Hs.152925	Hs.152925:KIAA1268 protein	2.55
	410012	AW015832	Hs.57898	(locuslink)NM_017819:Homo sapiens hypoth	2.55
	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	2.55
20	449042	AW294985	Hs.30715	Hs.30715:potassium voltage-gated channel	2.55
	420281	AI623693	Hs.323494	(locuslink)NM_017964:Homo sapiens hypoth	2.55
	418581	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	2.55
	406629	AW277078	Hs.181165	Hs.181165:eukaryotic translation elongat	2.55
	421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens 8D6 an	2.54
25	446715	AJ337735	Hs.173919	Hs.173919:ESTs, Weakly similar to neuron	2.54
	431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	2.54
	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyrido	2.54
	427368	BE041451	Hs.177507	Hs.177507:hypothetical protein HSPC155	2.54
	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	2.54
30	409532	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cyste)	2.54
	442875	BE623003	Hs.23625	Hs.23625:Homo sapiens clone TCCCTA00142	2.54
	455031	AA335996	Hs.355907	Hs.355907:ESTs, Weakly similar to protei	2.54
	442432	BE093589	Hs.38178	NM_024629:Homo sapiens hypothetical prot	2.54
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	2.54
35	448775	AB025237	Hs.388	NM_002452:Homo sapiens nudix (nucleoside	2.54
	414368	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	2.54
	432876	AW248272	Hs.279652	NM_015856:Homo sapiens mitochondrial rib	2.53
	431731	BE265322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	2.53
	425994	AK000207	Hs.165803	NM_017708:Homo sapiens hypothetical prot	2.53
40	445982	BE410233	Hs.13501	(locuslink)NM_014303:Homo sapiens pescad	2.53
	444232	W56010	Hs.347297	(locuslink)NM_013397:Homo sapiens over-e	2.53
	435655	AW105663	Hs.6947	(locuslink)NM_014159:Homo sapiens Huntin	2.53
	417686	AA769155	Hs.235498	Hs.235498:hypothetical protein FLJ14075	2.53
	417933	X02308	Hs.82962	NM_001071:Homo sapiens thymidylate synth	2.53
45	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	2.53
	452313	Y00486	Hs.28914	Hs.28914:adenine phosphoribosyltransfera	2.53
	438317	AA826401	Hs.122393	Hs.122393:ESTs	2.53
	409299	AA045650	Hs.53125	NM_004597:Homo sapiens small nuclear rib	2.53
	423599	AI805664	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	2.53
50	412525	AA581439	Hs.152328	Hs.152328:ESTs	2.53
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	2.53
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite molit-	2.53
	414987	AA524394	Hs.294022	NM_032665:Homo sapiens hypothetical prot	2.53
	434274	AA628539	Hs.57783	Hs.57783:eukaryotic translation initiati	2.53
55	400282		Hs.289101	NM_005313:Homo sapiens glucose regulated	2.53
	425322	U63630	Hs.155637	NM_006904:Homo sapiens protein kinase, D	2.53
	453344	BE349075	Hs.44571	Hs.44571:ESTs	2.53
	449915	NM_004529	Hs.404	NM_004529:Homo sapiens myeloid/lymphoid	2.53
	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of olig	2.52
60	439012	BE383814	Hs.6455	NM_006666:Homo sapiens RuvB-like 2 (E. c	2.52
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	2.52
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidase	2.52
	442315	AA173992	Hs.7956	Hs.7956:ESTs	2.52
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	2.52
65	422385	BE549407	Hs.115823	(locuslink)NM_006638:Homo sapiens ribonu	2.52
	433517	AW022133	Hs.189838	Hs.189838:ESTs	2.52
	450230	AW016607	Hs.201582	Hs.201582:ESTs	2.52
	432866	BE395875	Hs.279609	NM_014342:Homo sapiens mitochondrial car	2.52
	433001	AF217513	Hs.279905	NM_016359:Homo sapiens nucleolar protein	2.52
70	440773	AA352702	Hs.37747	NM_022767:Homo sapiens hypothetical prot	2.52
	440587	AL138461	Hs.323084	(locuslink)NM_031209:Homo sapiens tRNA-g	2.52
	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	2.52
	424259	AK001776	Hs.143954	(locuslink)NM_018270:Homo sapiens chromo	2.52
	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	2.52
75	453204	R10799	Hs.191990	Hs.191990:ESTs	2.52
	453665	AA626250	Hs.326184	Hs.326184:Homo sapiens nuclear protein p	2.52
	432353	NM_016558	Hs.274411	NM_016558:Homo sapiens SCAN domain conta	2.52
	433271	BE621697	Hs.14317	NM_018848:Homo sapiens nucleolar protein	2.51
	431770	BE221880	Hs.268555	NM_012255:Homo sapiens 5'-3' exoninucel	2.51
80	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	2.51
	428839	AI767756	Hs.82302	(locuslink)NM_147174:Homo sapiens hepara	2.51
	404826				2.51
	429669	BE185499	Hs.2471	NM_014878:Homo sapiens KIAA0020 gene pro	2.51
	434474	AL042935	Hs.211571	(locuslink)NM_005333:Homo sapiens holoxy	2.51
	424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	2.51
	450422	AA743525	Hs.60300	NM_033414:Homo sapiens hypothetical prot	2.51
	440214	AA247118	Hs.7049	(locuslink)NM_018386:Homo sapiens hypoth	2.51

5	421168	AF182277	Hs.330780	Hs.330780:cytochrome P450, subfamily IIB	2.51
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	2.51
	452101	T60298	Hs.10844	NM_052972:Homo sapiens leucine-rich alph	2.51
	436043	AW963838	Hs.168830	Hs.168830:Homo sapiens cDNA FLJ12136 fis	2.51
	424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	2.51
	435677	AA694142	Hs.6685	Hs.6685:thyroid hormone receptor interac	2.51
	406363				2.51
	452018	AW102941	Hs.211265	Hs.211265:ESTs	2.51
10	409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	2.51
	421937	AI878857	Hs.109705	NM_016185:Homo sapiens hematological and	2.51
	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	2.51
	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	2.50
	434584	D57341	Hs.188361	Hs.188361:Homo sapiens cDNA FLJ12807 fis	2.50
15	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	2.50
	426053	U68105	Hs.172182	NM_002568:Homo sapiens poly(A) binding p	2.50
	432642	BE297635	Hs.3069	NM_004134:Homo sapiens heat shock 70kD p	2.50
	452390	AI864142	Hs.29288	(locuslink)NM_022759:Homo sapiens endo-b	2.50
	429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inacti	2.50
	400076				2.50
20	420596	NM_002692	Hs.99185	NM_002692:Homo sapiens polymerase (DNA d	2.50
	422244	Y08890	Hs.113503	NM_002271:Homo sapiens karyopherin (impo	2.50
	410723	AA100683	Hs.372108	Hs.372108:ESTs	2.50
	435496	AW840171	Hs.265398	Hs.265398:ESTs, Moderately similar to hy	2.50
25	425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	2.50
	433626	AF078859	Hs.86347	NM_013341:Homo sapiens hypothetical prot	2.50
	448391	H71025	Hs.21075	NM_016328:Homo sapiens GTF2I repeat doma	2.50

TABLE 10B

30	Pkey:	Uniqe Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
35	Play	CAT Number	Accession
	406685	0_0	M18728
	434414	35978_1	AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298 AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175 BF854337
40	432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG951122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AI075321 L13823 AA216700 BF771864 AW861859 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
	406708	0_0	AI282759
	459306	223120_4	AW578452
50	447349	1063443_1	BE743847 AW809603 BM469626 AI375546
	441153	264480_3	BE562826 BE378727

TABLE 10C

55	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA -- sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
60	Pkey	Ref	Strand	Nt_position
	404519	8152000	Plus	12817-13000
	405399	9256288	Minus	63448-63554
	403220	7630969	Plus	64338-64517
65	404661	9797073	Plus	33374-33675,33769-34008
	402496	9797769	Minus	8615-9103
	403055	8748904	Minus	109532-110225
	400965	7770576	Minus	173043-173564
70	403218	7630969	Plus	58039-58149
	401866	8018106	Plus	73126-73623
	403221	7630969	Plus	66294-66438,66936-67124
	401519	6649315	Plus	157315-157950
75	405451	7622517	Minus	145949-146227
	403532	8076842	Minus	81750-81901
	402944	9368423	Plus	110411-110716,111173-111640
	403219	7630969	Plus	61858-61995
80	403381	9438267	Minus	26009-26178
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
	404684	9797403	Minus	110881-111020
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	405506	6466489	Plus	80014-80401,80593-81125
	403739	7630882	Plus	44563-44766,48209-48483,52255-52495

406545	7711510	Plus	145662-145781,147854-147984,148098-14824
401405	7768126	Minus	69276-69452,69548-69958
400750	8119067	Plus	198991-199168,199316-199548
401179	9438647	Plus	113477-113893
400529	9796988	Plus	138232-138423
403817	8962065	Plus	110297-111052
400448	9887687	Minus	177372-177674
406122	9144087	Minus	30940-31386
406180	7283201	Minus	38923-39107
402829	8918414	Plus	101532-101852,102006-102263
400995	8099094	Plus	141186-141601
404826	6572184	Plus	47726-48046
406363	9256114	Plus	14403-14602,17000-17147,17241-17368

Table 11A lists about 958 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium) that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" colon to "average" normal adult tissues was greater than or equal to 3.0, the "average" colon level was set to the 90th percentile value amongst colon primary cancer specimens and colon liver derived metastases, the "average" normal adult tissue level was set to the 70th percentile value amongst non-malignant tissues minus the colonic derived samples, the "average" colon value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of have an oncogenic function or of transducing an intracellular signal, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 11A: 958 genes up-regulated in colon cancer compared to normal adult tissues excluding non-malignant colon tissues (whole colon and colon epithelium)

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

Pkey	ExAccn	UnigeneID	Unigene Title	R1
436749	AA584890	Hs.5302	NM_008149:Homo sapiens lectin, galactosi	37.18
406690	M29540	Hs.220529	(locuslink)NM_004363:Homo sapiens carcin	31.24
407242	M18728		(locuslink)NM_002483:Homo sapiens carcin	24.81
406685	M18728		(locuslink)NM_002483:Homo sapiens carcin	20.54
431912	AI660552	Hs.356183	Hs.356183:ESTs, Weakly similar to S3B4_H	20.38
428934	AF039401	Hs.194659	NM_001285:Homo sapiens chloride channel,	20.13
406667	M12523			19.89
437935	AW339591	Hs.5840	NM_033049:Homo sapiens mucin 13, epithel	19.68
446787	U67167	Hs.315	NM_002457:Homo sapiens mucin 2, intesti	19.55
423541	AA296922	Hs.129778	NM_014471:Homo sapiens serine protease i	18.33
421341	AJ243212	Hs.374281	NM_007329:Homo sapiens deleted in malign	17.47
414386	X00442	Hs.75990	NM_005143:Homo sapiens haptoglobin (HP),	17.37
416768	AA363733	Hs.1032	NM_006507:Homo sapiens regenerating isle	16.99
422578	AF239666	Hs.1545	NM_001804:Homo sapiens caudal type homeo	15.15
441031	AI110684	Hs.7645	NM_005141:Homo sapiens fibrinogen, B bet	15.02
421582	AB910275	Hs.350470	NM_003225:Homo sapiens trefol factor 1	14.23
407243	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	14.12
422260	AA315993	Hs.105484	NM_032044:Homo sapiens regenerating gene	13.64
432542	AW083920	Hs.16098	NM_020384:Homo sapiens claudin 2 (CLDN2)	13.48
424212	NM_005814	Hs.143131	NM_005814:Homo sapiens glycoprotein A33	13.43
418888	AU076801	Hs.89436	NM_004063:Homo sapiens cadherin 17, U c	13.20
453863	X02544	Hs.572	Hs.572:orosemucoid 1	13.06
413719	BE439580	Hs.75498	NM_004591:Homo sapiens small inducible c	12.58
436217	T53925	Hs.107	NM_004467:Homo sapiens fibrinogen-like 1	12.34
421100	AW351839	Hs.124660	Hs.124660:ESTs, Moderately similar to 21	11.72
409153	W03754	Hs.50813	NM_017625:Homo sapiens intelectin (ITLN)	11.72
452316	AA298484	Hs.61265	NM_138805:Homo sapiens family with seque	11.49
406399				11.25
414463	T69078	Hs.76177	NM_001633:Homo sapiens alpha-1-microglob	11.18
421964	X73079	Hs.288579	NM_002644:Homo sapiens polymeric immunog	11.12
407007	U22961	Hs.184411	NM_000477:Homo sapiens albumin (ALB), mR	11.01
423673	BE003054	Hs.1695	NM_002426:Homo sapiens matrix metallopro	10.70
447400	AK000322	Hs.18457	NM_017763:Homo sapiens hypothetical prot	10.69
450685	L15533	Hs.423	NM_138938:Homo sapiens pancreatitis-asso	10.57
427583	M82962	Hs.179704	NM_005588:Homo sapiens meprin A, alpha (10.48
418007	M13509	Hs.83169	NM_002421:Homo sapiens matrix metallopro	10.39
406741	AA058357	Hs.74466	(locuslink)NM_006890:Homo sapiens carcin	10.20
422424	AI186431	Hs.296638	Hs.296638:prostate differentiation facto	10.19
423371	AU076819	Hs.1650	NM_000111:Homo sapiens solute carrier fa	9.91
452304	AA025386	Hs.61311	Hs.61311:ESTs, Weakly similar to S10590	9.72
422106	D84239	Hs.111732	NM_003890:Homo sapiens IgG Fc binding pr	9.70
430569	AF241254	Hs.178098	NM_021804:Homo sapiens angiotensin I con	9.65
406687	M31126	Hs.352054	Hs.352054:pregnancy specific beta-1-glyc	9.52
428355	BE256452	Hs.2257	NM_000638:Homo sapiens vitronectin (seru	9.47
422281	M36803	Hs.346935	NM_000613:Homo sapiens hemopexin (HPX)	9.41
413585	AI133452	Hs.75431	NM_000509:Homo sapiens fibrinogen, gamma	9.39
422664	AA315933	Hs.120879	Hs.120879:Homo sapiens, clone MGC:32871	9.31
417931	W95642	Hs.82961	Hs.82961:Homo sapiens, clone MGC:22588 I	9.30

5	422487	AJ010901	Hs.198267	NM_018406:Homo sapiens mucin 4, tracheob	9.01
	413936	AF113676	Hs.297681	NM_000295:Homo sapiens serine (or cystei	8.99
	424687	J05070	Hs.151738	NM_004994:Homo sapiens matrix metallopro	8.80
	420344	BE463721	Hs.97101	NM_014373:Homo sapiens putative G protei	8.71
	446921	AB012113	Hs.16530	NM_002988:Homo sapiens small inducible c	8.67
	428470	AC002301	Hs.184507	Hs.184507:Homo sapiens, similar to Homol	8.47
	452594	AU076405	Hs.29981	Hs.29981:solute carrier family 26 (sulfa	8.47
	422310	AA316622	Hs.98370	(locuslink)NM_030522:Homo sapiens cytoch	8.43
10	421907	BE018556	Hs.109358	Hs.109358:ATPase, Class V, type 10B	8.34
	424326	NM_014479	Hs.145296	NM_014479:Homo sapiens ADAM-like, decysl	8.12
	435538	AB011540	Hs.4930	Hs.4930:low density lipoprotein receptor	8.09
	413881	L00190	Hs.75599	(locuslink)NM_000488:Homo sapiens serine	7.96
	443426	AF098158	Hs.9329	(locuslink)NM_012112:Homo sapiens chromo	7.92
15	436972	AA284679	Hs.25640	Hs.25640:claudin 3	7.89
	430677	Z26317	Hs.359784	NM_001943:Homo sapiens desmoglein 2 (DSG	7.87
	406632	W74001	Hs.55279	NM_002639:Homo sapiens serine (or cystei	7.71
	423803	NM_005709	Hs.132945	(locuslink)NM_005709:Homo sapiens PDZ-73	7.58
	430272	X04898	Hs.237658	Hs.237658:apolipoprotein A-II	7.48
20	451035	AU076785	Hs.430	NM_002670:Homo sapiens plastin 1 (I lsof	7.31
	422330	D30783	Hs.115263	NM_001432:Homo sapiens epiregulin (EREG)	7.31
	425976	C75094	Hs.334514	NM_025257:Homo sapiens chromosome 6 open	7.29
	411825	AK000334	Hs.352415	NM_017767:Homo sapiens solute carrier fa	7.23
	451917	AW391351	Hs.50820	Hs.50820:hypothetical cardiac/skeletal m	7.21
25	410418	D31382	Hs.63325	NM_019894:Homo sapiens transmembrane pro	7.12
	418318	U47732	Hs.84072	NM_004616:Homo sapiens transmembrane 4 s	7.12
	414617	AI339520	Hs.288817	(locuslink)NM_025130:Homo sapiens hypoth	7.10
	447342	AI199268	Hs.19322	Hs.19322:Homo sapiens, Similar to RIKEN	7.06
	452194	AI694413	Hs.373599	Hs.373599:EST	7.02
30	414816	Y13709	Hs.77399	NM_001265:Homo sapiens caudal type homeo	6.97
	417491	AW376842	Hs.1085	NM_004963:Homo sapiens guanylate cyclase	6.96
	423445	NM_014324	Hs.128749	NM_014324:Homo sapiens alpha-methylacyl-	6.96
	403220				6.95
35	415992	C05837	Hs.145807	Hs.145807:hypothetical protein FLJ13593	6.87
	449722	BE280074	Hs.23960	Hs.23960:cyclin B1	6.87
	414798	AI286323	Hs.97411	Hs.97411:hypothetical protein MGC12335	6.80
	415214	AI445236	Hs.125124	NM_004442:Homo sapiens EphB2 (EPHB2), tr	6.78
	411975	AI916058	Hs.144583	Hs.144583:Homo sapiens, clone IMAGE:3462	6.76
	422511	AU076442	Hs.117938	NM_000494:Homo sapiens collagen, type XV	6.66
40	408983	NM_000492	Hs.663	NM_000492:Homo sapiens cystic fibrosis t	6.65
	431301	AA502384	Hs.151529	Hs.151529:ESTs	6.62
	428970	BE276891	Hs.194691	NM_003979:Homo sapiens retinoic acid ind	6.59
	424273	W40460	Hs.144442	NM_003561:Homo sapiens phospholipase A2,	6.56
	431657	AI345227	Hs.105448	Hs.105448:protein kinase, lysine defic	6.54
45	431330	X69532	Hs.2777	NM_002215:Homo sapiens inter-alpha (glob	6.53
	425983	AK000226	Hs.165619	NM_031285:Homo sapiens mucin and cadheri	6.50
	408243	Y00787	Hs.624	NM_000584:Homo sapiens interleukin 8 (IL	6.47
	428187	AI687303	Hs.285529	Hs.285529:G protein-coupled receptor 49	6.46
	408704	AA056635	Hs.5366	NM_139053:Homo sapiens epidermal growth	6.45
50	428753	AW939252	Hs.192927	NM_017726:Homo sapiens protein phosphata	6.41
	426227	U87058	Hs.154299	(locuslink)NM_005242:Homo sapiens coagul	6.41
	419354	M62839	Hs.1252	NM_000042:Homo sapiens apolipoprotein H	6.27
	414987	AA524394	Hs.294022	NM_032865:Homo sapiens hypothetical prot	6.20
	422627	BE336857	Hs.118787	Hs.118787:transforming growth factor, be	6.19
55	407786	AA687538	Hs.38972	NM_005727:Homo sapiens tetraspan 1 (TSPA	6.19
	414809	AI434699	Hs.77356	Hs.77356:transferrin receptor (p90, CD71	6.18
	425280	U31519	Hs.1872	NM_002591:Homo sapiens phosphoenolpyruva	6.16
	432179	X75208	Hs.2913	NM_004443:Homo sapiens EphB3 (EPHB3), mR	6.16
	443957	AA521049	Hs.353013	Hs.353013:chromosome 20 open reading fra	6.15
60	426174	AA547959	Hs.115838	Hs.115838:ESTs	6.10
	430135	NM_000035	Hs.234234	NM_000035:Homo sapiens aldolase B, fruct	6.07
	420542	NM_000505	Hs.1321	NM_000505:Homo sapiens coagulation facto	6.06
	409453	AI885516	Hs.95612	Hs.95612:ESTs	6.06
	408482	NM_000676	Hs.45743	NM_000676:Homo sapiens adenosine A2b rec	6.03
65	444151	AW972917	Hs.128749	(locuslink)NM_014324:Homo sapiens alpha-	5.99
	444381	BE387335	Hs.283713	NM_138455:Homo sapiens collagen triple h	5.97
	421408	AI688223	Hs.91096	NM_052818:Homo sapiens tripartite motif	5.95
	430204	AA618335	Hs.356664	Hs.356664:hypothetical protein FLJ32334	5.92
70	443991	NM_002250	Hs.10082	NM_002250:Homo sapiens potassium interne	5.90
	428874	W32133	Hs.194366	Hs.194366:transferrin (prealbumin, amy	5.88
	408908	BE296227	Hs.250822	(locuslink)NM_003158:Homo sapiens serine	5.88
	411142	NM_014256	Hs.69009	NM_014256:Homo sapiens UDP-GlcNAc:betaGa	5.86
	452281	T93500	Hs.28792	Hs.28792:Homo sapiens cDNA FLJ11041 fis,	5.82
	412115	AK001763	Hs.73239	Hs.73239:hypothetical protein FLJ10901	5.77
75	421379	Y15221	Hs.103982	NM_005409:Homo sapiens small inducible c	5.76
	433083	AL042759	Hs.191762	Hs.191762:hypothetical protein MGC20258	5.75
	403218				5.74
80	412104	AW205197	Hs.240951	(locuslink)NM_033120:Homo sapiens naked	5.72
	449027	AI271216	Hs.22880	NM_005700:Homo sapiens dipeptidylpeptida	5.72
	429345	R11141	Hs.199695	Hs.199695:hypothetical protein MAC30	5.72
	414753	AF158255	Hs.77225	NM_006437:Homo sapiens ADP-ribosyltransf	5.72
	415000	AW025529	Hs.239812	Hs.239812:serologically defined breast c	5.71
	425206	NM_002153	Hs.165109	NM_002153:Homo sapiens hydroxysteroid (1	5.70
	432978	AF126743	Hs.279884	NM_013238:Homo sapiens DNAJ domain-conta	5.70

	409889	AW630041	Hs.56937	NM_021978:Homo sapiens suppression of tu	5.67
	414052	AW578849	Hs.283552	Hs.283552:hypothetical protein BC016153	5.67
	413916	N49813	Hs.75615	NM_000483:Homo sapiens apolipoprotein C-	5.63
5	418322	AA284166	Hs.84113	NM_005192:Homo sapiens cyclin-dependent	5.62
	433437	U20536	Hs.3280	NM_001226:Homo sapiens caspase 6, apopto	5.60
	424010	AL080188	Hs.137556	NM_033100:Homo sapiens MT-protocadherin	5.59
	438746	AI885815	Hs.184727	Hs.184727:ESTs, Weakly similar to T45738	5.58
	414590	NM_000506	Hs.76530	NM_000506:Homo sapiens coagulation facto	5.56
10	457001	J03258	Hs.2062	Hs.2062:vitamin D (1,25- dihydroxyvitami	5.56
	423164	AK000232	Hs.124835	NM_019062:Homo sapiens hypothetical prot	5.54
	409757	NM_001898	Hs.123114	NM_001898:Homo sapiens cystatin SN (CST1	5.53
	425397	J04088	Hs.156346	NM_001067:Homo sapiens topoisomerase (DN	5.53
	403221				5.52
15	420981	L40904	Hs.100724	NM_005037:Homo sapiens peroxisome profil	5.52
	417165	R80137	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	5.48
	419508	AW997939	Hs.90786	NM_003786:Homo sapiens ATP-binding casse	5.44
	410850	AW362867	Hs.302738	Hs.302738:Homo sapiens cDNA: FLJ21425 fi	5.42
	436251	BE515065	Hs.296585	(locuslink)NM_006392:Homo sapiens nucleo	5.41
20	430603	AA148164	Hs.247280	Hs.247280:chromosome 20 open reading fra	5.38
	450505	NM_004572	Hs.25051	NM_004572:Homo sapiens plakophilin 2 (PK	5.34
	422535	AA311914	Hs.154578	Hs.154578:Homo sapiens mRNA for FLJ00256	5.33
	441384	AA447849	Hs.288660	Hs.288660:Homo sapiens cDNA: FLJ22182 fi	5.32
	425834	NM_001639	Hs.1957	Hs.1957:amyloid P component, serum	5.31
25	430680	AW139724	Hs.168974	Hs.168974:ESTs	5.25
	432378	AI493046	Hs.146133	Hs.146133:ESTs	5.25
	419693	AA133749	Hs.301350	Hs.301350:FXFD domain-containing ion tra	5.24
	422163	AF027208	Hs.112360	Hs.112360:prominin-like 1 (mouse)	5.21
	447320	AI675419	Hs.164464	Hs.164464:Homo sapiens, clone MGC:23656	5.21
30	415927	AL120168	Hs.78919	NM_021083:Homo sapiens Kell blood group	5.21
	418203	X54942	Hs.83758	NM_001827:Homo sapiens CDC28 protein kin	5.20
	407944	R34008	Hs.239727	NM_024422:Homo sapiens desmocollin 2 (DS	5.20
	428289	M26301	Hs.2253	Hs.2253:complement component 2	5.19
	409231	AA446644	Hs.692	NM_002354:Homo sapiens tumor-associated	5.19
35	446051	BE048061	Hs.37054	Hs.37054:ephrin-A3	5.15
	432269	NM_002447	Hs.2942	Hs.2942:macrophage stimulating 1 recepto	5.13
	427557	NM_002659	Hs.179657	NM_002659:Homo sapiens plasminogen activ	5.11
	414639	X67055	Hs.76716	NM_002217:Homo sapiens pre-alpha (globul	5.09
	422765	AW409701	Hs.1578	NM_001168:Homo sapiens baculoviral IAP r	5.08
40	428479	Y00272	Hs.334562	NM_001786:Homo sapiens cell division cyc	5.08
	425873	NM_013390	Hs.160417	Hs.160417:transmembrane protein 2	5.07
	432575	AA553722	Hs.194346	Hs.194346:Sp1-2 protein	5.07
	409142	AL136877	Hs.50758	Hs.50758:SMC4 structural maintenance of	5.07
	427747	AW411425	Hs.180655	(locuslink)NM_004217:Homo sapiens serine	5.06
45	422609	Z46023	Hs.118721	NM_000434:Homo sapiens siradase 1 (lyso	5.06
	414361	AI086138	Hs.204044	Hs.204044:ESTs	5.04
	452940	AA029722	Hs.2173	NM_002033:Homo sapiens fucosyltransferas	5.03
	435849	BE305242	Hs.16098	Hs.16098:claudin 2	5.03
	411257	AA628967	Hs.115274	Hs.115274:Indian hedgehog homolog (Droso	5.01
50	416065	BE267931	Hs.78996	NM_002592:Homo sapiens proliferating cel	5.00
	406873	M34996	Hs.198253	Hs.198253:major histocompatibility compl	4.99
	451541	BE279383	Hs.26557	NM_007183:Homo sapiens plakophilin 3 (PK	4.99
	429833	NM_012079	Hs.288627	NM_012079:Homo sapiens diacylglycerol O-	4.98
	411393	AW797437	Hs.69771	NM_001710:Homo sapiens B-factor, properd	4.98
55	445109	AF039916	Hs.12330	NM_001247:Homo sapiens ectorucleoside tr	4.98
	431548	AI834273	Hs.9711	NM_017515:Homo sapiens novel protein (HS	4.97
	419574	AK001989	Hs.91165	Hs.91165:hypothetical protein FLJ11127	4.97
	428450	NM_014791	Hs.184339	NM_014791:Homo sapiens maternal embryoni	4.95
	431211	M86849	Hs.323733	Hs.323733:gap junction protein, beta 2,	4.95
60	437009	AF127026	Hs.5394	NM_005379:Homo sapiens myosin IA (MYO1A)	4.93
	439453	BE264974	Hs.6566	Hs.6566:thyroid hormone receptor interac	4.93
	430696	AA531276	Hs.59509	Hs.59509:ESTs, Weakly similar to similar	4.93
	431779	AW971178	Hs.268571	(locuslink)NM_001645:Homo sapiens apolip	4.92
	436469	AK001455	Hs.5198	Hs.5198:Down syndrome critical region ge	4.91
65	414108	AI267592	Hs.75761	NM_003137:Homo sapiens SFRS protein kina	4.91
	422539	AJ009936	Hs.118138	NM_033013:Homo sapiens nuclear receptor	4.89
	428024	Z29087	Hs.2236	Hs.2236:NIMA (never in mitosis gene a)-r	4.89
	428407	NM_003963	Hs.184194	NM_003963:Homo sapiens transmembrane 4 s	4.89
	407811	AW190902	Hs.40093	Hs.40093:cysteine knot superfamily 1, BM	4.88
	409162	H25530	Hs.50868	Hs.50868:solute carrier family 22 (organ	4.88
70	434370	AF130988	Hs.58346	NM_022336:Homo sapiens ectodysplasin 1,	4.87
	413753	U17760	Hs.75517	NM_000228:Homo sapiens laminin, beta 3 (4.87
	405484				4.87
	410639	BE269047	Hs.65234	(locuslink)NM_017895:Homo sapiens DEAD/H	4.87
75	428953	AA306610	Hs.348183	NM_003823:Homo sapiens tumor necrosis fa	4.86
	447343	AA256641	Hs.236894	Hs.236894:ESTs, Highly similar to S02392	4.83
	421462	AF016495	Hs.104624	NM_020980:Homo sapiens aquaporin 9 (AQP9	4.81
	415474	NM_014252	Hs.78457	NM_014252:Homo sapiens solute carrier fa	4.79
	415099	AI492170	Hs.77917	NM_006002:Homo sapiens ubiquitin carboxy	4.79
80	417115	AW952782	Hs.334612	NM_003094:Homo sapiens small nuclear rib	4.79
	426761	AI015709	Hs.172089	Hs.172089:pro-oncosis receptor inducing	4.78
	453751	R36762	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	4.77
	452721	AJ269529	Hs.301871	Hs.301871:solute carrier family 37 (glyc	4.76
	424905	NM_002497	Hs.153704	NM_002497:Homo sapiens NIMA (never in mi	4.76

	421943	BE616520	Hs.343912	NM_033504:Homo sapiens CAC-1 (CAC-1), mR	4.75
	400529				4.75
	407233	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	4.75
5	447472	AW207347	Hs.211101	Hs.211101:ESTs	4.74
	447966	AA340605	Hs.105887	(locuslink)NM_145252:Homo sapiens simila	4.72
	439963	AW247529	Hs.6793	Hs.6793:platelet-activating factor acely	4.72
	407103	AA424881	Hs.256301	Hs.256301:hypothetical protein MGC13170	4.70
	405556				4.70
10	421506	BE302796	Hs.105097	Hs.105097:thymidine kinase 1, soluble	4.70
	444700	NM_003645	Hs.11729	NM_003645:Homo sapiens fatty-acid-Coenzy	4.70
	443464	BE548446	Hs.321579	NM_021095:Homo sapiens solute carrier fa	4.70
	441623	AA315805	Hs.348710	Hs.348710:Homo sapiens, clone IMAGE:4242	4.70
	423068	M25529	Hs.123107	NM_002257:Homo sapiens kallikrein 1, ren	4.65
15	422714	AB018335	Hs.119387	NM_014698:Homo sapiens KIAA0792 gene pro	4.64
	403739				4.61
	427490	Z95152	Hs.178695	NM_002754:Homo sapiens mitogen-activated	4.61
	426088	AF038007	Hs.166196	NM_005603:Homo sapiens ATPase, Class I,	4.61
	412723	AA648459	Hs.335951	Hs.335951:hypothetical protein AF301222	4.60
20	424825	AF207069	Hs.153357	NM_001084:Homo sapiens procollagen-lysin	4.60
	447335	BE617695	Hs.286192	NM_032192:Homo sapiens protein phosphata	4.59
	424441	X14850	Hs.147097	Hs.147097:H2A histone family, member X	4.59
	432150	AK000224	Hs.272789	NM_017716:Homo sapiens membrane-spanning	4.59
	414695	BE439915	Hs.76913	Hs.76913:proteasome (prosome, macropain)	4.59
25	450737	AW007152	Hs.63325	Hs.63325:transmembrane protease, serine	4.58
	435327	BE301871	Hs.4867	Hs.4867:mannosyl (alpha-1,3-)glycoprote	4.57
	411263	BE297802	Hs.69360	NM_006845:Homo sapiens kinesin-like 6 (m	4.57
	408056	AA312329	Hs.42331	Hs.42331:ephrin-AA	4.55
	409964	AW368226	Hs.67928	Hs.67928:ESTs	4.54
30	417576	AA339449	Hs.82285	NM_000819:Homo sapiens phosphoribosylgly	4.54
	432407	AA221036		AF134164:Homo sapiens Human endogenous r	4.54
	439975	AW328081	Hs.6817	NM_033453:Homo sapiens inosine triphosph	4.53
	409213	U61412	Hs.51133	NM_005975:Homo sapiens PTK6 protein tyro	4.53
	403219				4.53
35	412974	R18978	Hs.75105	NM_006579:Homo sapiens emopamil binding	4.52
	408194	AA601038	Hs.191797	Hs.191797:ESTs	4.52
	422237	M13149	Hs.1498	NM_000412:Homo sapiens histidine-rich gl	4.51
	456906	AF117646	Hs.156637	NM_012116:Homo sapiens Cas-Br-M (murine)	4.51
	425123	AW205274	Hs.154695	NM_000303:Homo sapiens phosphomannomulas	4.51
40	425743	BE396495	Hs.159428	NM_138761:Homo sapiens BCL2-associated X	4.50
	406684	X16354	Hs.50964	(locuslink)NM_001712:Homo sapiens carcin	4.50
	439580	AF086401	Hs.293847	Hs.293847:ESTs	4.50
	411126	NM_001202	Hs.68879	(locuslink)NM_001202:Homo sapiens bone m	4.49
	428385	AF112213	Hs.184062	Hs.184062:chromosome 20 open reading fra	4.48
45	434263	N34895	Hs.79187	Hs.79187:coxsackie virus and adenovirus	4.47
	431945	AW000827	Hs.11962	NM_030766:Homo sapiens apoptosis regulat	4.47
	422616	BE300330	Hs.118725	NM_012248:Homo sapiens selenophosphate s	4.46
	452299	AW206330	Hs.355663	Hs.355663:ESTs	4.46
	414998	NM_002543	Hs.77729	NM_002543:Homo sapiens oxidised low dens	4.46
50	452888	AW955454	Hs.30942	NM_004093:Homo sapiens ephrin-B2 (EPNB2)	4.46
	442013	AA506476	Hs.375009	Hs.375009:Homo sapiens mRNA; cDNA DKFZp6	4.46
	450334	AF035959	Hs.24879	Hs.24879:phosphatidic acid phosphatase 1	4.45
	445417	AK001058	Hs.12680	Hs.12680:Homo sapiens cDNA FLJ10196 fis,	4.44
	433662	W07162	Hs.150826	NM_020387:Homo sapiens RAB25, member RAS	4.44
55	419559	Y07828	Hs.91096	NM_007028:Homo sapiens tripartite motif	4.44
	425860	L29339	Hs.1964	NM_000343:Homo sapiens solute carrier fa	4.43
	408847	AW290997	Hs.190153	Hs.190153:Homo sapiens cDNA FLJ33988 fis	4.43
	431836	AF178532	Hs.271411	NM_138992:Homo sapiens beta-site APP cle	4.43
	435777	AW419202	Hs.286192	NM_032192:Homo sapiens protein phosphata	4.42
60	422867	L32137	Hs.1584	Hs.1584:cartilage oligomeric matrix prot	4.41
	431350	AH192528	Hs.164537	Hs.164537:ESTs	4.39
	432593	AW301003	Hs.51483	Hs.51483:Homo sapiens, Similar to RIKEN	4.39
	421975	AW961017	Hs.6459	(locuslink)NM_024531:Homo sapiens hypoth	4.39
	412870	N22788	Hs.82407	NM_022059:Homo sapiens chemokine (C-X-C	4.38
65	412133	U83460	Hs.104557	NM_001859:Homo sapiens solute carrier fa	4.38
	422293	X94453	Hs.114366	Hs.114366:pyruvate-5-carboxylate synthet	4.38
	425998	AU076629	Hs.165950	NM_002011:Homo sapiens fibroblast growth	4.38
	453082	H18835	Hs.31608	(locuslink)NM_017636:Homo sapiens transi	4.37
	453111	AB014598	Hs.31720	NM_014799:Homo sapiens hephaestin (HEPH)	4.36
70	432677	NM_004482	Hs.278611	NM_004482:Homo sapiens UDP-N-acetyl-atph	4.36
	429271	AF039850	Hs.198515	NM_005224:Homo sapiens dead ringer-like	4.35
	426108	AA622037	Hs.166468	NM_004708:Homo sapiens programmed cell d	4.34
	412612	NM_000047	Hs.74131	NM_000047:Homo sapiens arylsulfatase E (4.34
	424865	AF011333	Hs.153563	NM_002349:Homo sapiens lymphocyte antigen	4.34
75	427239	BE270447	Hs.356512	Hs.356512:ESTs, Weakly similar to UBCA_A	4.33
	413254	U40272	Hs.75253	NM_004135:Homo sapiens isocitrate dehydr	4.32
	439659	AW970780	Hs.59483	Hs.59483:leucine-rich repeat-containing	4.32
	417526	AA568906	Hs.82240	Hs.82240:syntaxin 3A	4.32
	413186	AU077141	Hs.374548	Hs.374548:solute carrier family 16 (mono	4.31
80	436391	AJ227892	Hs.146274	Hs.146274:ESTs	4.30
	413219	AA878200	Hs.118727	Hs.118727:Homo sapiens cDNA FLJ33803 fis	4.29
	452017	AF109302	Hs.27495	Hs.27495:prostate cancer associated prot	4.29
	408113	T82427	Hs.194101	Hs.194101:Homo sapiens cDNA: FLJ20869 fi	4.29
	425638	AI916662	Hs.211577	(locuslink)NM_004986:Homo sapiens kinase	4.29

5	432636	AA340864	Hs.278562	NM_001307:Homo sapiens claudin 7 (CLDN7)	4.29
	412869	AA290712	Hs.82407	Hs.82407:chemokine (C-X-C motif) ligand	4.29
	443639	BE269042	Hs.9561	Hs.9561:proteasome (prosome, macropain)	4.28
	418245	AA088767	Hs.83883	NM_020182:Homo sapiens transmembrane, pr	4.27
	409636	AA305729	Hs.18272	(locustink)NM_030574:Homo sapiens solute	4.27
	408989	AW381666	Hs.49500	Hs.49500:KIAA0746 protein	4.27
	428023	AL038843	Hs.374530	Hs.374530:Homo sapiens cDNA: FLJ23802 fi	4.27
	410199	AW377424	Hs.205126	Hs.205126:Homo sapiens cDNA: FLJ22667 fi	4.24
10	431685	AW296135	Hs.267659	NM_006113:Homo sapiens vav 3 oncogene (V	4.24
	409956	AW103364	Hs.727	NM_002192:Homo sapiens inhibin, beta A (4.24
	413278	BE563085	Hs.833	Hs.833:interferon-stimulated protein, 15	4.23
	431193	AW749505	Hs.296770	Hs.296770:KIAA1719 protein	4.23
	436856	AI469355	Hs.127310	(locustink)NM_144624:Homo sapiens kinase	4.23
	456629	AW891965	Hs.367942	Hs.367942:Homo sapiens, clone IMAGE:4701	4.23
15	426682	AV660038	Hs.2056	Hs.2056:UDP glycosyltransferase 1 family	4.23
	418054	NM_002318	Hs.83354	NM_002318:Homo sapiens lysyl oxidase-like	4.22
	418526	BE019020	Hs.85838	NM_004207:Homo sapiens solute carrier fa	4.22
	437897	AA770561	Hs.146170	Hs.146170:hypothetical protein FLJ22969	4.21
20	435099	AC004770	Hs.4756	NM_004111:Homo sapiens flap structure-sp	4.21
	419378	R24922	Hs.90078	Hs.90078:nucleotide-sugar transporter si	4.21
	421585	U95626	Hs.302043	NM_003965:Homo sapiens chemokine (C-C mo	4.20
	420039	NM_004605	Hs.376147	Hs.376147:Homo sapiens cDNA FLJ39099 fis	4.20
	426427	M86699	Hs.169840	Hs.169840:TTK protein kinase	4.19
25	425263	NM_001197	Hs.155419	NM_001197:Homo sapiens BCL2-interactng	4.19
	426031	AA295251	Hs.166066	(locustink)NM_006697:Homo sapiens displa	4.19
	441085	AW136551	Hs.181245	Hs.181245:Homo sapiens cDNA FLJ12532 fis	4.19
	412939	AW411491	Hs.75069	Hs.75069:serine hydroxymethyltransferase	4.18
	430514	AA318501	Hs.241587	NM_021246:Homo sapiens lymphocyte antige	4.17
30	431842	NM_005764	Hs.271473	Hs.271473:epithelial protein up-regulate	4.17
	430387	AW372884	Hs.240770	Hs.240770:nuclear cap binding protein su	4.17
	404826				4.17
	414198	AW505308	Hs.75812	NM_004563:Homo sapiens phosphoenolpyruva	4.17
	434203	BE262677	Hs.283558	NM_018509:Homo sapiens hypothetical prot	4.17
35	426378	U80082	Hs.169600	Hs.169600:KIAA0826 protein	4.16
	433020	AI375726	Hs.227152	NM_016391:Homo sapiens hypothetical prot	4.16
	420319	AW406289	Hs.96593	NM_019034:Homo sapiens ras homolog gene	4.15
	446696	AF279265	Hs.298476	NM_022911:Homo sapiens solute carrier fa	4.15
	400130		Hs.155560	NM_001746:Homo sapiens calnexin (CANX)	4.14
40	431890	X17033	Hs.271986	NM_002203:Homo sapiens integrin, alpha 2	4.14
	425003	AF119046	Hs.154149	NM_014481:Homo sapiens APEX nuclease (ap	4.13
	417386	AL037228	Hs.301957	NM_018144:Homo sapiens Sec51 alpha form	4.13
	424837	BE276113	Hs.333034	NM_003491:Homo sapiens ARD1 homolog, N-a	4.13
	424534	D87682	Hs.150275	Hs.150275:KIAA0241 protein	4.13
45	445462	AA378776	Hs.288649	(locustink)NM_024051:Homo sapiens hypoth	4.12
	428471	X57348	Hs.184510	Hs.184510:stathmin	4.12
	409012	AL117435	Hs.49725	Hs.49725:OKFZP434I216 protein	4.11
	424154	AF026004	Hs.141660	NM_004366:Homo sapiens chloride channel	4.10
	400290	I18836	Hs.31608	(locustink)NM_017636:Homo sapiens transi	4.10
50	409152	AA176585	Hs.194346	Hs.194346:Spir-2 protein	4.10
	427333	AF067797	Hs.176658	NM_001169:Homo sapiens aquaporin 8 (AQP8	4.10
	413835	AI272727	Hs.249163	NM_024306:Homo sapiens fatty acid hydrox	4.09
	444664	N26362	Hs.11615	NM_016086:Homo sapiens map kinase phosph	4.09
	421959	AW751497	Hs.98370	NM_030622:Homo sapiens cytochrome P450,	4.09
55	407777	AA161071	Hs.71465	Hs.71465:squalene epoxidase	4.09
	414806	D14694	Hs.77329	(locustink)NM_014754:Homo sapiens phosph	4.08
	421190	U95031	Hs.102482	Hs.102482:mucin 5, subtype B, tracheobro	4.08
	408683	R58665	Hs.46847	NM_016614:Homo sapiens TRAF and TNF rece	4.08
	419488	AA316241	Hs.90691	NM_006993:Homo sapiens nucleophosmin/nuc	4.06
60	414907	X90725	Hs.77597	NM_000998:Homo sapiens ribosomal protein	4.06
	425247	NM_005940	Hs.155324	Hs.155324:matrix metalloproteinase 11 (s	4.06
	443802	AW504924	Hs.9805	Hs.9805:exportin 5	4.04
	411165	NM_000169	Hs.69089	NM_000169:Homo sapiens galactosidase, al	4.04
	434808	AF155108	Hs.256150	Hs.256150:NY-REN-41 antigen	4.04
65	428376	AF119665	Hs.184011	Hs.184011:pyrophosphatase (inorganic)	4.04
	418216	AA662240	Hs.283099	Hs.283099:AF15q14 protein	4.02
	436278	BE396290	Hs.5097	Hs.5097:synaptogyrin 2	4.02
	421910	NM_014586	Hs.109437	NM_014586:Homo sapiens hormonally upregu	4.02
	417866	AW067903	Hs.82772	Hs.82772:collagen, type XI, alpha 1	4.02
70	449057	AB037784	Hs.22941	Hs.22941:KIAA1363 protein	4.01
	414561	AI064813	Hs.195155	Hs.195155:solute carrier family 38, memb	4.00
	414812	X72755	Hs.77367	NM_002416:Homo sapiens monokine induced	4.00
	456362	AW973003	Hs.179909	(locustink)NM_024831:Homo sapiens nuclea	3.99
	431958	X63629	Hs.2877	NM_001793:Homo sapiens cadherin 3, type	3.98
75	418661	NM_001949	Hs.1189	NM_001949:Homo sapiens E2F transcription	3.98
	419092	J05581	Hs.89603	NM_002456:Homo sapiens mucin 1, transmem	3.98
	414013	AA766605	Hs.47099	NM_024642:Homo sapiens hypothetical prot	3.98
	409083	BE243834	Hs.50441	NM_015936:Homo sapiens CGI-04 protein (L	3.97
	445873	AA250970	Hs.251946	Hs.251946:Homo sapiens cDNA FLJ11840 fis	3.96
80	436485	X59135	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.96
	422164	NM_014312	Hs.112377	Hs.112377:cortical thymocyte receptor (X	3.95
	437016	AI076916	Hs.5398	Hs.5398:guanine monophosphate synthetase	3.94
	449437	AI702038	Hs.100057	Hs.100057:serine/threonine kinase 35	3.94
	446946	AI878932	Hs.317	NM_003286:Homo sapiens topoisomerase (DN	3.94

5	420162	BE378432	Hs.95577	NM_052984:Homo sapiens cyclin-dependent	3.94
	443180	R15875	Hs.258576	NM_012129:Homo sapiens claudin 12 (CLDN1	3.93
	418738	AW388633	Hs.6682	Hs.6682:solute carrier family 7, (cation	3.93
	409463	AA58165	Hs.17296	NM_023930:Homo sapiens hypothetical prot	3.92
	447495	AW401864	Hs.18720	NM_004208:Homo sapiens programmed cell d	3.92
10	448093	AW977382	Hs.15898	Hs.15898:2,4-dienoyl CoA reductase 2, pe	3.91
	426698	AA852773	Hs.334838	Hs.334838:KIAA1866 protein	3.90
	438485	W57578	Hs.378718	Hs.378718:Homo sapiens cDNA FLJ33433 fis	3.89
	436827	H72187	Hs.356668	(locuslink)NM_005274:Homo sapiens guanin	3.89
	407971	AI469117	Hs.62918	Hs.62918:CDK91 cell division cycle 91-i	3.89
15	440750				3.89
	448140	AF145761	Hs.20450	NM_020125:Homo sapiens B lymphocyt acti	3.89
	413880	AI660842	Hs.110915	NM_021258:Homo sapiens interleukin 22 re	3.89
	453258	AW293134	Hs.32597	NM_005977:Homo sapiens ring finger prote	3.89
	428788	AF082283	Hs.193516	NM_003921:Homo sapiens B-cell CLL/lympho	3.88
20	443044	N26522	Hs.8935	NM_014298:Homo sapiens quinolinate phosph	3.88
	413095	AA494359	Hs.30715	Hs.30715:potassium voltage-gated channel	3.88
	417129	AI381800	Hs.300684	Hs.300684:calcitonin gene-related peptid	3.87
	410268	AA316181	Hs.61635	NM_012449:Homo sapiens six transmembrane	3.87
	425047	U34038	Hs.154299	NM_005242:Homo sapiens coagulation facto	3.87
25	416084	L16991	Hs.79006	NM_012145:Homo sapiens deoxythymidylate	3.86
	449667	AB023227	Hs.23860	Hs.23860:KIAA1010 protein	3.86
	400298	AA032279	Hs.61635	Hs.61635:six transmembrane epithelial an	3.85
	407770	AW607831	Hs.38738	NM_014343:Homo sapiens claudin 15 (CLDN1	3.85
	418313	BE244231	Hs.84038	NM_015937:Homo sapiens CGI-06 protein (L	3.85
30	413380	AI904232	Hs.75323	Hs.75323:prohibitin	3.85
	452220	BE158006	Hs.212296	Hs.212296:ESTs	3.85
	413588	AA971014	Hs.75432	NM_000884:Homo sapiens IMP (inosine mono	3.85
	433658	L03678	Hs.156110	Hs.156110:immunoglobulin kappa constant	3.84
	428474	AB023182	Hs.184523	Hs.184523:serine/threonine kinase 38 lik	3.84
35	430237	AI272144	Hs.236522	Hs.236522:DKFZP434P106 protein	3.84
	414862	BE621310	Hs.923	Hs.923:single-stranded DNA binding prote	3.84
	437967	BE277414	Hs.5947	NM_005370:Homo sapiens mel transforming	3.84
	427318	AF186081	Hs.175783	NM_014579:Homo sapiens solute carrier fa	3.83
	459306	AW578452		AW578452:RC1-CT0262-030100-023-b07 CT025	3.83
40	446342	BE298665	Hs.14846	Hs.14846:Homo sapiens mRNA; cDNA DKFZp56	3.83
	432866	BE159028	Hs.279704	Hs.279704:chromatin accessibility comple	3.82
	434845	BE267057	Hs.325321	Hs.325321:WD repeat domain 18	3.82
	426514	BE616633	Hs.170195	Hs.170195:bone morphogenetic protein 7 (3.82
	410315	AI638871	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	3.82
45	421905	AI660247	Hs.32699	Hs.32699:Homo sapiens, Similar to RIKEN	3.81
	421481	AW391972	Hs.104696	Hs.104696:KIAA1324 protein	3.81
	445921	AW015211	Hs.153799	Hs.153799:Homo sapiens cDNA FLJ38333 fis	3.80
	414358	W70171	Hs.75939	NM_012474:Homo sapiens uridine monophosp	3.80
	457284	AF102850	Hs.227933	NM_013338:Homo sapiens Alg5, S. cerevisi	3.80
50	413813	M96956	Hs.75561	NM_003212:Homo sapiens teratocarcinoma-d	3.80
	414602	AW630088	Hs.76550	NM_052886:Homo sapiens mal, T-cell diffe	3.80
	410219	T98226	Hs.171952	Hs.171952:occludin	3.80
	407137	T97307			3.78
	430462	AI584156	Hs.105640	Hs.105640:hypothetical protein BC007772	3.78
55	432680	T47364	Hs.278613	(locuslink)NM_005532:Homo sapiens interf	3.78
	450010	AW293801	Hs.255052	Hs.255052:ESTs	3.78
	440334	BE276112	Hs.7165	NM_003804:Homo sapiens zinc finger prote	3.78
	440676	NM_004987	Hs.112378	(locuslink)NM_004987:Homo sapiens LIM an	3.77
	428072	BE258602	Hs.182368	NM_016292:Homo sapiens heat shock protei	3.77
60	407722	BE252241	Hs.38041	NM_003681:Homo sapiens pyridoxal (pyrido	3.77
	426459	AF151812	Hs.169992	NM_015966:Homo sapiens serologically def	3.77
	443323	BE560621	Hs.9222	Hs.9222:estrogen receptor binding site a	3.76
	406621	X57809	Hs.181125	Hs.181125:immunoglobulin lambda locus	3.76
	423198	M81933	Hs.1634	Hs.1634:cell division cycle 25A	3.76
65	428206	AB020643	Hs.183006	Hs.183006:likely homolog of mouse hepari	3.75
	447200	BE543146	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.74
	425209	AL049761	Hs.155140	NM_001895:Homo sapiens casein kinase 2,	3.74
	411950	T28407	Hs.81564	NM_002619:Homo sapiens platelet factor 4	3.74
	418681	AA287786	Hs.23449	Hs.23449:insulin receptor tyrosine kinas	3.74
70	421532	AW138207	Hs.146170	NM_022842:Homo sapiens hypothetical prot	3.74
	446291	BE397753	Hs.14623	Hs.14623:interferon, gamma-inducible pro	3.74
	435886	BE265839	Hs.12126	NM_018487:Homo sapiens hepatocellular ca	3.73
	417286	AA122237	Hs.81874	NM_002413:Homo sapiens microsomal glutat	3.73
	421743	T35958	Hs.107614	Hs.107614:DKFZP564I1171 protein	3.73
75	400419	AF084545		AF084545:Homo sapiens versican Vint isof	3.73
	421357	AK000609	Hs.103808	NM_017896:Homo sapiens chromosome 20 ope	3.73
	420665	AW469240	Hs.371581	Hs.371581:ESTs	3.73
	418703	NM_014448	Hs.87435	Hs.87435:Rho guanine exchange factor (GE	3.73
	452679	Z42387	Hs.83883	(locuslink)NM_020182:Homo sapiens transm	3.72
80	419743	AW408762	Hs.5957	Hs.5957:Homo sapiens clone 24416 mRNA se	3.72
	435730	AB020635	Hs.4984	Hs.4984:KIAA0828 protein	3.72
	431512	BE270734	Hs.2795	Hs.2795:lactate dehydrogenase A	3.72
	444006	BE395085	Hs.334762	(locuslink)NM_032832:Homo sapiens hypoth	3.72
	442875	BE623003	Hs.23625	Hs.23625:Homo sapiens clone TCCCTA00142	3.71
	413431	AW246428	Hs.75355	NM_003348:Homo sapiens ubiquitin-conjuga	3.71
	413950	AA249096	Hs.32793	Hs.32793:Homo sapiens cDNA FLJ31108 fis,	3.71
	411125	AA151647	Hs.68877	Hs.68877:cytochrome b-245, alpha polypep	3.71

5	406722	H27498	Hs.293441	Hs.293441:Homo sapiens SNC73 protein (SN	3.71
	418416	U11700	Hs.84999	NM_000053:Homo sapiens ATPase, Cu++ tran	3.71
	421038	AL080192	Hs.101282	Hs.101282:Homo sapiens mRNA; cDNA DKFZp4	3.70
	409327	L41162	Hs.53563	NM_001853:Homo sapiens collagen, type IX	3.70
	413476	U25849	Hs.75393	NM_004300:Homo sapiens acid phosphatase	3.70
	400846				3.70
	415003	M11437	Hs.77741	Hs.77741:kininogen	3.70
	408137	A1594131	Hs.29002	Hs.29002:KIAA1706 protein	3.70
10	418650	BE386750	Hs.86978	Hs.86978:prolyl endopeptidase	3.70
	413179	N99692	Hs.75227	NM_005002:Homo sapiens NADH dehydrogenas	3.69
	425843	BE313280	Hs.159627	NM_004632:Homo sapiens death associated	3.69
	432215	AU076609	Hs.2934	NM_001033:Homo sapiens ribonucleotide re	3.69
	413781	J05272	Hs.850	(locuslink)NM_000883:Homo sapiens IMP (i	3.69
	429344	R94038	Hs.374664	NM_005538:Homo sapiens inhibin, beta C (3.69
15	442315	AA173992	Hs.7956	Hs.7956:ESTs	3.68
	452875	BE275760	Hs.30928	NM_006114:Homo sapiens translocase of ou	3.68
	401179				3.67
	410174	AA305007	Hs.59461	Hs.59461:DKFZP434C245 protein	3.67
20	418558	AW082266	Hs.86131	Hs.86131:Fas (TNFRSF6)-associated via de	3.67
	440086	NM_005402	Hs.6906	NM_005402:Homo sapiens v-ral s/mian leuk	3.66
	409402	AF208234	Hs.695	Hs.695:cystatin B (stefin B)	3.66
	436014	AF281134	Hs.283741	NM_020158:Homo sapiens exosome component	3.66
	432633	AJ796390	Hs.210667	Hs.210667:ESTs	3.66
25	412599	AU076782	Hs.248267	(locuslink)NM_021126:Homo sapiens mercap	3.66
	453857	AL080235	Hs.35861	Hs.35861:Ras-induced senescence 1	3.65
	432211	BE274530	Hs.273333	Hs.273333:hypothetical protein FLJ10986	3.65
	430720	U85768	Hs.247838	NM_002991:Homo sapiens small inducible c	3.65
	432320	AW411066	Hs.274351	NM_016032:Homo sapiens zinc finger, DHHC	3.64
30	420186	NM_015925	Hs.95697	Hs.95697:liver-specific bHLH-Zip transcr	3.64
	441128	AA570256	Hs.348504	Hs.348504:hypothetical protein BC014072	3.64
	444184	T87841	Hs.282990	(locuslink)NM_033550:Homo sapiens chromo	3.64
	411678	AI907114	Hs.71465	NM_003129:Homo sapiens squalene epoxidase	3.63
	423750	AF165883	Hs.298229	NM_012394:Homo sapiens prefoldin 2 (PFND	3.62
35	412948	BE243313	Hs.334851	Hs.334851:LIM and SH3 protein 1	3.62
	452098	AI858183		BF755039:QV0-CT0583-181000-428-f07 CT058	3.62
	430024	AI808780	Hs.227730	NM_000210:Homo sapiens integrin, alpha 6	3.62
	416412	NM_014742	Hs.79305	Hs.79305:KIAA0255 gene product	3.61
	437712	X04588	Hs.85844	Hs.85844:neurotrophic tyrosine kinase, r	3.61
	400847				3.60
40	406671	AA129547	Hs.285754	NM_000245:Homo sapiens met proto-oncogen	3.60
	412641	M16660	Hs.74335	Hs.74335:heat shock 90kD protein 1, beta	3.60
	404854				3.60
	400448				3.60
45	453331	AI240665	Hs.352537	Hs.352537:Homo sapiens cDNA FLJ31066 fis	3.60
	441406	Z45957	Hs.7837	Hs.7837:phosphoprotein regulated by mito	3.60
	417389	BE260964	Hs.82045	Hs.82045:midkine (neurite growth-promoti	3.59
	419607	R52557	Hs.91579	NM_033416:Homo sapiens similar to HYPOTH	3.59
	447250	AI878909	Hs.17883	NM_002707:Homo sapiens protein phosphata	3.59
50	446356	AI816736	Hs.14896	Hs.14896:zinc finger, DHHC domain contai	3.59
	431236	AV656840	Hs.285115	NM_001560:Homo sapiens interleukin 13 re	3.59
	426722	U53823	Hs.171952	NM_002538:Homo sapiens occludin (OCLN),	3.58
	420531	AI652069	Hs.98614	NM_004587:Homo sapiens ribosome binding	3.58
	416933	BE561850	Hs.80506	NM_003090:Homo sapiens small nuclear rib	3.57
55	447698	AI420156	Hs.326733	NM_052858:Homo sapiens similar to RIKEN	3.57
	434457	AF141332	Hs.200333	NM_018690:Homo sapiens apolipoprotein B4	3.57
	424241	AW995948	Hs.8364	Hs.8364:pyruvate dehydrogenase kinase, I	3.57
	452264	AU077013	Hs.28757	Hs.28757:transmembrane 9 superfamily mem	3.57
	420614	AL110291	Hs.99364	Hs.99364:abhydrolase domain containing 1	3.56
60	434224	AA380731	Hs.84	NM_000206:Homo sapiens Interleukin 2 rec	3.56
	425322	U63630	Hs.155637	NM_006904:Homo sapiens protein kinase, D	3.56
	438407	AI457122	Hs.129673	Hs.129673:eukaryotic translation initiat	3.56
	413859	AW992356	Hs.8364	Hs.8364:pyruvate dehydrogenase kinase, I	3.56
	427268	X78520	Hs.174139	NM_001829:Homo sapiens chloride channel	3.55
65	436127	W94824	Hs.11565	NM_080748:Homo sapiens chromosome 20 ope	3.55
	411704	AI499220	Hs.71573	(locuslink)NM_017988:Homo sapiens hypoth	3.55
	452700	AI859390	Hs.288940	NM_021259:Homo sapiens transmembrane pro	3.54
	418803	U50079	Hs.88556	NM_004964:Homo sapiens histone deacetyla	3.54
	453323	AF034102	Hs.32951	NM_001532:Homo sapiens solute carrier fa	3.54
70	422813	AV656571	Hs.121068	(locuslink)NM_003270:Homo sapiens transm	3.54
	452488	N74921	Hs.184389	Hs.184389:ESTs, Moderately similar to S1	3.54
	432268	BE311856	Hs.274230	Hs.274230:3'-phosphoadenosine 5'-phospho	3.54
	425811	AL039104	Hs.159557	NM_002266:Homo sapiens karyopherin alpha	3.53
	437741	BE561610	Hs.5809	NM_020470:Homo sapiens putative transmem	3.53
75	421802	BE261458	Hs.108408	(locuslink)NM_016022:Homo sapiens CGI-78	3.53
	428582	BE336699	Hs.185055	Hs.185055:BENE protein	3.53
	446147	AL133064	Hs.14051	(locuslink)NM_145698:Homo sapiens endoza	3.53
	408716	AI567839	Hs.151714	(locuslink)NM_033405:Homo sapiens perox	3.52
	450825	AC005954	Hs.25527	(locuslink)NM_014428:Homo sapiens tight	3.52
80	442007	AA301116	Hs.142838	NM_032390:Homo sapiens MKI67 (FHA domain	3.52
	453454	AW052006	Hs.374973	NM_004697:Homo sapiens PRP4 pre-mRNA pro	3.52
	421612	AF161254	Hs.106196	(locuslink)NM_016579:Homo sapiens BD6 an	3.51
	428371	AB012193	Hs.183874	NM_003589:Homo sapiens cullin 4A (CUL4A)	3.51
	421340	F07783	Hs.1369	NM_000574:Homo sapiens decay accelerat	3.50

	429023	NM_000312	Hs.2351	NM_000312:Homo sapiens protein C (inact)	3.50
	452862	AW378065	Hs.8687	Hs.8687:ESTs	3.50
	442893	BE018682	Hs.166196	Hs.166196:ATPase, Class I, type 8B, memb	3.50
	404240				3.50
5	424909	S78187	Hs.153752	(locuslink)NM_004358:Homo sapiens cell d	3.50
	429583	NM_006412	Hs.209119	NM_006412:Homo sapiens 1-acylglycerol-3-	3.50
	445937	AI452943	Hs.321231	(locuslink)NM_003779:Homo sapiens UDP-Ga	3.49
	424954	NM_000546	Hs.1846	NM_000546:Homo sapiens tumor protein p53	3.49
10	424142	AI678727	Hs.378970	Hs.378970:Homo sapiens cDNA FLJ35102 fis	3.49
	428028	U52112	Hs.182018	Hs.182018:interleukin-1 receptor-associat	3.49
	456534	X91195	Hs.100623	NM_138689:Homo sapiens protein phosphata	3.49
	424685	W21223	Hs.151734	Hs.151734:nuclear transport factor 2	3.49
	419170	BE002798	Hs.287850	NM_002219:Homo sapiens integral membrane	3.49
	439841	AF038961	Hs.6710	NM_004870:Homo sapiens mannosyl-P-dolicho	3.49
15	428390	AI640377	Hs.350077	NM_000982:Homo sapiens ribosomal protein	3.48
	430589	AJ002744	Hs.245315	NM_017423:Homo sapiens UDP-N-acetyl-alpha	3.48
	431183	NM_006855	Hs.250696	NM_006855:Homo sapiens KDEL (Lys-Asp-Glu	3.48
	422599	BE387202	Hs.118638	Hs.118638:non-metastatic cells 1, protei	3.48
	457635	AV660976	Hs.3569	Hs.3569:chromosome 20 open reading frame	3.48
20	419705	AW368634	Hs.154331	Hs.154331:ESTs	3.48
	454390	AB020713	Hs.56956	(locuslink)NM_024923:Homo sapiens hypoth	3.48
	402829				3.47
	451707	AW051061	Hs.60973	Hs.60973:Homo sapiens cDNA FLJ40829 fis,	3.47
25	433604	NM_013442	Hs.3439	Hs.3439:stomatin (EPB72)-like 2	3.47
	420085	AI741909	Hs.44680	Hs.44680:hypothetical protein FLJ20979	3.47
	437704	AA766142	Hs.131810	Hs.131810:Homo sapiens cDNA FLJ35976 fis	3.47
	439223	AW238299	Hs.250818	NM_025217:Homo sapiens UL16 binding prot	3.46
	452203	X57522	Hs.352018	NM_000593:Homo sapiens transporter 1, AT	3.46
30	450273	AW296454	Hs.24743	Hs.24743:hypothetical protein FLJ20171	3.46
	408089	H59799	Hs.42644	Hs.42644:thioredoxin-like 2	3.46
	446950	AA305800	Hs.5672	(locuslink)NM_030799:Homo sapiens golgi	3.46
	437379	AL359575	Hs.23765	Hs.23765:membrane metallo-endopeptidase-	3.45
	427581	NM_014788	Hs.179703	NM_014788:Homo sapiens tripartite motif	3.45
35	433627	AF078866	Hs.284296	NM_033161:Homo sapiens surfactant 4 (SURF4)	3.45
	400263		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.45
	433570	AI580053	Hs.109007	Hs.109007:Homo sapiens, Similar to LOC16	3.45
	410636	AA088177	Hs.172870	Hs.172870:KIAA1913 protein	3.45
	456950	AF111170	Hs.306165	Hs.306165:ESTs, Highly similar to unknow	3.44
40	432391	AI732374	Hs.339827	Hs.339827:ESTs, Weakly similar to protea	3.44
	428144	BE269243	Hs.182625	Hs.182625:VAMP (vesicle-associated membr	3.44
	417144	AA382104	Hs.81337	Hs.81337:lectin, galactoside-binding, so	3.44
	458778	AW451034	Hs.326525	NM_001669:Homo sapiens arylsulfatase D (3.44
	425274	BE281191	Hs.155462	Hs.155462:MCM6 minichromosome maintenanc	3.44
45	448913	AA194422	Hs.22584	NM_004999:Homo sapiens myosin VI (MYO6),	3.44
	448847	AI587180	Hs.110906	Hs.110906:hypothetical protein BC004501	3.44
	420166	AW732276	Hs.95583	NM_012339:Homo sapiens transmembrane 4 s	3.44
	412420	AL035668	Hs.73853	NM_001200:Homo sapiens bone morphogeneti	3.43
	424482	BE268621	Hs.149155	(locuslink)NM_003374:Homo sapiens voltag	3.43
	414186	U33446	Hs.75799	Hs.75799:protease, serine, 8 (proctasin)	3.43
50	422396	W21872	Hs.7907	(locuslink)NM_145059:Homo sapiens L-fuco	3.43
	428093	AW594506	Hs.104830	Hs.104830:ESTs	3.43
	428293	BE250944	Hs.183556	Hs.183556:solute carrier family 1 (neur	3.42
	445580	AF167572	Hs.12912	NM_006109:Homo sapiens SKB1 homolog (S.	3.42
55	442821	BE391929	Hs.8752	Hs.8752:transmembrane protein 4	3.42
	427597	D15049	Hs.179770	NM_002842:Homo sapiens protein tyrosine	3.42
	427648	AI376722	Hs.180062	Hs.180062:proteasome (prosome, macropain	3.41
	428734	BE303044	Hs.192023	NM_003757:Homo sapiens eukaryotic transl	3.41
	453902	BE502341	Hs.3402	NM_139177:Homo sapiens chromosome 17 ope	3.41
60	441565	AW953575	Hs.303125	Hs.303125:p53-induced protein PIGPC1	3.41
	414045	NM_002951	Hs.75722	NM_002951:Homo sapiens ribophornin II (RP	3.41
	423323	AI951628	Hs.127007	NM_003740:Homo sapiens potassium channel	3.41
	443303	U67319	Hs.9216	NM_033340:Homo sapiens caspase 7, apopto	3.41
	426268	AF083420	Hs.168913	NM_003576:Homo sapiens serine/threonine	3.40
	422256	M64673	Hs.1499	NM_005526:Homo sapiens heat shock transc	3.40
65	451129	BE072881		BE072881:RC2-BT0548-200300-012-e09 BT054	3.40
	400205		Hs.81848	NM_006265:Homo sapiens RAD21 homolog (S.	3.40
	428109	AW732918	Hs.182490	Hs.182490:leucine-rich PPR-motif contain	3.39
	448440	AA173467	Hs.62402	Hs.62402:p21/Cdc42/Rac1-activated kinase	3.39
70	426858	NM_004182	Hs.172791	NM_004182:Homo sapiens ubiquitously-expr	3.39
	417457	AA378907	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.39
	406363				3.39
	444758	AL044878	Hs.11899	NM_000859:Homo sapiens 3-hydroxy-3-methy	3.39
	423309	BE006775	Hs.126782	NM_014467:Homo sapiens sushi-repeat prot	3.38
75	426125	X87241	Hs.166994	Hs.166994:FAT tumor suppressor homolog 1	3.38
	452835	AK001269	Hs.30738	NM_018087:Homo sapiens hypothetical prot	3.38
	419493	AF001212	Hs.90744	Hs.90744:proteasome (prosome, macropain)	3.38
	457670	AF119666	Hs.23449	NM_018842:Homo sapiens insulin receptor	3.38
	400125		Hs.125078	(locuslink)NM_004152:Homo sapiens ornith	3.38
80	429404	NM_005738	Hs.10706	NM_005738:Homo sapiens ADP-ribosylation	3.37
	410293	AK000047	Hs.61960	NM_018992:Homo sapiens hypothetical prot	3.37
	434826	AF155661	Hs.22265	Hs.22265:pyruvate dehydrogenase phosphat	3.37
	423599	AI005664	Hs.31731	(locuslink)NM_012094:Homo sapiens peroxi	3.37
	427715	BE245274	Hs.180428	Hs.180428:KIAA1181 protein	3.37

5	446715	AI337735	Hs.173919	Hs.173919:ESTs, Weakly similar to neuron	3.36
	426788	U66615	Hs.172280	NM_003074:Homo sapiens SWI/SNF related,	3.36
	429747	M87507	Hs.2490	Hs.2490:caspase 1, apoptosis-related cys	3.36
	406698	X03068	Hs.73931	Hs.73931:major histocompatibility comple	3.36
	439778	AL109729	Hs.99384	Hs.99384:abhydrolase domain containing 1	3.36
	418862	BE550864	Hs.89399	NM_005176:Homo sapiens ATP synthase, H+	3.36
	421140	AA289741	Hs.102135	NM_006280:Homo sapiens signal sequence r	3.36
	451932	AA360954	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.36
10	449042	AW294985	Hs.30715	Hs.30715:potassium voltage-gated channel	3.36
	426746	J03626	Hs.2057	NM_000373:Homo sapiens uridine monophosp	3.36
	425725	NM_012243	Hs.159322	(locuslink)NM_012243:Homo sapiens solute	3.35
	444734	NM_001360	Hs.11806	NM_001360:Homo sapiens 7-dehydrocholesta	3.35
	436415	BE265254	Hs.343258	NM_006191:Homo sapiens proliferation-ass	3.35
15	457329	AI634860	Hs.359682	(locuslink)NM_016442:Homo sapiens type 1	3.35
	432169	Y00871	Hs.2910	NM_002765:Homo sapiens phosphoribosyl py	3.35
	412525	AA581439	Hs.152328	Hs.152328:ESTs	3.35
	416391	AI878927	Hs.79284	NM_002402:Homo sapiens mesoderm specific	3.35
	419193	D29643	Hs.34789	NM_005216:Homo sapiens dolichyl-diphosph	3.35
20	432065	AA401039	Hs.2903	Hs.2903:protein phosphatase 4 (formerly	3.34
	400262		Hs.75309	NM_001961:Homo sapiens eukaryotic transl	3.34
	423598	BE247600	Hs.377968	NM_020400:Homo sapiens G protein-coupled	3.34
	424291	AL120051	Hs.144700	NM_004429:Homo sapiens ephrin-B1 (EFNB1)	3.34
	450506	NM_004460	Hs.418	(locuslink)NM_004460:Homo sapiens fibrob	3.34
25	437296	AA350894	Hs.20281	Hs.20281:MAPK phosphatase-7	3.34
	431731	BE266322	Hs.211374	(locuslink)NM_145051:Homo sapiens hypoth	3.34
	425159	NM_004341	Hs.154868	NM_004341:Homo sapiens carbamoyl-phospha	3.34
	427349	AA360154	Hs.177415	(locuslink)NM_001997:Homo sapiens Finkel	3.34
	439246	AI980072	Hs.351474	Hs.351474:Homo sapiens cDNA FLJ30002 fis	3.34
30	448775	AB025237	Hs.388	NM_002452:Homo sapiens nudix (nucleoside	3.34
	407236	W79485	Hs.173960	Hs.173960:nuclear matrix protein NMP200	3.34
	445350	AF052112	Hs.12540	NM_006330:Homo sapiens lysophospholipase	3.34
	444706	AK000398	Hs.11747	(locuslink)NM_017798:Homo sapiens chromo	3.34
	429574	BE268321	Hs.208912	Hs.208912:hypothetical protein MGC861	3.33
35	427647	W19744	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.33
	415938	BE383507	Hs.78921	NM_003488:Homo sapiens A kinase (PRKA) a	3.33
	414271	AK000275	Hs.75871	(locuslink)NM_012408:Homo sapiens protei	3.33
	424394	BE277024	Hs.146381	Hs.146381:RNA binding motif protein, X c	3.33
	437186	AA338305	Hs.377816	Hs.377816:Homo sapiens cDNA FLJ36808 fis	3.32
40	430542	AI557486	Hs.119122	Hs.119122:ribosomal protein L13a	3.32
	444019	BE173977	Hs.10098	NM_019082:Homo sapiens putative nucleola	3.32
	434931	AW968941	Hs.166254	Hs.166254:likely ortholog of rat vacuole	3.32
	426158	NM_001982	Hs.199067	NM_001982:Homo sapiens v-erb-b2 erythro	3.32
	430393	BE185030	Hs.241305	(locuslink)NM_006470:Homo sapiens tripar	3.32
45	402104				3.32
	446620	AA128808	Hs.179902	(locuslink)NM_022109:Homo sapiens CDw92	3.32
	443425	AI056776	Hs.133397	Hs.133397:ESTs	3.32
	414883	AA926960	Hs.348669	Hs.348669:CDK28 protein kinase 1	3.31
50	413063	AL035737	Hs.75184	Hs.75184:chitinase 3-like 1 (cartilage g	3.31
	451564	AU076698	Hs.132760	(locuslink)NM_001467:Homo sapiens glucos	3.31
	437822	AW450485	Hs.4437	NM_000991:Homo sapiens ribosomal protein	3.31
	441866	BE464341	Hs.21201	Hs.21201:nectin 3	3.31
	438930	AW843633	Hs.343261	Hs.343261:histocompatibility (minor) 13	3.31
55	422192	AA305159	Hs.113019	NM_015931:Homo sapiens fts485 (LOC51066)	3.31
	446506	AI123118	Hs.15159	(locuslink)NM_016326:Homo sapiens chemok	3.31
	415323	BE269352	Hs.949	NM_000433:Homo sapiens neutrophil cyto	3.31
	449644	AW960707	Hs.148324	Hs.148324:ESTs	3.31
	422611	AA158177	Hs.118722	(locuslink)NM_004480:Homo sapiens fucosy	3.31
60	417640	D30857	Hs.82353	NM_006404:Homo sapiens protein C recepto	3.30
	428157	AI738719	Hs.198427	NM_000189:Homo sapiens hexokinase 2 (HK2	3.30
	447321	AW271217	Hs.281434	Hs.281434:Homo sapiens cDNA FLJ31373 fis	3.30
	450447	AF212223	Hs.25010	NM_018698:Homo sapiens hypothetical prot	3.30
	422691	NM_003365	Hs.119251	NM_003365:Homo sapiens ubiquinol-cytochr	3.30
65	426375	AK000597	Hs.169549	NM_017893:Homo sapiens sema domain, immu	3.30
	449230	BE613348	Hs.356392	Hs.356392:ESTs, Highly similar to S-ph	3.29
	424756	AW504657	Hs.152931	(locuslink)NM_002296:Homo sapiens lamin	3.29
	442772	AW503680	Hs.5957	Hs.5957:Homo sapiens clone 24416 mRNA se	3.29
	430281	AI878842	Hs.237924	NM_016016:Homo sapiens CGI-69 protein (L	3.29
	448153	Y10805	Hs.20521	NM_001536:Homo sapiens HMT1 hnRNP methyl	3.29
70	420332	NM_001756	Hs.1305	NM_001756:Homo sapiens serine (or cystei	3.29
	417691	AU076610	Hs.82399	NM_007357:Homo sapiens component of o6g	3.29
	412926	AI879076	Hs.75061	Hs.75061:macrophage myristoylated alanin	3.28
	427308	D26067	Hs.174905	Hs.174905:KIAA0033 protein	3.28
	432026	AA524545	Hs.224630	Hs.224630:Homo sapiens cDNA FLJ33318 fis	3.28
75	449199	AI990122	Hs.196988	Hs.196988:ESTs	3.28
	442739	NM_007274	Hs.8679	(locuslink)NM_007274:Homo sapiens cyto	3.28
	422051	AW327546	Hs.111024	(locuslink)NM_005984:Homo sapiens solute	3.28
	452714	AW770994	Hs.30340	Hs.30340:hypothetical protein KIAA1165	3.28
	431884	AA521246	Hs.210792	Hs.210792:Homo sapiens cDNA FLJ36591 fis	3.28
80	402260				3.28
	408686	AK000002	Hs.55879	(locuslink)NM_033450:Homo sapiens multidi	3.28
	409267	NM_012453	Hs.52515	NM_012453:Homo sapiens transducin (beta)	3.28
	447783	AF054178	Hs.19561	NM_005001:Homo sapiens NADH dehydrogenas	3.27
	426812	AF105365	Hs.172613	NM_006598:Homo sapiens solute carrier fa	3.27

	429671	BE379335	Hs.211594	Hs.211594:proteasome (prosome, macropain	3.27
	434521	NM_002267	Hs.3885	Hs.3885:karyopherin alpha 3 (importin al	3.27
	454128	AL031259	Hs.367900	Hs.367900:programmed cell death 2	3.27
5	445033	AV652402	Hs.72901	NM_078487:Homo sapiens cyclin-dependent	3.27
	448752	AA593867	Hs.300842	NM_024820:Homo sapiens KIAA1608 protein	3.26
	425221	AV649864	Hs.155188	NM_005642:Homo sapiens TAF7 RNA polymera	3.26
	440285	U29589	Hs.7138	NM_000740:Homo sapiens cholinergic recep	3.26
	413745	AW247252	Hs.75514	NM_000270:Homo sapiens nucleoside phosph	3.26
10	412338	AA151527	Hs.69485	(locuslink)NM_024661:Homo sapiens hypoth	3.26
	426520	BE545684	Hs.343566	Hs.343566:KIAA0251 protein	3.26
	427640	AF08293	Hs.180015	NM_001355:Homo sapiens D-dopachrome taut	3.26
	440943	AW082298	Hs.145161	NM_032331:Homo sapiens hypothetical prot	3.26
	425966	NM_001761	Hs.1973	NM_001761:Homo sapiens cyclin F (CCNF),	3.25
	416448	L13210	Hs.79339	NM_005567:Homo sapiens lectin, galactosi	3.25
15	449944	AF290512	Hs.58215	(locuslink)NM_033046:Homo sapiens rhotek	3.25
	424381	AA285249	Hs.146329	NM_007194:Homo sapiens CHK2 checkpoint h	3.25
	426784	U03749	Hs.172216	NM_001275:Homo sapiens chromogranin A (p	3.25
	420190	AI816209	Hs.95867	(locuslink)NM_024112:Homo sapiens chromo	3.25
	438085	R52518	Hs.7967	Hs.7967:ESTs, Weakly similar to extensin	3.24
20	419216	AU076718	Hs.164021	NM_002993:Homo sapiens small inducible c	3.24
	430154	AW583058	Hs.234726	NM_001085:Homo sapiens serine (or cystei	3.24
	458376	AB023179	Hs.9059	Hs.9059:KIAA0962 protein	3.24
	410600	AW575742	Hs.351676	Hs.351676:Homo sapiens cDNA FLJ25921 fis	3.24
25	420676	AI434780	Hs.4248	Hs.4248:Homo sapiens PP3781 mRNA, comple	3.24
	435640	AF220053	Hs.54960	NM_018468:Homo sapiens uncharacterized h	3.23
	427775	R26944	Hs.180777	Hs.180777:Homo sapiens mRNA; cDNA DKFZp5	3.23
	412600	L28824	Hs.74101	Hs.74101:spleen tyrosine kinase	3.23
	430250	NM_016929	Hs.283021	NM_016929:Homo sapiens chloride intracel	3.23
30	432871	NM_016142	Hs.279617	Hs.279617:hydroxysteroid (17-beta) dehyd	3.23
	432731	R31178	Hs.287820	Hs.287820:fibronectin 1	3.23
	410340	AW182833	Hs.112188	(locuslink)NM_021826:Homo sapiens hypoth	3.23
	410047	AI167810	Hs.379753	Hs.379753:Homo sapiens cDNA FLJ33176 fis	3.23
	430567	NM_003028	Hs.244542	Hs.244542:Homo sapiens cDNA FLJ38908 fis	3.23
35	425907	AA365752	Hs.155965	Hs.155965:ESTs	3.23
	436075	BE090176	Hs.179902	NM_080546:Homo sapiens CDw92 antigen (CD	3.22
	403912				3.22
	429782	NM_005754	Hs.220689	Hs.220689:Ras-GTPase-activating protein	3.22
	416178	AI808527	Hs.192822	NM_030949:Homo sapiens protein phosphata	3.22
40	445229	BE276013	Hs.343828	Hs.343828:Homo sapiens mRNA; cDNA DKFZp7	3.22
	422030	X51416	Hs.110849	(locuslink)NM_004451:Homo sapiens estrogen	3.22
	409591	AA532963	Hs.9100	Hs.9100:hypothetical gene supported by A	3.22
	411531	AB014511	Hs.70604	Hs.70604:ATPase, Class II, type 9A	3.22
	414820	AA371931	Hs.77422	Hs.77422:proteolipid protein 2 (colonic	3.22
45	450770	AA019924	Hs.28803	Hs.28803:ESTs	3.22
	433233	AB040927	Hs.301804	Hs.301804:KIAA1494 protein	3.22
	414172	AW954324	Hs.75790	(locuslink)NM_002642:Homo sapiens phosph	3.21
	428781	AF164799	Hs.193384	Hs.193384:putative 28 kDa protein	3.21
	432078	BE314877	Hs.24553	(locuslink)NM_022369:Homo sapiens hypoth	3.21
50	454358	AW792876	Hs.288936	NM_031420:Homo sapiens mitochondrial rib	3.21
	447140	AF070537	Hs.17481	NM_138391:Homo sapiens hypothetical prot	3.21
	409132	AJ224538	Hs.50732	NM_005399:Homo sapiens protein kinase, A	3.21
	400836				3.20
	420281	AI623693	Hs.323494	(locuslink)NM_017964:Homo sapiens hypoth	3.20
55	414343	AL036166	Hs.75914	NM_006815:Homo sapiens coated vesicle me	3.20
	447096	BE539199	Hs.62112	(locuslink)NM_003457:Homo sapiens zinc f	3.20
	412276	BE262621	Hs.73798	Hs.73798:macrophage migration inhibitory	3.20
	425261	BE385099	Hs.355814	Hs.355814:Homo sapiens clone IMAGE:29333	3.20
	407736	N41744	Hs.349326	Hs.349326:Homo sapiens cDNA FLJ30677 fis	3.20
60	400845				3.20
	407082	Z47055			3.20
	452012	AA307703	Hs.279766	(locuslink)NM_012310:Homo sapiens kinase	3.20
	403217				3.20
	414249	AI797994	Hs.279929	(locuslink)NM_017510:Homo sapiens gp25L2	3.19
65	431243	U46455	Hs.252189	NM_002999:Homo sapiens syndecan 4 (amphi	3.19
	417777	AB23763	Hs.7055	Hs.7055:Homo sapiens cDNA FLJ33420 fis,	3.19
	457274	AW674193	Hs.227152	NM_016391:Homo sapiens hypothetical prot	3.19
	445139	AB037848	Hs.12365	Hs.12365:synaptotagmin XIII	3.19
	430280	AA361258	Hs.237868	Hs.237868:Homo sapiens mRNA; cDNA DKFZp6	3.19
70	422197	AW974265	Hs.111632	Hs.111632:Lsm3 protein	3.19
	422938	NM_001809	Hs.1594	NM_001809:Homo sapiens centromere protei	3.18
	435575	AF213457	Hs.44234	NM_018965:Homo sapiens triggering recept	3.18
	449704	AK000733	Hs.23900	Hs.23900:Rac GTPase activating protein 1	3.18
	426925	NM_001196	Hs.172694	Hs.172694:BH3 interacting domain death a	3.18
75	414814	D14697	Hs.77393	(locuslink)NM_002004:Homo sapiens farnes	3.18
	405387				3.18
	444108	R55784	Hs.140942	Hs.140942:Homo sapiens cDNA FLJ38396 fis	3.18
	424089	AL036662	Hs.144949	Hs.144949:ESTs	3.17
80	414788	X78342	Hs.77313	Hs.77313:cyclin-dependent kinase (CDC2-I	3.17
	424927	AW973666	Hs.153850	Hs.153850:hypothetical protein C321D2.4	3.17
	451452	BE560065	Hs.26433	NM_001382:Homo sapiens dolichyl-phosphat	3.17
	426924	BE222542	Hs.128782	Hs.128782:Homo sapiens cDNA FLJ31512 fis	3.17
	447032	AK000310	Hs.17138	(locuslink)NM_017755:Homo sapiens hypoth	3.17
	410683	AA194952	Hs.36093	Hs.36093:Homo sapiens cDNA FLJ12885 fis,	3.17

5	415402	AA164687	Hs.177576	Hs.177576:mannosyl (alpha-1,3)-glycopro	3.17
	451032	W03692	Hs.323079	Hs.323079:Homo sapiens mRNA; cDNA DKFZp5	3.17
	412146	M92444	Hs.73722	Hs.73722:APEX nuclease (multifunctional	3.17
	417018	M16038	Hs.80887	Hs.80887:y-yes-1 Yamaguchi sarcoma viral	3.16
	425244	AK002127	Hs.155313	NM_022105:Homo sapiens death associated	3.16
	417878	U90916	Hs.82845	Hs.82845:Homo sapiens cDNA: FLJ21930 fis	3.16
	426675	AW084791	Hs.133122	Hs.133122:hypothetical protein FLJ14524	3.16
	432728	NM_006979	Hs.278721	NM_006979:Homo sapiens HLA class II regi	3.16
10	442643	U82756	Hs.374973	(locuslink)NM_004697:Homo sapiens PRP4 p	3.16
	418462	BE001596	Hs.85266	Hs.85266:Integrin, beta 4	3.16
	429922	Z97630	Hs.226117	NM_005318:Homo sapiens H1 histone family	3.16
	429556	AW139399	Hs.314807	Hs.314807:hypothetical protein MGC2655	3.15
	418127	BE243982	Hs.83532	(locuslink)NM_002389:Homo sapiens membra	3.15
15	416293	BE244454	Hs.79162	Hs.79162:structure specific recognition	3.15
	435968	AW161481	Hs.111577	(locuslink)NM_030926:Homo sapiens Integr	3.15
	414702	L22005	Hs.76932	NM_004359:Homo sapiens cell division cyc	3.15
	437672	AW748265	Hs.5741	NM_016230:Homo sapiens flavohemoprotein	3.15
	435750	AB029012	Hs.4990	Hs.4990:KIAA1089 protein	3.14
20	432710	AA609685	Hs.278672	NM_005898:Homo sapiens membrane componen	3.14
	407961	AW672939	Hs.41694	Hs.41694:origin recognition complex, sub	3.14
	438203	BE540090	Hs.7345	Hs.7345:MAD1 mitotic arrest deficient-II	3.14
	426410	BE298446	Hs.305890	NM_138578:Homo sapiens BCL2-like 1 (BCL2	3.14
	422282	AF019225	Hs.114309	(locuslink)NM_003661:Homo sapiens apolip	3.14
25	450295	AI766732	Hs.210528	Hs.210628:ESTs	3.14
	413900	AW409747	Hs.75612	NM_006819:Homo sapiens stress-induced-ph	3.13
	452695	AW780199	Hs.30327	NM_003668:Homo sapiens mitogen-activated	3.13
	407797	AK000524	Hs.39850	Hs.39850:uridine kinase-like 1	3.13
	412006	AW451618	Hs.290216	Hs.290216:ESTs	3.13
30	424247	X14008	Hs.234734	NM_000239:Homo sapiens lysozyme (renal a	3.13
	447627	AF090922	Hs.152738	NM_016050:Homo sapiens mitochondrial rib	3.13
	422753	AI928995	Hs.1575	Hs.1575:small nuclear ribonucleoprotein	3.12
	441321	H17182	Hs.7771	NM_007273:Homo sapiens repressor of estr	3.12
	411358	R47479	Hs.94761	Hs.94761:KIAA1691 protein	3.12
35	438444	AI064707	Hs.301226	Hs.301226:Homo sapiens, clone IMAGE:3456	3.12
	424727	AW590378	Hs.378965	Hs.378965:Homo sapiens cDNA FLJ37658 fis	3.12
	435975	AL118990	Hs.373554	(locuslink)NM_130786:Homo sapiens alpha-	3.12
	426680	AA320160	Hs.171811	NM_001625:Homo sapiens adenylate kinase	3.12
40	412326	R07566	Hs.73817	NM_002983:Homo sapiens small inducible c	3.12
	409220	BE243323	Hs.51233	(locuslink)NM_003842:Homo sapiens tumor	3.12
	428699	AW578252	Hs.190161	Hs.190161:LR8 protein	3.12
	422675	BE018517	Hs.119140	NM_001970:Homo sapiens eukaryotic transl	3.12
	444301	AK000136	Hs.10760	NM_017680:Homo sapiens asporin (LRR clas	3.12
	409932	AI376750	Hs.57600	NM_001283:Homo sapiens adaptor-related p	3.12
45	419152	L12711	Hs.89643	(locuslink)NM_001064:Homo sapiens transk	3.12
	410240	AL157424	Hs.61289	Hs.61289:synaptotagmin 2	3.12
	413073	AL038165	Hs.75187	NM_014765:Homo sapiens translocase of ou	3.11
	406865	AI025931	Hs.181357	Hs.181357:lamrin receptor 1 (67kD, ribo	3.11
	405203				3.11
50	441028	AI333660	Hs.17558	Hs.17558:Homo sapiens, clone IMAGE:40704	3.11
	417211	T97617	Hs.269092	Hs.269092:ESTs	3.11
	421684	BE281591	Hs.105768	NM_018120:Homo sapiens hypothetical prot	3.11
	429824	AA296363	Hs.121520	Hs.121520:Homo sapiens cDNA FLJ35792 fis	3.11
	426234	BE314534	Hs.168159	Hs.168159:bifunctional apoptosis regulat	3.11
55	408606	H69912	Hs.48269	NM_003384:Homo sapiens vaccinia related	3.10
	417821	BE245149	Hs.82643	NM_002822:Homo sapiens protein tyrosine	3.10
	416976	BE243985	Hs.80680	Hs.80680:major vault protein	3.10
	410013	AF067173	Hs.57904	Hs.57904:mago-nashi homolog, proliferati	3.10
	429597	NM_003816	Hs.2442	Hs.2442:a disintegrin and metalloprotein	3.10
60	453518	AW503205	Hs.27268	Hs.27268:Homo sapiens cDNA: FLJ21933 fis	3.10
	429238	NM_002849	Hs.198288	NM_002849:Homo sapiens protein tyrosine	3.10
	433409	AI278802	Hs.25661	Hs.25661:ESTs, Moderately similar to hyp	3.10
	426440	BE382756	Hs.169902	NM_006516:Homo sapiens solute carrier fa	3.10
	435472	AW972330	Hs.283022	NM_018643:Homo sapiens triggering recept	3.10
65	427609	AK000436	Hs.179791	NM_017817:Homo sapiens RAB20, member RAS	3.10
	408201	AK000568	Hs.43654	NM_017882:Homo sapiens ceroid-lipofuscin	3.10
	418181	U37012	Hs.83727	NM_013291:Homo sapiens cleavage and poly	3.10
	445176	AI878907	Hs.12379	NM_001419:Homo sapiens ELAV (embryonic l	3.10
	436906	H95980	Hs.181244	Hs.181244:major histocompatibility compl	3.10
70	427337	Z46223	Hs.176663	NM_000569:Homo sapiens Fc fragment of Ig	3.10
	433435	BE545277	Hs.340959	NM_005726:Homo sapiens Ts translation el	3.09
	408150	BE620274	Hs.43112	Hs.43112:Homo sapiens mRNA; cDNA DKFZp43	3.09
	431738	AW237726	Hs.288549	NM_032828:Homo sapiens ubiquitin UBF-4	3.09
	449703	H61001	Hs.171802	Hs.171802:Homo sapiens, clone IMAGE:3956	3.09
75	423184	NM_004428	Hs.1624	NM_004428:Homo sapiens ephrin-A1 (EFNA1)	3.09
	400278		Hs.2280	NM_002950:Homo sapiens ribophorin I (RPN	3.09
	449051	AW961400	Hs.333526	NM_032339:Homo sapiens hypothetical prot	3.09
	428297	AA236291	Hs.183583	NM_030666:Homo sapiens serine (or cystei	3.09
	430066	AI929659	Hs.237825	Hs.237825:signal recognition particle 72	3.09
	428044	AA093322	Hs.301404	NM_006743:Homo sapiens RNA binding motif	3.09
80	426989	AI815206	Hs.100293	Hs.100293:O-linked N-acetylglucosamine (3.08
	447887	AA114050	Hs.211610	NM_001228:Homo sapiens caspase 8, apopto	3.08
	422010	AA302049	Hs.31181	Hs.31181:Homo sapiens cDNA: FLJ23230 fis	3.08
	444823	BE262989	Hs.12045	Hs.12045:C2I protein	3.08

	410668	BE379794	Hs.159551	NM_014452:Homo sapiens tumor necrosis fa	3.08
	415173	AW501735	Hs.180059	Hs.180059:Homo sapiens cDNA FLJ31360 fis	3.08
	419757	AA773820	Hs.63970	Hs.63970:ESTs	3.08
5	427725	U66839	Hs.180533	NM_002756:Homo sapiens mitogen-activated	3.08
	424408	AI754813	Hs.146428	Hs.146428:collagen, type V, alpha 1	3.08
	453914	NM_000507	Hs.574	NM_000507:Homo sapiens fructose-1,6-bisph	3.08
	420187	AK001714	Hs.95744	NM_019028:Homo sapiens hypothetical prot	3.08
	431498	AK001777	Hs.258551	NM_012100:Homo sapiens aspartyl aminopep	3.07
10	411423	AW845987	Hs.68864	(locuslink)NM_139248:Homo sapiens membra	3.07
	449954	AA641636	Hs.37477	Hs.37477:ESTs, Weakly similar to T46220	3.07
	423671	AW860155	Hs.234101	Hs.234101:Homo sapiens, similar to choli	3.07
	448719	AA033627	Hs.21858	Hs.21858:serine (or cysteine) proteinase	3.07
	451455	AI937227	Hs.8821	NM_021175:Homo sapiens hepcidin antidiur	3.07
15	450876	AF189062	Hs.285976	(locuslink)NM_013384:Homo sapiens LAG1 I	3.07
	432465	D56165	Hs.275163	NM_002512:Homo sapiens non-metastatic ce	3.07
	421808	AK000157	Hs.108502	NM_017688:Homo sapiens hypothetical prot	3.07
	430014	H59354	Hs.374303	(locuslink)NM_144691:Homo sapiens hypoth	3.07
	436553	AW407157	Hs.181125	Hs.181125:immunoglobulin lambda locus	3.08
20	458814	AI498957	Hs.351937	Hs.351937:ribosomal protein, large P2	3.06
	450247	AF123303	Hs.24713	NM_013386:Homo sapiens hypothetical prot	3.06
	418062	AW630656	Hs.83383	NM_005406:Homo sapiens peroxiredoxin 4 (3.06
	407223	H96850		H96850:Yw03b12.s1 Soares melanocyte 2NbH	3.06
	418641	BE243136	Hs.86947	NM_001109:Homo sapiens a disintegrin and	3.06
25	450690	AA296696	Hs.333418	(locuslink)NM_014164:Homo sapiens FXVD d	3.06
	408124	U89337	Hs.42653	NM_004381:Homo sapiens cAMP responsive e	3.06
	435550	AI224456	Hs.324507	Hs.324507:hypothetical protein FLJ20986	3.06
	421779	AI879159	Hs.108219	NM_004626:Homo sapiens wingless-type MMT	3.05
	440246	W52010	Hs.191379	Hs.191379:ESTs	3.05
30	446770	AV660309	Hs.154986	Hs.154986:ESTs, Weakly similar to PLLP_H	3.05
	440708	AF038962	Hs.7361	Hs.7361:voltage-dependent anion channel	3.05
	425118	AU076611	Hs.154672	Hs.154672:methylene tetrahydrofolate deh	3.05
	453830	AA534295	Hs.20953	Hs.20953:hypothetical protein BC010003	3.05
	412867	AU076861	Hs.74637	Hs.74637:testis enhanced gene transcript	3.05
35	422032	AA476866	Hs.110857	NM_016310:Homo sapiens polymerase (RNA)	3.05
	441238	AI372555	Hs.322456	NM_032039:Homo sapiens hypothetical prot	3.05
	408524	D87942	Hs.46328	Hs.46328:fucosyltransferase 2 (secretor	3.05
	408102	U46351	Hs.621	Hs.621:lectin, galactoside-binding, solu	3.05
	430508	AI015435	Hs.104637	Hs.104637:solute carrier family 1 (gluta	3.04
40	432281	AK001239	Hs.274263	Hs.274263:hypothetical protein FLJ10377	3.04
	443883	AA114212	Hs.9930	Hs.9930:serine (or cysteine) proteinase	3.04
	423570	AW838306	Hs.128819	NM_018344:Homo sapiens hypothetical prot	3.04
	443653	AA137043	Hs.9663	NM_013374:Homo sapiens programmed cell d	3.04
	451711	AK000461	Hs.26890	NM_017829:Homo sapiens cat eye syndrome	3.04
45	444736	AA533491	Hs.23317	NM_032824:Homo sapiens hypothetical prot	3.04
	407687	AK002011	Hs.37558	NM_018339:Homo sapiens hypothetical prot	3.04
	423022	AA320525	Hs.201076	Hs.201076:ESTs	3.04
	453450	AW797627	Hs.347459	Hs.347459:Homo sapiens cDNA FLJ13900 fis	3.04
50	412708	R26830	Hs.106137	Hs.106137:Homo sapiens mRNA for OK/SW-CL	3.04
	448569	BE382657	Hs.21486	Hs.21486:signal transducer and activator	3.04
	443329	BE262943	Hs.9234	NM_032635:Homo sapiens seven transmembra	3.03
	439018	AW300887	Hs.26638	NM_031457:Homo sapiens membrane-spanning	3.03
	412627	BE391959	Hs.74276	Hs.74276:chloride intracellular channel	3.03
	444309	U83236	Hs.10803	Hs.10803:calcium and Integrin binding 1	3.03
55	412969	AI373162	Hs.75103	NM_003406:Homo sapiens tyrosine 3-monoox	3.03
	430354	AA954810	Hs.239784	Hs.239784:scribble	3.03
	414774	X02419	Hs.77274	NM_002658:Homo sapiens plasminogen activ	3.03
	450607	AL050373	Hs.25213	NM_015677:Homo sapiens hypothetical prot	3.03
	421179	U72664	Hs.148495	NM_002810:Homo sapiens proteasome (proso	3.02
60	451798	BE297567	Hs.27047	Hs.27047:hypothetical protein FLJ20392	3.02
	428428	AL037544	Hs.184298	NM_001799:Homo sapiens cyclin-dependent	3.02
	447656	NM_003726	Hs.19126	NM_003726:Homo sapiens src family associ	3.02
	436823	AW749865	Hs.117077	Hs.117077:zinc finger protein 264	3.02
	417896	AA379770	Hs.82890	Hs.82890:defender against cell death 1	3.02
65	444193	Y17801	Hs.10574	Hs.10574:solute carrier family 2, (facil	3.02
	418741	H83265	Hs.8881	Hs.8881:Homo sapiens cDNA FLJ32163 fis,	3.01
	414421	AI521130	Hs.355126	(locuslink)NM_144686:Homo sapiens hypoth	3.01
	424867	AI024860	Hs.153591	NM_005787:Homo sapiens Not56 (D. melanog	3.01
	442504	BE503373	Hs.334335	NM_022484:Homo sapiens hypothetical prot	3.01
70	437651	BE560672	Hs.13543	(locuslink)NM_145214:Homo sapiens tripar	3.01
	436540	BE397032	Hs.14468	NM_020230:Homo sapiens peter pan homolog	3.00
	438000	AI825880	Hs.5985	Hs.5985:non-kinase Cdc42 effector protei	3.00
	415697	AI365603	Hs.279696	Hs.279696:DKFZP566H1024 protein	3.00
	437469	AW753112	Hs.15514	Hs.15514:hypothetical protein MGC3260	3.00
75	436319	H90727	Hs.5123	Hs.5123:hypothetical protein BC008246	3.00
	450126	BE018138	Hs.24447	(locuslink)NM_005866:Homo sapiens type I	3.00
	445985	BE621800	Hs.29444	Hs.29444:putative small membrane protein	3.00
	406868	AA505445	Hs.300697	Hs.300697:immunoglobulin heavy constant	3.00
	424439	AA579635	Hs.1770	Hs.1770:ligase I, DNA, ATP-dependent	3.00
80	408452	AA054683	Hs.222728	Hs.222728:Homo sapiens cDNA FLJ39004 fis	3.00
	417831	H16423	Hs.82685	Hs.82685:CD47 antigen (Rb-related anti	3.00

TABLE 11B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	406685	Q_0	M18728
10	432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104 AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849 AA584918 BG959570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AJ075321 L13823 AA216700 BF771864 AW861859 BE537058 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928 AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
15	459306	223120_-4	AW578452
	452098	161393_1	BG028348 BF772844 H83066 AW817969 H90985 BF755039 AI858183
	451129	1455511_1	BE072881 AI762181 BE072946

TABLE 11C

20 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 25 NL_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
	406399	9256288	Minus	63448-63554
	403220	7630969	Plus	64338-64517
30	403218	7630969	Plus	58039-58149
	403221	7630969	Plus	66294-66438,66936-67124
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
	400529	9796988	Plus	138232-138423
35	405556	1552511	Plus	163497-163623,164715-164968,165369-16550
	403739	7630882	Plus	44563-44766,48209-48483,52255-52495
	403219	7630969	Plus	61858-61995
	404826	6572184	Plus	47726-48046
	400750	8119067	Plus	198991-199168,199316-199548
40	400846	9188605	Plus	39310-39474
	401179	9438647	Plus	113477-113893
	400847	9188605	Plus	44643-44835
	404854	7143420	Plus	14260-14537
	400448	9887687	Minus	177372-177674
45	404240	5002624	Minus	116132-116407,116553-116922
	402829	8918414	Plus	101532-101852,102006-102263
	405363	9256114	Plus	14403-14602,17000-17147,17241-17368
	402104	8119072	Plus	122409-122600
	402260	3398665	Minus	113765-113910,115653-115765,116808-11694
50	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
	400836	8954179	Plus	677-1188
	400845	9188605	Plus	34428-34612
	403217	7630969	Plus	54089-54163,55427-55623
	405387	6587915	Minus	3769-3833,5708-5895
55	405203	7230116	Plus	125295-125463

60 Table 12A lists about 1006 genes up-regulated in cervical cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" cervical cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" cervical cancer level was set to the 93rd percentile value amongst cervical cancers. The "average" normal adult tissue level was set to the 93rd percentile value amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 12A: 1006 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES

65 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 70 R1: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
75	402075	U19557	Hs.123035	squamous cell carcinoma antigen 2 (SCCA2)	81.1
	425650	NM_001944	Hs.1925	desmoglein 3 (permpigus vulgaris antigen)	43.6
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial coll	38.9
	435094	AI560129	Hs.329062	EST	30.3
	439606	W79123	Hs.58561	G protein-coupled receptor 87	28.8
80	452240	AI591147	Hs.61232	ESTs	27.0
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), actin bi	26.0
	417034	NM_006183	Hs.80962	neurotensin	25.5
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor, cl	24.5
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	23.7

	435505	AF200492	Hs.211238	interleukin-1 homolog 1	21.2
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	20.5
	418345	AJ001696	Hs.241407	serine proteinase inhibitor 13 (PI13; serpin	20.1
	452461	N78223	Hs.108106	transcription factor	19.8
5	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor, cl	19.2
	429432	AI678059	Hs.202676	synaptonemal complex protein 2	17.5
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-type,	16.4
	435243	AW292886	Hs.261373	hypothetical protein dJ434O14.3	16.3
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	16.2
10	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cys-X-C	15.9
	421373	AA808229	Hs.167771	ESTs	15.7
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolo	15.4
	441459	AI919142	Hs.214233	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	14.6
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	13.8
15	412719	AW016610	Hs.129911	ESTs	13.4
	417366	BE185289	Hs.1076	small proline-rich protein 1B (comitin)	13.3
	431753	X76029	Hs.2841	neuromedin U	13.2
	438817	AI023799	Hs.163242	ESTs	13.1
	404996			Target Exon	13.1
20	443211	AI128388	Hs.143655	ESTs	12.9
	414764	AW013887	Hs.72047	ESTs	12.9
	428618	AA885360	Hs.160199	Target CAT	12.7
	416651	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	12.7
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribosomal	12.6
25	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	12.6
	432666	AW204069	Hs.312716	ESTs, Weakly similar to unnamed protein produ	12.6
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaphyseal	12.6
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin D 24	12.3
30	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	12.2
	422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psoriasin 1)	11.6
	415989	AI267700	Hs.317584	ESTs	11.5
	452838	U65011	Hs.30743	preferentially expressed antigen in melanoma	11.4
	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	11.3
35	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeas	11.0
	449260	AA741180	Hs.29879	ESTs	11.0
	423049	X59373	Hs.188023	ESTs, Moderately similar to HXDA_HUMAN HOMEOB	10.7
	406467			Target Exon	10.5
	439926	AW014875	Hs.137007	ESTs	10.2
40	426368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin 1, pr	10.2
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fs, clone HEMBA10	10.2
	414422	AA147224	Hs.337232	Homeo box A13	10.2
	442660	AW138174	Hs.130651	ESTs	10.1
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu or sig	10.0
45	408572	AA055511	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN ALU SU	9.9
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDNA clo	9.8
	400195	NM_007057		NM_007057: Homo sapiens ZW10 interactor (ZW1N	9.8
	422426	W79117	Hs.58559	ESTs	9.7
	447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypothetical p	9.7
50	458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN ALU SU	9.4
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	9.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR/MRP)	9.4
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypothetical p	9.4
	419247	S65791	Hs.89764	fragile X mental retardation 1	9.1
	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fs, clone NT2RP40	9.1
55	420602	AF060877	Hs.99236	regulator of G-protein signalling 20	9.0
	428845	AL157579	Hs.153610	KIAA0751 gene product	9.0
	426427	M86699	Hs.169840	TTK protein kinase	9.0
	429538	BE182592	Hs.11261	small proline-rich protein 2A	9.0
	446232	AI281848	Hs.194691	retinoic acid induced 3	8.9
60	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	8.9
	439772	AL365406	Hs.10268	Homo sapiens mRNA full length insert cDNA clo	8.9
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related kinase	8.9
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	8.9
	430486	BE062109	Hs.241551	chloride channel, calcium activated, family m	8.7
65	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, h	8.7
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	8.7
	407642	AW178953		gb:MR0-ST0032-200899-001-b11 ST0032 Homo sapi	8.7
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfamily, m	8.7
	458027	L49054	Hs.85195	myeloid leukemia factor 1	8.4
70	424086	AI351010	Hs.102267	lysyl oxidase	8.3
	420092	AA814043	Hs.88045	ESTs	8.3
	449034	AI624049		gb:ts41a09.x1 NCL_CGAP_Ut1 Homo sapiens cDNA	8.3
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human, odont	8.2
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (melanom	8.2
75	436279	AW900372	Hs.180793	ESTs, Weakly similar to S65657 alpha-1C-adren	8.2
	440834	AA907027	Hs.128606	ESTs	8.2
	452724	R84810	Hs.30464	cyclin E2	8.1
	423849	AL157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (from c	8.1
80	410044	BE566742	Hs.58169	highly expressed in cancer, rich in leucine h	8.0
	429228	AI553633	Hs.337139	ESTs	7.9
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome region 14	7.9
	425710	AF030880	Hs.159275	solute carrier family, member 4	7.8
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	7.8

	435159	AA658879	Hs.116649	ESTs	7.7
	439232	N48590	Hs.46693	ESTs	7.7
	437616	AI797163	Hs.207954	ESTs	7.6
5	406554			Target Exon	7.4
	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated protein	7.4
	424098	AF077374	Hs.139322	small proline-rich protein 3	7.3
	418134	AA397769	Hs.86617	ESTs	7.2
	446364	AB006624	Hs.14912	KIAA0286 protein	7.2
10	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (yeast	7.1
	414148	BE084049		gb:PM0-BT0651-270400-003-f02 BT0651 Homo sapi	7.0
	429548	AW138872	Hs.135288	ESTs	7.0
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	7.0
	450192	AA263143	Hs.24596	RAD51-interacting protein	7.0
15	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophila ho	6.9
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone COL0454	6.9
	427821	AA470158	Hs.98202	ESTs	6.9
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794 prote	6.9
	425761	AW664214	Hs.195729	ESTs	6.9
20	450028	AI912012	Hs.200737	ESTs	6.8
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated protein N	6.8
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane glyco	6.8
	413573	AI733859	Hs.149089	ESTs	6.8
	422330	D30783	Hs.115263	epiregulin	6.8
25	454988	AW850140		gb:IL3-CT0219-261099-023-D11 CT0219 Homo sapi	6.8
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010317E2	6.8
	403471			Target Exon	6.7
	409041	AB033025	Hs.50081	KIAA1199 protein	6.7
30	407839	AA045144	Hs.161566	ESTs	6.6
	415652	T79213	Hs.272073	ESTs	6.6
	420900	AL045633	Hs.44269	ESTs	6.6
	444271	AW452569	Hs.149804	ESTs	6.6
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	6.5
	448693	AW004854	Hs.226320	hypothetical protein FLJ23537	6.5
35	431622	AW979271	Hs.293184	ESTs	6.5
	457405	AA504860		gb:ab03a10.s1 Stratagene fetal retina 937202	6.4
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 fis, clone NT2RP20	6.4
	414812	X72755	Hs.77367	monokine induced by gamma interferon	6.4
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxygenase	6.3
40	446435	AW205737	Hs.253582	ESTs	6.3
	421948	L42583	Hs.334309	keratin 6A	6.3
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	6.3
	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-protein	6.2
	406747	AI925153	Hs.217493	annexin A2	6.2
45	453884	AA355925	Hs.36232	KIAA0186 gene product	6.2
	423735	AA330259		gb:EST33963 Embryo, 12 week II Homo sapiens c	6.2
	421773	W69233	Hs.112457	ESTs	6.2
	457435	AW972024	Hs.142653	ret finger protein	6.1
50	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HEMBB10	6.1
	427043	AA397679	Hs.3991	ESTs	6.1
	409723	AW885757	Hs.257862	ESTs	6.1
	459462	AA481396	Hs.105167	ESTs	6.1
55	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif,	6.0
	427217	AA399272	Hs.144341	ESTs	6.0
	441820	AA969119	Hs.143502	ESTs, Weakly similar to envelope protein [H.s	6.0
	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferritin a	6.0
	430791	AA486293	Hs.272068	ESTs, Weakly similar to ALU3_HUMAN ALU SUBFAM	5.9
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein [H.s	5.9
60	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	5.9
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced prote	5.9
	414299	AA142989	Hs.71730	ESTs	5.8
	439292	AA090421	Hs.5555	hypothetical protein MGC5347	5.8
	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin (140	5.8
	413625	AW451103	Hs.71371	ESTs	5.8
65	416049	AI970536	Hs.16603	hypothetical protein FLJ13163	5.8
	415064	AA159804	Hs.149305	hypothetical protein MGC2603	5.7
	425695	NM_005401	Hs.159238	protein tyrosine phosphatase, non-receptor ty	5.7
	451381	BE241831	Hs.172330	hypothetical protein MGC2705	5.7
	415900	Z43758	Hs.26037	ESTs	5.7
70	444478	W07318	Hs.240	M-phase phosphoprotein 1	5.7
	449611	AI970394	Hs.197075	ESTs	5.7
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo sapi	5.7
	438639	AI278360	Hs.31409	ESTs	5.7
	414972	BE263782	Hs.77695	KIAA0008 gene product	5.7
75	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-like 1	5.6
	428365	AA295331	Hs.183861	Homo sapiens cDNA FLJ20042 fis, clone COL0042	5.6
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	5.6
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein	5.5
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase 3)	5.5
80	451307	AW293207	Hs.211516	ESTs	5.5
	441531	AW291239	Hs.271111	ESTs	5.5
	418663	AK001100	Hs.41690	desmocollin 3	5.5
	410659	AI080175	Hs.68826	ESTs	5.5
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo sapi	5.5

5	431255	AA497043	Hs.115685	ESTs	5.5
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequence.	5.5
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	5.4
	418502	R99288	Hs.35152	ESTs	5.4
	440320	AA879294		gb:ntw85e09.s1 NCL_CGAP_Pr12 Homo sapiens cDNA	5.4
	439579	AF086400		gb:Homo sapiens full length insert cDNA clone	5.4
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7 (gale	5.4
	408536	AW381532	Hs.135188	ESTs	5.4
10	408758	NM_003686	Hs.47504	exonuclease 1	5.4
	451411	AA017492	Hs.135655	EST	5.4
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	5.3
	407853	AA336797	Hs.40499	clckopf (Xenopus laevis) homolog 1	5.3
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin 6)	5.2
15	420026	AI831190	Hs.166676	ESTs	5.2
	427356	AW023482	Hs.97849	ESTs	5.2
	420440	NM_002407	Hs.97644	mammaglobin 2	5.2
	430082	AW514083	Hs.190135	ESTs	5.2
	445259	AI798994	Hs.152923	ESTs	5.2
20	457345	AI699933	Hs.192175	ESTs	5.2
	453161	AA628608	Hs.61655	ESTs	5.2
	445019	AI205540	Hs.281295	ESTs	5.2
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	5.2
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH-ASSO	5.2
25	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	5.2
	443179	AI928402	Hs.6933	hypothetical protein FLJ12684	5.2
	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, choline, at	5.2
	441020	W79283	Hs.35962	ESTs	5.1
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 gene	5.1
30	419520	AB009303	Hs.90800	matrix metalloproteinase 16 (membrane-inserte	5.1
	430663	AA481269	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP)	5.1
	405547			NM_018833*:Homo sapiens transporter 2, ATP-bi	5.1
	435206	AI432364	Hs.160594	ESTs	5.1
	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	5.1
35	439223	AW238299	Hs.250618	UL16 binding protein 2	5.1
	413251	AI932903	Hs.211535	ESTs	5.1
	426320	W47596	Hs.169300	transforming growth factor, beta 2	5.1
	458829	AI557388		gb:PT2.1_6_G03.r tumor2 Homo sapiens cDNA 3,	5.0
40	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PR	5.0
	432473	AI202703	Hs.152414	ESTs	5.0
	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino acid	5.0
	423634	AW559908	Hs.1690	heparin-binding growth factor binding protein	5.0
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, protein-gl	5.0
	432867	AW016936	Hs.233364	ESTs	5.0
45	449448	D60730	Hs.57471	ESTs	5.0
	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (from c	4.9
	405657			C7000246:gij72477[pir][DVHY1C multidrug resis	4.9
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromosomes 1	4.9
	446704	AI337228	Hs.197083	ESTs	4.9
50	434376	AA631492	Hs.23921	hypothetical protein DKFZp547A023	4.9
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypothetical	4.9
	421155	H87879	Hs.102267	lysyl oxidase	4.9
	443335	T89697	Hs.16645	ESTs	4.9
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell growt	4.8
55	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-induc	4.8
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage elast	4.8
	441720	AI346487	Hs.28739	ESTs	4.8
	442980	AA857025	Hs.8878	kinesin-like 1	4.8
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase domain 12	4.8
60	417592	AA204664	Hs.182437	ESTs, Weakly similar to I54383 chromosome seg	4.8
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosyltran	4.8
	418939	AW630803	Hs.89497	lamin B1	4.7
	417235	AA810278	Hs.24250	ESTs	4.7
	411958	AA099020		gb:zn45h01.s1 Stratagene HeLa cell s3 937216	4.7
65	433858	N69243	Hs.192974	hypothetical protein FLJ12735	4.7
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	4.7
	418379	AA218940	Hs.137516	fidgelfin-like 1	4.7
	401747			Homo sapiens keratin 17 (KRT17)	4.7
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDNA do	4.7
70	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	4.7
	457465	AW301344	Hs.122908	DNA replication factor	4.6
	433159	AB035898	Hs.150587	kinesin-like protein 2	4.6
	412333	AW937485		gb:QV3-DT0044-221299-045-b09 DT0044 Homo sapi	4.6
	401137			Target Exon	4.6
75	401576			Target Exon	4.6
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone COL0667	4.6
	421978	AJ243662	Hs.110196	NICE-1 protein	4.6
	409728	AL137379	Hs.47125	hypothetical protein FLJ13912	4.6
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PLACE10	4.6
80	450510	AA010056	Hs.242998	ESTs	4.6
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	4.6
	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, type II	4.6
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino acid	4.5
	449416	AI651016	Hs.246311	ESTs	4.5

	416168	H23687		gb:yn72d12r1 Soares adult brain N2b5HB55Y Ho	4.5
	447033	AI357412	Hs.157601	ESTs	4.5
	446353	AI290919	Hs.153661	ESTs	4.5
5	443715	AI583187	Hs.9700	cyclin E1	4.5
	454707	AW814989		gb:MR1-ST0206-170400-024-g05 ST0206 Homo sapi	4.5
	435435	T89473	Hs.192328	ESTs	4.5
	412099	U64198	Hs.73165	interleukin 12 receptor, beta 2	4.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma c	4.4
10	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	4.4
	430919	AA489041	Hs.295448	ESTs	4.4
	435313	AI769400	Hs.189729	ESTs	4.4
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	4.4
	433322	H50621	Hs.134156	ESTs, Weakly similar to I38022 hypothetical p	4.4
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (p150)	4.4
15	408908	BE296227	Hs.250822	serine/threonine kinase 15	4.4
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated protein ho	4.4
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	4.4
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibitor, cl	4.4
20	418216	AA682240	Hs.283099	AF15q14 protein	4.4
	446252	AI283125	Hs.150009	ESTs	4.4
	447519	U46258	Hs.339665	ESTs	4.4
	425916	NM_006786	Hs.162200	urotensin 2	4.3
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalinin (10	4.3
25	416320	H47867	Hs.34024	ESTs	4.3
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth facto	4.3
	441582	BE550200	Hs.127197	ESTs	4.3
	414132	AI801235	Hs.48480	ESTs	4.3
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homology to	4.3
30	411835	U29343	Hs.72550	hyaluronan-mediated motility receptor (RHAMM)	4.3
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	4.3
	428613	AB037749	Hs.186928	KIAA1328 protein	4.3
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter tra	4.3
	447078	AW685727	Hs.301570	ESTs	4.3
35	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HEMBB10	4.3
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	4.3
	405708			Target Exon	4.3
	433405	AW157566	Hs.156892	ESTs	4.3
	456443	AW967500	Hs.133543	ESTs	4.3
40	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to M	4.2
	448621	AI097144	Hs.5250	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	4.2
	412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequence	4.2
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.2
45	455365	AW948343		gb:RC0-MT0015-130400-031-c01 MT0015 Homo sapi	4.2
	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypothetical p	4.2
	430134	BE380149	Hs.105223	ESTs, Weakly similar to T33188 hypothetical p	4.2
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	4.2
	427666	AI791495	Hs.180142	calmodulin-like skin protein	4.2
	444602	AI174456	Hs.271925	ESTs, Moderately similar to I38022 hypothetic	4.2
50	417791	AW965339	Hs.111471	ESTs	4.2
	444266	AI424984	Hs.125465	ESTs	4.2
	439394	AA149250	Hs.56105	ESTs	4.2
	457336	AW969657	Hs.291029	ESTs	4.2
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypothetical p	4.2
55	404440			NM_021048:Homo sapiens melanoma antigen, fami	4.2
	449228	AJ403107	Hs.148590	protein related with psoriasis	4.2
	437144	ALD49466	Hs.7859	ESTs	4.2
	448599	AW860912		gb:QV0-CT0387-170200-121-c05 CT0387 Homo sapi	4.2
	431810	X67155	Hs.270845	kinesin-like 5 (mitotic kinesin-like protein	4.2
60	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.2
	444361	W76027	Hs.23920	hypothetical protein FLJ11105	4.2
	458116	AW977549	Hs.47367	KIAA1785 protein	4.1
	444105	AW189097	Hs.166597	ESTs	4.1
	426010	AA136563	Hs.1975	hypothetical protein FLJ21007	4.1
65	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor, cl	4.1
	408096	BE250162	Hs.83765	dihydrofolate reductase	4.1
	457620	AA602711	Hs.335753	EST	4.1
	402048			Target Exon	4.1
	427025	AA397589	Hs.97523	ESTs	4.1
70	423515	AA327017	Hs.162204	ESTs	4.1
	423891	AK002042	Hs.134795	Homo sapiens cDNA FLJ11180 fis, clone PLACE10	4.1
	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo sapi	4.1
	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	4.1
	426642	AW068223	Hs.171581	ubiquitin C-terminal hydrolase UCH37	4.1
75	423738	AB002134	Hs.132195	atray trypsin-like protease	4.1
	448243	AW369771	Hs.52620	integrin, beta 8	4.1
	411559	BE144081		gb:MR0-HT0165-030200-007-d06 HT0165 Homo sapi	4.1
	423553	AA405635	Hs.96854	ESTs, Weakly similar to DYX_HUMAN CYTOPLASM	4.1
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	4.1
	424115	AA335497	Hs.293965	ESTs, Weakly similar to I38022 hypothetical p	4.1
80	432374	W69815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PLACE10	4.1
	424745	AA214618	Hs.152759	activator of S phase kinase	4.0
	433384	AI021992	Hs.124244	ESTs	4.0
	448995	AI613276	Hs.5662	guanine nucleotide binding protein (G protein	4.0

	448504	AI858128	Hs.171136	ESTs	4.0
	432009	AL137424	Hs.306458	Homo sapiens mRNA; cDNA DKFZp761G2123 (from c	4.0
	432441	AW292425	Hs.163484	ESTs	4.0
5	424794	M85545	Hs.210696	ESTs	4.0
	432184	AW971125		gb:EST383212 MAGE resequences, MAGL Homo sapi	4.0
	408321	AW405882	Hs.44205	coristatin	4.0
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like repeat d	4.0
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.0
10	447724	AW298375	Hs.24477	ESTs	4.0
	446155	AI553695	Hs.159422	Homo sapiens cDNA FLJ13997 fis, clone Y79AA10	4.0
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.0
	420252	AW270404	Hs.193161	ESTs	4.0
	412811	H06382	Hs.21400	ESTs	4.0
15	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA10	4.0
	438390	AI422017		gb:tf45f12.x1 NCI_CGAP_Brn23 Homo sapiens cDN	4.0
	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	4.0
	429500	AA460421	Hs.30875	ESTs	4.0
	421270	H56037	Hs.108146	ESTs	3.9
20	430733	AW975920	Hs.283361	ESTs	3.9
	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo sapi	3.9
	424131	AA335714	Hs.199665	ESTs	3.9
	457059	BE561665	Hs.177677	exosome component Rrp40	3.9
	424717	H03754	Hs.152213	wingless-type MMTV integration site family, m	3.9
25	404959			NM_025001*:Homo sapiens hypothetical protein	3.9
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	3.9
	428536	AI143139	Hs.2288	visinin-like 1	3.9
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H.sapi	3.9
	432757	AF113013	Hs.278919	PRO0806 protein	3.9
30	418686	Z36830	Hs.87258	annexin A8	3.9
	437845	AA769578	Hs.90488	ESTs	3.9
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein produ	3.9
	419312	AA831850	Hs.58149	hypothetical protein MGC14136	3.9
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member), pro	3.9
35	410553	AW016824	Hs.255527	hypothetical protein MGC14128	3.9
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.9
	438014	N71183	Hs.121806	Homo sapiens cDNA FLJ11971 fis, clone HEMBB10	3.9
	442163	AI791749	Hs.128896	ESTs	3.9
	438656	H85310	Hs.209456	ESTs, Weakly similar to NG22 [H.sapiens]	3.9
40	406560			ENSP0000016943*:CDNA	3.8
	407395	AF005082		gb:Homo sapiens skin-specific protein (xp33)	3.8
	404132			Target Exon	3.8
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	3.8
	439238	N47305	Hs.46668	ESTs	3.8
45	433289	AF005258		gb:Homo sapiens laminin alpha 3b chain mRNA,	3.8
	436149	AI754308	Hs.159452	ESTs	3.8
	446292	AF081497	Hs.279682	Rh type C glycoprotein	3.8
	444078	BE246919	Hs.10290	U5 snRNP-specific 40 kDa protein (hPrp8-bind	3.8
	405545			(MDR/TAP) (TAP2)	3.8
50	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequence	3.8
	409687	T51125	Hs.8493	ESTs	3.8
	407291	AA001464		gb:ze45b01.r1 Soares retina NZb4HR Homo sapie	3.8
	415532	R14780	Hs.12826	ESTs	3.8
	402047	AK001921	Hs.169575	hypothetical protein MGC2550	3.8
55	415317	Z43388		gb:HSC1AF121 normalized infant brain cDNA Hom	3.8
	438777	AA825487	Hs.142179	ESTs	3.8
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.7
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolysis bu	3.7
	405943			Target Exon	3.7
60	430686	NM_001942	Hs.2633	desmoglein 1	3.7
	458242	BE295688	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone HEP024	3.7
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	3.7
	418582	BE244318	Hs.213194	hypothetical protein MGC10895	3.7
	453900	AW003592	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAM	3.7
65	433849	BE465884	Hs.280728	ESTs	3.7
	449592	AI655494	Hs.195718	ESTs	3.7
	453028	AB006532	Hs.31442	RecQ protein-like 4	3.7
	435612	AA693537	Hs.321411	ESTs	3.7
	417742	R64719		gb:EST22d11 WATM1 Homo sapiens cDNA clone 22d	3.7
70	418735	N48769	Hs.44609	ESTs	3.7
	444707	AI188613	Hs.41690	desmocollin 3	3.7
	421508	NM_004833	Hs.105115	absent in melanoma 2	3.7
	450613	AI702055		gb:tt20g10.x1 NCI_CGAP_U11 Homo sapiens cDNA	3.7
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	3.7
	432837	AA310693	Hs.87329	HSPC072 protein	3.7
75	442353	BE379594	Hs.19136	ESTs, Moderately similar to ALU7_HUMAN ALU SU	3.7
	423441	R68649	Hs.278359	absent in melanoma 1 like	3.7
	449978	AI806335	Hs.200829	ESTs, Weakly similar to T30171 ninein - mouse	3.7
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo sapi	3.7
80	409582	R27430	Hs.271555	ESTs	3.6
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANTIGEN	3.6
	458446	AW394104	Hs.43744	ESTs, Moderately similar to I54374 gene NF2 p	3.6
	433040	H70423	Hs.300511	ESTs	3.6
	452193	AA987351	Hs.184993	ESTs	3.6

5	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed-rect	3.6
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.6
	459575	BE080825		gb:QV1-BT0631-180200-078-c08 BT0631 Homo sapi	3.6
	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	3.6
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	3.6
	417830	AW504786	Hs.122579	hypothetical protein FLJ10461	3.6
	427131	AA448460	Hs.112017	GE36 gene	3.6
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	3.6
10	420373	AW968228		gb:EST380198 MAGE resequences, MAGJ Homo sapi	3.6
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromosomes 2	3.6
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.6
	424639	AI917494	Hs.9812	Homo sapiens cDNA FLJ14388 fis, clone HEMBA10	3.6
	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	3.6
15	434321	AA629368		gb:zu78a11.s1 Soares_testis_NHT Homo sapiens	3.6
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic prot	3.6
	427335	AA448542	Hs.251677	G antigen 7B	3.6
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity	3.6
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	3.6
20	426749	AI623718	Hs.105618	ESTs	3.6
	443899	AW842283	Hs.79933	cyclin I	3.6
	440684	AI253123	Hs.127356	ESTs, Highly similar to S21424 nestin [H.sapi	3.6
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	3.6
	408591	AF015224	Hs.46452	mammaglobin 1	3.5
25	408867	AA497199	Hs.656	cell division cycle 25C	3.5
	428508	BE252383	Hs.184668	SB8131 protein	3.5
	431120	AA492588		gb:ng99c08.s1 NCL_CGAP_Thy1 Homo sapiens cDNA	3.5
	401780			NM_005557:Homo sapiens keratin 16 (focal non	3.5
	409695	AA296961		gb:EST112514 Adrenal gland tumor Homo sapiens	3.5
30	456671	AB011142	Hs.114293	KIAA0570 gene product	3.5
	412155	R38167	Hs.12449	Homo sapiens transmembrane protein HTMP10 (HT	3.5
	435244	N77221	Hs.187824	ESTs	3.5
	435246	AW450963	Hs.119991	ESTs	3.5
	431917	D16181	Hs.2868	peripheral myelin protein 2	3.5
35	443113	AI040686	Hs.132908	ESTs	3.5
	443341	AW631480	Hs.8688	ESTs	3.5
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.5
40	418347	AA216419		gb:nc16e03.s1 NCL_CGAP_Pr1 Homo sapiens cDNA	3.5
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo sapi	3.5
	408633	AW963372	Hs.46677	PRO2000 protein	3.5
	427878	CG5766	Hs.181022	CGI-07 protein	3.5
	419945	AW290975	Hs.118923	ESTs	3.5
	448372	AW445166	Hs.170802	ESTs	3.5
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen 1NFLS	3.5
45	411274	NM_002776	Hs.69423	kallikrein 10	3.5
	400666			NM_002425:Homo sapiens matrix metalloproteinase	3.5
	426920	AA393351	Hs.132121	ESTs	3.5
	402639			Target Exon	3.4
	454891	AW837349		gb:QV2-LT0038-270300-108-d12 LT0038 Homo sapi	3.4
50	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet-de	3.4
	456296	AA829976	Hs.239114	mannosidase, alpha, class 1A, member 2	3.4
	450650	T65617	Hs.101257	hypothetical protein MGC3295	3.4
	429274	AI379772	Hs.99206	ESTs	3.4
	430704	AW813091	Hs.335799	ESTs	3.4
55	419807	R77402		gb:y175f11.s1 Soares placenta Nb2HP Homo sapi	3.4
	451778	AI826131	Hs.71243	ESTs, Weakly similar to zinc finger protein [3.4
	430397	AI924533	Hs.105607	bicarbonate transporter related protein 1	3.4
	432113	AA935065	Hs.152385	ESTs	3.4
	449722	BE280074	Hs.23960	cyclin B1	3.4
60	455092	BE152428		gb:CM0-HT0323-151299-126-b04 HT0323 Homo sapi	3.4
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.4
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37kD)	3.4
	417009	AA191719	Hs.314714	ESTs	3.4
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moiety X	3.4
65	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen induci	3.4
	413219	AA878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PLACE20	3.4
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	3.4
	438993	AA828995		gb:pd77b08.s1 NCL_CGAP_Ov2 Homo sapiens cDNA	3.4
	403274			Target Exon	3.4
70	435360	AF105366	Hs.4876	solute carrier family 12 (potassium/chloride	3.4
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2 prote	3.4
	443462	AI054690	Hs.171176	ESTs	3.3
75	444910	AI201849		gb:qs76g04.x1 NCL_CGAP_Pr28 Homo sapiens cDNA	3.3
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (from c	3.3
	449101	AA205847	Hs.23016	G protein-coupled receptor	3.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	3.3
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone CAE066	3.3
	419751	AW195581	Hs.93121	KIAA0761 protein	3.3
80	404782			C7001692-gij5724096[gb]AAF26844.1 (AF195021	3.3
	415613	R20233		gb:yg18h11.s1 Soares infant brain 1NIB Homo s	3.3
	452198	AI097560	Hs.61210	ESTs, Weakly similar to I38022 hypothetical p	3.3
	406599			Target Exon	3.3
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	3.3

412879	BE092219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo sapi	3.3
421107	AA283822	Hs.55606	ESTs, Weakly similar to S47072 finger protein	3.3
436985	AA740946	Hs.150896	ESTs	3.3
443903	AI220547	Hs.135223	ESTs	3.3
432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp58600724 (from c	3.3
447153	AA805202	Hs.315562	ESTs	3.3
450769	AA057418	Hs.33654	ESTs	3.3
421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cys-X-C	3.3
402481			NM_001821*-Homo sapiens choroideremia-like (R	3.3
459394	BE409894	Hs.126522	Homo sapiens, clone MGC:16722, mRNA, complete	3.3
424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-1 [H.	3.3
417708	N74392	Hs.50495	ESTs	3.3
414869	AA157291	Hs.21479	ubiquitin 1	3.3
441690	R81733	Hs.33106	ESTs	3.3
414774	X02419	Hs.77274	plasminogen activator, urokinase	3.3
412246	AI160873	Hs.69233	zinc finger protein	3.3
412903	BE007967	Hs.155795	ESTs	3.3
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placental)	3.3
451177	AI969716	Hs.13034	ESTs	3.3
409990	AA079337		gb:zmm95b09.r1 Stratagene colon HT29 (937221)	3.3
418462	BE001596	Hs.85266	integrin, beta 4	3.3
424567	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92k	3.3
405196			C2000662*gi7512792 pir T12482 hypothetical	3.3
459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA libra	3.3
432917	NM_014125	Hs.279812	PRO0327 protein	3.3
448251	BE280486	Hs.84045	hypothetical protein FLJ20288	3.3
415025	AW207091	Hs.72307	ESTs	3.3
420218	AW958037	Hs.288	ribosomal protein L4	3.2
429594	AK001128	Hs.210297	Homo sapiens cDNA FLJ10266 fis, clone HEMBB10	3.2
447762	AI939461	Hs.161370	ESTs	3.2
414147	BE091634		gb:IL2-BT0731-240400-069-C03 BT0731 Homo sapi	3.2
445038	AI635444	Hs.143917	dJ467N11.1 protein	3.2
448666	NM_014953	Hs.323346	KIAA1008 protein	3.2
402800			Target Exon	3.2
411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated	3.2
424308	AW975531	Hs.154443	minichromosome maintenance deficient (S. cere	3.2
455203	AW865450		gb:PM4-SN0020-010400-008-b09 SN0020 Homo sapi	3.2
459666	W27362		gb:30g7 Human retina cDNA randomly primed sub	3.2
401458			Target Exon	3.2
432361	AI378562	Hs.159585	ESTs	3.2
444008	BE544855	Hs.220756	ESTs, Weakly similar to SFR4_HUMAN SPLICING F	3.2
405336			Target Exon	3.2
446563	BE326588	Hs.141454	ESTs	3.2
449276	AW241510	Hs.252713	ESTs	3.2
455838	BE145808		gb:MR0-HT0208-101299-103-f11 HT0208 Homo sapi	3.2
420591	X53655	Hs.99171	neurotrophin 3	3.2
401486			C4000647*gi4758508 ref NP_004253.1 airway	3.2
432979	AA573263	Hs.120860	ESTs	3.2
413833	Z15005	Hs.75573	centromere protein E (312kd)	3.2
438325	AA804258	Hs.123229	ESTs	3.2
421751	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha-1C-a	3.2
431938	AA938471	Hs.54431	specific granule protein (28 kDa); cysteine-r	3.2
421777	BE562088	Hs.108196	HSPC037 protein	3.2
408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone ADKA02	3.2
427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone LNG004	3.2
402337			Target Exon	3.2
420930	AW888650		gb:CM4-NT0007-130500-551-f05 NT0007 Homo sapi	3.2
436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HEMBA10	3.2
443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	3.1
437641	AA811452	Hs.291911	ESTs	3.1
414761	AJ077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.1
434208	T92641	Hs.127648	hypothetical protein PRO2176	3.1
433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN ALU SU	3.1
452934	AA581322	Hs.4213	hypothetical protein MGC16207	3.1
458923	Y12812	Hs.24422	regulatory factor X-associated protein	3.1
448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A receptor, ep	3.1
439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDNA clo	3.1
422283	AW411307	Hs.114311	COCA45 (cell division cycle 45, S.cerevisiae,	3.1
445885	AI734009	Hs.127699	KIAA1603 protein	3.1
441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone HEP010	3.1
424653	AW977534	Hs.151459	calcium/calmodulin-dependent serine protein k	3.1
431322	AW970522		gb:EST382704 MAGE resequences, MAGK Homo sapi	3.1
423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription factor	3.1
455987	BE178323		gb:RC3-HT0600-240400-023-g05 HT0600 Homo sapi	3.1
421426	AA291101	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA, part	3.1
423887	AL080207	Hs.134585	DKFZP434G232 protein	3.1
408296	AL117452	Hs.44155	DKFZP586G1517 protein	3.1
447815	AI432199	Hs.247084	ESTs	3.1
441974	AI683782	Hs.128245	ESTs	3.1
446474	AI301227	Hs.150186	hypothetical protein DKFZp566K1946	3.1
452166	AI948607	Hs.264680	ESTs	3.1
451659	BE379761	Hs.14248	ESTs	3.1
439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1

5	447701	BE619526	Hs.255527	hypothetical protein MGC14128	3.1
	443648	AI085377	Hs.143610	ESTs	3.1
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	3.1
	449441	AI656040	Hs.195532	ESTs	3.1
	458145	AI239457	Hs.130794	ESTs	3.1
10	444588	AI221321	Hs.167559	ESTs	3.1
	450832	AW970602	Hs.105421	ESTs	3.1
	449425	AW103433	Hs.195684	ESTs	3.1
	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ113051 fis, clone NTZRP30	3.1
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKALP)	3.1
15	416120	H46739		gb:yo14h02.s1 Soares adult brain N2b5HB55Y Ho	3.1
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S. cere	3.1
	404107			Target Exon	3.1
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HEMBB10	3.1
	417168	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp588L1121 (from c	3.1
20	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM040	3.1
	442824	BE178065	Hs.144081	ESTs	3.1
	435061	AI651474	Hs.163944	ESTs	3.1
	420589	AA419360	Hs.192708	ESTs	3.0
	434559	AI311295	Hs.8294	KIAA0196 gene product	3.0
25	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B, membe	3.0
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptional act	3.0
	402892			Target Exon	3.0
	405087			Target Exon	3.0
	411770	NM_014278	Hs.71992	heat shock protein (hsp110 family)	3.0
30	459687	AA031956		gb:zk15e04.s1 Soares_pregnan_uterus_NbHPU Ho	3.0
	435990	AI015862	Hs.131793	ESTs	3.0
	442577	AA292988	Hs.163900	ESTs	3.0
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitter tra	3.0
	458154	AW816379	Hs.335018	ESTs	3.0
35	416809	N67253	Hs.271691	ESTs	3.0
	444946	AW139205	Hs.156457	hypothetical protein FLJ22408	3.0
	437938	AI950087		gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapiens cDN	3.0
	413281	AA861271	Hs.222024	transcription factor BMAL2	3.0
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 281002701	3.0
40	445505	AI971156	Hs.148891	ESTs	3.0
	425005	AI565851		gb:tn07g03.x1 NCI_CGAP_Bm25 Homo sapiens cDN	3.0
	435673	AF202961	Hs.284200	Homo sapiens uncharacterized gastric protein	3.0
	432189	AA527941		gb:rh30c04.s1 NCI_CGAP_Pr3 Homo sapiens cDNA	3.0
	453509	AL040021	Hs.252674	ESTs, Weakly similar to alternatively spliced	3.0
45	455750	BE075114		gb:PM1-BT0585-110200-003-c11 BT0585 Homo sapi	3.0
	407777	AA161071	Hs.71465	squalene epoxidase	3.0
	424441	X14850	Hs.147097	H2A histone family, member X	3.0
	417734	Z42657	Hs.6724	ESTs	3.0
	449676	AW380579	Hs.209657	ESTs	3.0
50	445425	AI223511	Hs.300722	ESTs	3.0
	427061	AB032971	Hs.173392	KIAA1145 protein	3.0
	433584	AW295399		gb:UH-BI2-ahv-h-03-0-ULs1 NCI_CGAP_Sub4 Ho	3.0
	444477	AI150548	Hs.23155	ESTs	3.0
	446255	AI283257	Hs.257090	ESTs	3.0
55	400612			C10001034:gi7513113 pir T13078 KIAA0992 pro	3.0
	450841	AI741466	Hs.270515	ESTs	3.0
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone HEP091	3.0
	433871	W02410	Hs.205555	ESTs	3.0
	401994			Target Exon	3.0
60	449272	AW137658	Hs.197645	ESTs	3.0
	409703	NM_006187	Hs.56009	Z'-5'-oligoadenylate synthetase 3 (100 kD)	3.0
	400250			Eos Control	3.0
	408015	AW136771	Hs.244349	epidermal differentiation complex protein lik	3.0
	436414	BE264633	Hs.143638	WD repeat domain 4	3.0
65	432220	AI571305	Hs.232224	ESTs	3.0
	420531	AA280824	Hs.190035	ESTs	3.0
	433644	AW342028		gb:hb75d03.x1 NCI_CGAP_UI2 Homo sapiens cDNA	3.0
	447313	U92981	Hs.18081	Homo sapiens clone DT1P186 mRNA, CAG repeat r	3.0
	428262	AI651324	Hs.7298	biphenyl hydrolase-like (serine hydrolase; br	3.0
70	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone COL070	3.0
	417308	H60720	Hs.81892	KIAA0101 gene product	3.0
	436281	AW411194	Hs.85195	myeloid leukemia factor 1	3.0
	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2 (dihy	3.0
	423555	R72694	Hs.7720	dynenin, cytoplasmic, heavy polypeptide 1	3.0
75	426890	AA393167	Hs.41294	ESTs	2.9
	436333	AA709270	Hs.136672	EST	2.9
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	2.9
	402556			C1001383*gi538655 pir A61183 hypothetical	2.9
	411098	AW817238		gb:QV0-ST0247-090200-105-b07 ST0247 Homo sapi	2.9
80	435399	AA679463		gb:ac50c03.s1 Stratagene hNT neuron (937233)	2.9
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	2.9
	427986	NA5214	Hs.282387	Homo sapiens cDNA: FLJ21837 fis, clone HEP016	2.9
	410658	AW105231	Hs.192035	ESTs	2.9
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN 2 PR	2.9
	412279	BE245511		gb:TCBAP1D3235 Pediatric pre-B cell acute lym	2.9
	405277			ENSP00000211621* <i>Keratin, type II cytoskeletal</i>	2.9
	423733	AA330281		gb:EST33985 Embryo, 12 week II Homo sapiens c	2.9

5	455319	AW895387	gb:QV4-NN0038-300300-157-c10 NN0038 Homo sapi	2.9
	407638	AJ404672	Hs.334483 hypothetical protein FLJ23571	2.9
	413306	AW303544	Hs.118654 ESTs	2.9
	432215	AJ076609	Hs.2934 ribonucleotide reductase M1 polypeptide	2.9
	434423	NM_005769	Hs.3844 LIM domain only 4	2.9
	446269	AW263155	Hs.14559 hypothetical protein FLJ10540	2.9
	412367	AW945864	gb:QV0-ET0001-050500-228-e09 ET0001 Homo sapi	2.9
	436148	BE005252	Hs.321583 Homo sapiens cDNA FLJ20779 fis, clone COL0507	2.9
10	421190	U95031	Hs.102482 mucin 5, subtype B, tracheobronchial	2.9
	404981		ENSP00000252242*-Keratin, type II cytoskeletal	2.9
	448796	AA147829	Hs.301431 endothelial zinc finger protein induced by tu	2.9
	452732	BE300078	Hs.80449 Homo sapiens, clone IMAGE:3535294, mRNA, part	2.9
	401760		Target Exon	2.9
15	443859	NM_013409	Hs.9914 follistatin	2.9
	404253		NM_021058*-Homo sapiens H2B histone family, m	2.9
	432491	AA662910	Hs.42635 hypothetical protein DKFZp434K2435	2.9
	435867	AA954229	Hs.114052 ESTs	2.9
	429035	BE549781	Hs.270475 ESTs	2.9
20	446733	AA863360	Hs.26040 ESTs, Weakly similar to fatty acid omega-hydr	2.9
	446417	AJ299060	gb:qn14d12x1 NCL CGAP_Lu5 Homo sapiens cDNA	2.9
	437637	AJ003029	Hs.65792 syntrophin, gamma 2	2.9
	452452	BE393822	Hs.29645 Homo sapiens mRNA; cDNA DKFZp761C029 (from d	2.9
	442432	BE093589	Hs.38178 hypothetical protein FLJ23468	2.9
	450698	W31489	Hs.95044 ESTs, Weakly similar to I38022 hypothetical p	2.9
25	439430	AF124250	Hs.6564 cervical cancer anti-estrogen resistance 3	2.9
	434876	AF160477	Hs.61460 Ig superfamily receptor LNIR	2.9
	438268	AA782163	Hs.293502 ESTs	2.9
	401781		Target Exon	2.9
30	439625	AF086453	Hs.58611 ESTs	2.9
	425234	AW152225	Hs.165909 ESTs, Weakly similar to I38022 hypothetical p	2.9
	410743	AA089474	Hs.272153 ESTs	2.9
	414915	NM_002462	Hs.76391 myxovirus (influenza) resistance 1, homolog o	2.9
	449746	AI668594	Hs.176588 ESTs, Weakly similar to CP4Y_HUMAN CYTOCHROME	2.9
35	443479	AF027219	Hs.9443 zinc finger protein 202	2.9
	442601	AI684969	Hs.46772 ESTs	2.9
	405932		C15000305:gi 3806122 gb AAC69198.1 (AF097887	2.9
	405454		C12000541:gi 5729884 ref NP_006539.1 IGF-II	2.9
	418844	M62982	Hs.1200 arachidonate 12-lipoxygenase	2.9
40	408562	AI436323	Hs.31141 Homo sapiens mRNA for KIAA1568 protein, parti	2.9
	408829	NM_006042	Hs.48384 heparan sulfate (glucosamine) 3-O-sulfotransf	2.9
	414581	AA256213	Hs.72010 ESTs	2.9
	411268	AK000512	Hs.69388 hypothetical protein FLJ20505	2.9
	450024	AA005129	gb:zh90h08r1 Soares_fetal_liver_spleen_1NFLS	2.9
45	400297	AI127076	Hs.334473 hypothetical protein DKFZp564O1278	2.9
	436481	AA379597	Hs.5199 HSPC150 protein similar to ubiquitin-conjugat	2.9
	400631	AF173937	Hs.109494 secreted protein of unknown function	2.9
	429118	H20669	Hs.35406 ESTs, Highly similar to unnamed protein produ	2.9
	444381	BE387335	Hs.283713 ESTs, Weakly similar to S64054 hypothetical p	2.9
50	435711	AF226667	Hs.58553 CTP synthase II	2.9
	419088	AI538323	Hs.52620 integrin, beta 8	2.8
	431629	AJ077025	Hs.265827 interferon, alpha-inducible protein (clone IF	2.8
	429299	AI620463	Hs.293984 hypothetical protein MGC13102	2.8
	451702	AW665452	Hs.246503 ESTs	2.8
55	432162	AA584062	Hs.272798 hypothetical protein FLJ20413	2.8
	405281		NM_002864:Homo sapiens pregnancy-zone protein	2.8
	438161	BE089028	Hs.20158 ESTs, Weakly similar to S34159 transcription	2.8
	409103	AF251237	Hs.112208 XAGE-1 protein	2.8
	425599	AW366745	Hs.214140 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.8
60	425274	BE281191	Hs.155462 minichromosome maintenance deficient (mis5, S	2.8
	435099	AC004770	Hs.4756 flap structure-specific endonuclease 1	2.8
	445873	AA250970	Hs.251946 poly(A)-binding protein, cytoplasmic 1-like	2.8
	452730	AA027952	Hs.165216 ESTs	2.8
	413083	BE084528	gb:RC4-BT0311-250200-014-h06 BT0311 Homo sapi	2.8
65	437030	AA742577	Hs.303781 EST	2.8
	438113	AI467908	Hs.8882 ESTs	2.8
	442973	BE567665	Hs.288550 Homo sapiens cDNA: FLJ23156 fis, clone LNG096	2.8
	440994	AI160011	Hs.193341 ESTs	2.8
	442295	AI827248	Hs.224398 Homo sapiens cDNA FLJ11469 fis, clone HEMBA10	2.8
70	422689	AW856665	gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapi	2.8
	410310	J02931	Hs.62192 coagulation factor III (thromboplastin, tissu	2.8
	424408	AI754813	Hs.146428 collagen, type V, alpha 1	2.8
	433788	AI810534	Hs.161275 ESTs	2.8
	403806		Target Exon	2.8
75	437182	AL080098	gb:Homo sapiens mRNA; cDNA DKFZp564C1072 (fro	2.8
	453955	AW579207	Hs.304666 ESTs, Weakly similar to I78885 serine/threon	2.8
	420795	AA323037	Hs.128645 sorting nexin 16	2.8
	452696	AI826645	Hs.211534 ESTs	2.8
	432656	NM_000246	Hs.3076 MHC class II transactivator	2.8
80	438052	AA776564	Hs.41891 zinc finger 1111	2.8
	441755	AW450826	Hs.127786 ESTs	2.8
	427961	AW293165	Hs.143134 ESTs	2.8
	449785	AI225235	Hs.288300 hypothetical protein FLJ23231	2.8
	450451	AW591528	Hs.202072 ESTs	2.8

5	406831	N73448	Hs.50272	ESTs, Weakly similar to RS1A_HUMAN 40S RIBOSO	2.8
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A receptor, pi	2.8
	439453	BE264974	Hs.6565	thyroid hormone receptor/interactor 13	2.8
	413582	AW295647	Hs.71331	hypothetical protein MGC5350	2.8
	448979	AI611378	Hs.192610	ESTs	2.8
	409143	AW025980	Hs.138965	ESTs, Weakly similar to I38022 hypothetical p	2.8
	410664	NM_006033	Hs.65370	lipase, endothelial	2.8
	444550	BE250716	Hs.87614	ESTs	2.8
10	422109	S73265	Hs.1473	gastrin-releasing peptide	2.8
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.8
	445941	AI267371	Hs.172636	ESTs	2.8
	459719	AW749511	Hs.301554	ESTs, Weakly similar to AF133298 1 cytochrome	2.8
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT2RP20	2.8
	456456	AA477609	Hs.89563	nuclear cap binding protein subunit 1, 80kD	2.8
15	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypothetical p	2.8
	403000	BE247275	Hs.151787	U5 snRNP-specific protein, 116 kD	2.8
	413273	U75679	Hs.75257	stem-loop (histone) binding protein	2.8
	439846	T63959	Hs.228320	hypothetical protein FLJ23537	2.8
20	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9	2.8
	412970	AB026436	Hs.177534	dual specificity phosphatase 10	2.8
	455091	BE079752		gb:RC6-BT0627-140200-011-A04 BT0627 Homo sapi	2.8
	410049	AW579475		gb:RC0-DT0076-110100-031-d10 DT0076 Homo sapi	2.8
	452571	W31518	Hs.34665	ESTs	2.8
	455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318 Homo sapi	2.8
25	426343	NM_014642	Hs.169387	KIAA0036 gene product	2.8
	414853	U31116	Hs.77501	sarcoglycan, beta (43kD dystrophin-associated	2.8
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromosomes 4	2.7
	418592	X99226	Hs.294153	Fanconi anemia, complementation group A	2.7
30	429128	AA446869	Hs.119316	ESTs	2.7
	427651	AW405731	Hs.18498	Homo sapiens cDNA FLJ12277 fis, clone MAMMA10	2.7
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	2.7
	403763			NM_001059*Homo sapiens tachykinin receptor 3	2.7
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypothetic	2.7
35	406753	AA505665	Hs.217493	annexin A2	2.7
	415747	AA381209		gb:EST94257 Activated T-cells I Homo sapiens	2.7
	419875	AA853410	Hs.93557	proenkephalin	2.7
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothetical p	2.7
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.7
40	456181	L36463	Hs.1030	ras inhibitor	2.7
	416548	H62953		gb:yr4706.r1 Soares fetal liver spleen 1NFLS	2.7
	417995	AW974175	Hs.188751	ESTs, Weakly similar to MAPB_HUMAN MICROTUBUL	2.7
	435347	AW014873	Hs.116963	ESTs	2.7
	457339	AW971949	Hs.291252	ESTs, Weakly similar to ZN91_HUMAN ZINC FINGE	2.7
45	417398	N78541	Hs.177366	ESTs	2.7
	408380	AF123050	Hs.44532	diubiquitin	2.7
	437724	AW444828	Hs.184323	ESTs	2.7
	408680	AK000093	Hs.46821	hypothetical protein FLJ20086	2.7
	454202	AW178363		gb:RC3-HT0105-010999-002-H06 HT0105 Homo sapi	2.7
50	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli RecA ho	2.7
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.7
	406092			Target Exon	2.7
	447748	AI422023	Hs.161338	ESTs	2.7
	443236	AI079496	Hs.134169	ESTs	2.7
55	433743	AF075312	Hs.236760	Homo sapiens clone HQ0262	2.7
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related protein	2.7
	405675			Target Exon	2.7
	424625	AW904466	Hs.321197	PDZ domain protein (Drosophila InaD-like)	2.7
	416250	AA581386	Hs.73452	hypothetical protein MGC10791	2.7
60	448592	N69546	Hs.44563	hypothetical protein	2.7
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MAMMA10	2.7
	407287	AI678812		gb:tu59d08.x1 NCL_CGAP_Gas4 Homo sapiens cDNA	2.7
	448275	BE514434	Hs.20830	kinesin-like 2	2.7
	412977	AA125910	Hs.191461	ESTs	2.7
65	431721	AB032996	Hs.268044	KIAA1170 protein	2.7
	417357	AF260257	Hs.131917	retinitis pigmentosa GTPase regulator interac	2.7
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of the p	2.7
	416294	D86980	Hs.79170	KIAA0227 protein	2.7
	456201	AI989961	Hs.233477	ESTs, Moderately similar to A Chain A, Cyclop	2.7
70	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolog 2	2.7
	401230			NM_014191*Homo sapiens sodium channel, volta	2.7
	422058	AA862231	Hs.334443	ESTs	2.7
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	2.7
	430152	AB001325	Hs.234542	aquaporin 3	2.7
75	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	2.7
	443500	AV646388	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (from cl	2.7
	418030	BE207573	Hs.83321	neuromedin B	2.7
	445640	AV996626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapiens]	2.7
80	418869	AV516565		gb:qx01d05.x1 Soares_NHCCc_cervical_tumor Hom	2.7
	431688	AA513906		gb:ng67c08.s1 NCL_CGAP_Lip2 Homo sapiens cDNA	2.7
	427579	AA366143	Hs.179669	hypothetical protein FLJ20637	2.7
	423175	W27595	Hs.18653	hypothetical protein FLJ14627	2.7
	414737	AI160386	Hs.125087	ESTs	2.7
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.7

	446659	AI335361	Hs.226376	ESTs	2.7
	419833	AA251131	Hs.220697	ESTs	2.7
	411819	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo sapi	2.6
5	445592	AV654382	Hs.17947	ESTs, Weakly similar to T16534 hypothetical p	2.6
	446102	AW168067	Hs.252956	ESTs	2.6
	441408	AI733249	Hs.126897	ESTs	2.6
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse transc	2.6
	416283	NM_005429	Hs.79141	vascular endothelial growth factor C	2.6
10	421470	R27496	Hs.1378	annexin A3	2.6
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural arachnod	2.6
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	2.6
	431832	AW276856	Hs.192715	ESTs	2.6
	426698	AA394104	Hs.97489	ESTs	2.6
15	433288	AI368873	Hs.271257	ESTs, Weakly similar to I38022 hypothetical p	2.6
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	2.6
	432665	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypothetical p	2.6
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo sapi	2.6
	440048	AA897461	Hs.328737	ESTs, Weakly similar to envelope protein [H.s	2.6
20	401260			C1001031::gil7305041[ref][NP_038876.1] erythro	2.6
	435136	R27299	Hs.10172	ESTs	2.6
	412108	AA100293	Hs.185043	ESTs	2.6
	434442	AA737415	Hs.152826	ESTs	2.6
	443204	AW205878	Hs.29543	Homo sapiens cDNA FLJ13103 fis, clone NT2RP30	2.6
25	419667	AU077005	Hs.92208	a disintegrin and metalloproteinase domain 15	2.6
	422892	AA988176	Hs.121553	hypothetical protein FLJ20641	2.6
	409594	AA076118		gb:zm18e08.s1 Stratagene pancreas (937208) Ho	2.6
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (937208) Ho	2.6
	423038	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide	2.6
30	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyt growth factor	2.6
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.6
	434444	AI765276	Hs.101257	hypothetical protein MGC3295	2.6
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR/MRP)	2.6
	411465	AW847663		gb:IL3-CT0213-280100-056-F02 CT0213 Homo sapi	2.6
35	408625	AW243323	Hs.266785	ESTs	2.6
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.6
	439245	NM_013381	Hs.6510	thyrotropin-releasing hormone degrading ectoe	2.6
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subunit of	2.6
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin)	2.6
40	401050			NM_014155::Homo sapiens HSPC063 protein (HSPC	2.6
	405897			Target Exon	2.6
	451153	BE092900		gb:CM2-BT0742-100400-147-h04 BT0742 Homo sapi	2.6
	407327	AA487182	Hs.269414	ESTs, Weakly similar to Z195_HUMAN ZINC FINGE	2.6
	440159	AI637599	Hs.126127	ESTs	2.6
45	404184			NM_030903::Homo sapiens olfactory receptor, f	2.6
	428552	AW274560	Hs.129520	ESTs	2.6
	401367			Target Exon	2.6
	428450	NM_014791	Hs.184339	KIAA0175 gene product	2.6
	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
50	424783	AA913909	Hs.153088	TATA box binding protein (TBP)-associated fac	2.6
	449432	AW451361	Hs.196529	ESTs	2.6
	425062	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger protein)	2.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PLACE10	2.6
	450705	U03004	Hs.25351	Iroquois homeobox protein 5	2.6
55	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	2.6
	408391	AW859276		gb:MR1-CT0352-240200-105-d02 CT0352 Homo sapi	2.6
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mouse)	2.6
	431750	AA514986	Hs.283705	ESTs	2.6
	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to ARL-	2.6
60	453331	AI240665	Hs.8895	ESTs	2.6
	447175	AI365208	Hs.293606	ESTs	2.6
	451878	AI821027	Hs.8429	ESTs	2.6
	433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	2.6
	418282	AA215535	Hs.98133	ESTs	2.6
65	434557	AW855466	Hs.271866	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	2.6
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	2.6
	420894	AA744597	Hs.88854	ESTs	2.6
	435663	AI023707	Hs.134273	ESTs	2.6
	448037	AW195634	Hs.170401	ESTs	2.6
70	418067	AI127958	Hs.83393	cystatin E/M	2.6
	439524	BE542950	Hs.155548	ESTs	2.6
	402298			Target Exon	2.6
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.6
	407471	D55644		gb:Human spleen PABL (pseudoautosomal boundar	2.6
75	430994	AA490346	Hs.40530	Homo sapiens, clone MGC:17624, mRNA, complete	2.6
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (from c	2.6
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypothetical p	2.6
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (from c	2.6
	425415	M13903	Hs.157091	involutrin	2.6
80	444826	AI674482	Hs.148441	ESTs	2.6
	413331	BE083950		gb:PM0-BT0651-260200-001-b11 BT0651 Homo sapi	2.6
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.6
	405041			C3001706::gil1345652[sp][P15989]CA36_CHICK COL	2.6
	413864	BE175582		gb:RCS-HT0580-100500-022-C01 HT0580 Homo sapi	2.6

	438746	AI885815	Hs.184727	ESTs	2.5
	438966	AW979074		gb:EST391184 MAGE resequences, MAGP Homo sapi	2.5
	433365	AF026944	Hs.293797	ESTs	2.5
5	412723	AA648459	Hs.335951	hypothetical protein AF301222	2.5
	422656	AI870435	Hs.1569	LIM homeobox protein 2	2.5
	411171	AW820260		gb:QV2-ST0296-150200-040-c10 ST0296 Homo sapi	2.5
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo sapi	2.5
	459688	U72671	Hs.151290	intercellular adhesion molecule 5, telencepha	2.5
10	414883	AA926960	Hs.334883	CDC28 protein kinase 1	2.5
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	2.5
	437412	BE059288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (from cl	2.5
	427366	AA885108	Hs.223806	TATA box binding protein (TBP)-associated fac	2.5
	455549	AW994222		gb:RC3-BN0036-250200-012-e02 BN0036 Homo sapi	2.5
	409576	AA077118	Hs.197298	NS1-binding protein	2.5
15	448305	AA625207	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT2RP20	2.5
	429413	NM_014058	Hs.201877	DESC1 protein	2.5
	424420	BE614743	Hs.146688	prostaglandin E synthase	2.5
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, polypep	2.5
	452834	AI638627	Hs.105685	KIAA1688 protein	2.5
20	424354	NM_014314	Hs.145612	RNA helicase	2.5
	455095	AW855598		gb:CM1-CY0278-031199-032-e08 CT0278 Homo sapi	2.5
	431241	AA496799	Hs.36958	ESTs	2.5
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (connexin	2.5
	427239	BE270447	Hs.174070	ubiquitin carrier protein	2.5
25	407103	AA424881	Hs.256301	hypothetical protein MGC13170	2.5
	458175	AW296024	Hs.150434	ESTs	2.5
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein type	2.5
	453379	AA035261	Hs.61753	ESTs	2.5
30	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypothetical p	2.5
	412313	AW936832		gb:PM2-DT0023-050400-003-h03 DT0023 Homo sapi	2.5
	421733	AL119671	Hs.1420	fibroblast growth factor receptor 3 (achondro	2.5
	443757	H05479	Hs.62314	ESTs	2.5
	449300	AI656959	Hs.222165	ESTs	2.5
35	434913	AW872860	Hs.11056	RALBP1 protein	2.5
	448946	AI652855	Hs.23363	hypothetical protein FLJ10983	2.5
	437327	AL353942	Hs.306504	Homo sapiens mRNA; cDNA DKFZp76123121 (from	2.5
	450262	AW409872	Hs.184846	Homo sapiens, Similar to zinc finger protein	2.5
	453204	R10799	Hs.191990	ESTs	2.5
40	420170	U43374	Hs.95631	Human normal keratinocyte mRNA	2.5
	443344	AI640355	Hs.312691	ESTs	2.5
	439436	BE140845	Hs.57868	ESTs	2.5
	449867	AI672379	Hs.122970	hypothetical protein FLJ21579	2.5
	452220	BE158006	Hs.212296	ESTs	2.5
45	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	2.5
	429163	AA884766		gb:zm20a10.s1 Soares_NFL_T_GBC_S1 Homo sapien	2.5
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	2.5
	415030	D31118	Hs.191735	hypothetical protein MGC10520	2.5
	417975	AA641836	Hs.30085	hypothetical protein FLJ23186	2.5
50	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens cDNA	2.5
	400301	X03635	Hs.1657	estrogen receptor 1	2.5
	429386	AK001795	Hs.201179	hypothetical protein FLJ10933	2.5
	423949	AI014546	Hs.130912	ESTs	2.5
	411768	NM_013371	Hs.71979	Interleukin 19	2.5
55	436961	AW376974	Hs.156704	ESTs	2.5
	431124	AF284221	Hs.59506	doublesex and mab-3 related transcription fac	2.5
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	2.5
	418717	AI334430	Hs.86984	ESTs	2.5
	443270	NM_004272	Hs.337737	Homer, neuronal immediate early gene, 1B	2.5
60	448454	NM_005879	Hs.21254	TRAF interacting protein	2.5
	430072	X13294	Hs.300592	v-myb avian myeloblastosis viral oncogene hom	2.5
	442966	AI394036	Hs.132237	ESTs, Weakly similar to DUS8_HUMAN DUAL SPECI	2.5
	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HUMAN ALU SU	2.5
	418327	U70370	Hs.84136	paired-like homeodomain transcription factor	2.5
65	440381	AA917808	Hs.190495	ESTs	2.5
	403983			Target Exon	2.5
	451340	AW936273		gb:QV0-DT0020-090200-107-g07 DT0020 Homo sapi	2.5
	447888	BE620911	Hs.126889	ESTs	2.5
	441794	AW197794	Hs.253338	ESTs	2.5
70	424153	AA451737	Hs.141496	MAGE-like 2	2.5
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	2.5
	435647	AI653240	Hs.49823	ESTs	2.5
	428780	AI478578	Hs.50836	ESTs	2.5
	439108	AW163034	Hs.6467	synaptogyrin 3	2.5
75	422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fascin h	2.5
	428054	AI948588	Hs.266619	ESTs	2.5
	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	2.5
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S. cere	2.5
	443362	AI053464	Hs.166505	ESTs	2.5
80	433183	AF231338	Hs.222024	transcription factor BMAL2	2.5
	438214	H06076	Hs.26320	TRABID protein	2.5
	446745	AW118189	Hs.156400	ESTs	2.5
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	2.5
	426333	AW269088	Hs.118183	hypothetical protein FLJ22833	2.5

TABLE 12B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
407642	1007175_1	AW178963 AW845721 BE141041 AW806977 AW845690 AW845691 AW845724 AW176564 AW845705 AW845603 AW845729 AW845722 AW178966 AW845693 AW845585 AW845707 BE141053 BE141046 AW845570 AW845575 BE141043 BE141039 BE141070 AW062443 AW806980 AW845643 AW806969 AW845686 BE141054 BE141040 BE141044 AW845571 AW845604 BE141047 BE141071 AW062442 AW845633 AW178968
408391	1055687_1	AW859276 AW859274 AW190859 T91463
408690	107490_1	AW864542 AA056567 AW882724
409594	114249_1	AA076118 AA975618 AA076220
409695	114876_1	AA296961 AA296889 AA076945 AA077528 AA077497
409990	116644_1	AA079337 AA079338 AWZ72100
410008	116812_1	AA079552 BE142525 BE142527
410049	1172307_1	AW579475 AW939654 AW939655
410784	1221005_1	AW803201 BE079700 BE062940
411098	1232093_1	AW817238 AW993985 AW993998
411171	1234393_1	AW820260 AW820332 R94406
411465	1246769_1	AW847663 AW847861 AW861080
411559	1249417_1	BE144081 BE144190 AW851155
411819	1259748_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
411958	126717_1	AA099020 AW751275 AW751276 AW751289
412279	1267332_1	BE245511 BE246133 AW935247
412313	1288355_1	AW936832 AW936609 AW936657 AW936611 AW936739 AW936734 AW936779 AW936688 AW936659 AW936738 AW936827 AW936737 AW936736 AW936740 AW936833 AW936777 AW936830 AW936834 AW936829 AW936772 AW936638 AW936658 AW936636 AW936774 AW936778 AW936766 AW936776 AW936831 AW936760 AW936819
412333	1289037_1	AW937485 AW937589 AW937658 AW937654 AW937492
412367	1291505_1	AW945954 AW946020 AW946034 AW946027 AW946041 AW946044 AW946033 AW946024 AW946021 AW946029 AW946015 AW946016 AW946039 AW946045 AW946028 AW946036
412879	1334272_1	BE092219 BE092361 BE060789
413083	1348639_1	BE064528 BE064589 BE064561
413331	1361726_1	BE083950 BE084017 BE084016
413864	1395788_1	BE175582 BE175514 BE175505 BE175591 BE175530
414147	142127_1	BE091634
414148	142133_1	BE084049 AW292907 AA135984
415317	1533847_1	Z43388 F05453 R19673 R20275 H06917
415613	1540602_1	R20233 F12901 T74740
415747	155189_1	AA381209 AA381245 AA167683
416120	1571266_1	H46739 H51513 H19779
416168	1574545_1	H23687 H46460 H40239
416548	1600181_1	H62953 N76608 N72413
417742	1696282_1	R64719 Z44680 R12451
418347	174149_1	AA216419 F03238 AA229517
418869	179863_1	AW516565 AA229762 AA230035
419807	188252_1	R77402 AA262462 AA250988 R06794
420373	193194_1	AW868228 AA259146 W01465
420637	195241_1	AW976153 AA278945 AA747691
420930	197736_1	AW888650 AW888651 BE149946 BE149948 BE149951 BE149947 AW888649 AA281840 AA281822 AW888652
422689	219896_1	AW856665 AA315006 AW954733
423733	231476_1	AA330281 AA330232 AW962521
423735	231498_1	AA330259 AA661806 AA502431 AW974633 AA649496
423841	232507_1	AW753967 AA370795 AA331630 AW962550
425005	245908_1	AI565851 AA349556 R24798
429163	300543_1	AA884766 AW974271 AA592975 AA447312
431120	328264_1	AA492588 AA492498 AA492571
431322	331543_1	AW970622 AA503009 AA502958 AA502989 AA502805 T92188
431688	336609_1	AA513906 AA847734 AI357044
432184	342677_1	AW971125 AA527731 N52655 AI821508 AA532420
432189	342819_1	AA527941 AI810608 AI620190 AA635266
432869	355475_1	AW974094 AA569074 AA602574
433289	36202_1	AF005258
433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832
433644	371919_1	AW342028 AA641080 AA603282
434321	383473_1	AA629368 AW849574 AW849573
435399	405576_1	AA679463 AW813779 AW813709
437182	43421_1	AL080098 AL037472 AA432051
437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493 AA927794 AI560251 AW874058 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539542 AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI554269 F00531 H83488 W37181 W78802 R66056 AI002839 R57840 AA300207 AW959581 T63226 F04005
438390	45662_1	AI422017 AI422945 AI363249 AI423113 AI925592 AI420795 AI208187 AI423279 AI423645 AI424090 AI359637 ALD44732 D17003
438966	467436_1	AW979074 AA834841 AA828650
438993	467651_1	AA828995 AA834879 AI926361

439579	47404_1	AF086400 W79232 W73990
440320	491930_1	AA879294 N67538 A474541
444910	624951_1	AI201849 BE069007 AW946544
446417	676384_1	AI299050 BE256910
447197	711623_1	R36075 AI366546 R36167
448599	770766_1	AW860912 AI540866
449034	794817_1	AI624049 AW117770 AI858360
450024	82296_1	AA005129 AA679084 AA694399
450613	840016_1	AI702055 R89204 R86260
451105	859083_1	AI761324 AW880941 AW880937
451153	86054_1	BE092900 AA015877 AA018521
451340	86640_1	AW936273 AW340350 AA017208
454202	1050507_1	AW178363 AW846011 AW845964 AW845988 AW845977 AW846002
454241	1067807_1	BE144666 BE184942 AW238414 BE184946
454707	1230250_1	AW814989 AW814852 AW814808
454891	1239217_1	AW837349 AW837355 AW882717
454988	1248607_1	AW850140 AW850195 AW850192
455091	1252939_1	BE079752 BE079868 BE148989 AW855532 BE148818 BE148815 BE148796
455092	1252971_1	BE152428 AW855572 AW855607
455095	1252987_1	AW855598 AW855608 BE148763 BE148764 AW855645 AW855615 AW855596 AW855610 AW855601 AW855605
455203	1259973_1	AW865450 AW865119 AW865452 AW865461 AW865325 AW865114 AW865116 AW865321 AW865590 AW865390
455310	1278158_1	AW893961 AW893998 AW894034 AW894019
455319	1279172_1	AW895387 AW895547 AW895564 AW895323 AW895405 AW895539 AW895538
455365	1284681_1	AW948343 AW948341 AW902855 AW984737
455549	1324696_1	AW994222 AW994377
455666	1349545_1	BE065813 BE065788 BE065889 BE065832
455750	1355998_1	BE075114 BE075283 BE075118
455838	1374605_1	BE145808 BE145807 BE181883
455987	1397735_1	BE178323 BE177978
457405	333127_1	AA504860 AA504911
458829	773443_1	AI557388 BE158936
459267	966605_1	AJ003631 AJ003650 AJ003651

TABLE 12C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400612	9929646	Minus	151513-151662
400666	8118496	Plus	17982-18115,20297-20456
401050	8117628	Minus	78449-79425
401137	2547238	Minus	598-1009
401230	9929527	Minus	33835-34006,34539-34592,36461-36745,48925-49098,52604-52758
401260	8076883	Minus	86008-86355
401367	9796198	Minus	145356-145807
401458	9187886	Plus	76485-77597
401486	7341763	Plus	32585-32756,35281-36540,40791-40933,44018-44179
401575	7229804	Minus	76253-76364
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
402048	8072512	Plus	43936-44078
402298	6598824	Plus	36758-37953
402337	6957691	Plus	4116-4286,16811-16973,17107-17256,19715-20040,22029-22205
402481	9797406	Plus	87891-88991
402556	9863723	Plus	13579-14026
402639	9958129	Minus	20167-22383
402800	6010175	Plus	43921-44049,46181-46273
402892	8086844	Minus	194384-194645
403274	8072441	Minus	104069-104179,105683-105859
403471	9930659	Minus	85867-85983
403763	7229888	Minus	43575-43887
403806	8140491	Plus	145390-145678
403983	8576059	Minus	82441-82701
404107	8099028	Minus	201699-202363
404132	6981900	Plus	11307-12434
404184	4581418	Minus	12652-13548
404253	9367202	Minus	55675-56055
404440	7528051	Plus	80430-81581
404782	9910094	Minus	15455-15589
404959	7407964	Plus	45243-45368
404981	4432779	Minus	20626-20770,22513-22721
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405041	7547195	Plus	121230-121714
405196	7230083	Minus	135716-135851

5	405277	3980473	Plus	23471-23572
	405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
	405336	6094635	Plus	33267-33563
	405454	7656675	Plus	133807-134053
	405545	1054740	Plus	118677-118807,119091-119295,121626-121823
	405547	1054740	Plus	124361-124520,124914-125050
	405657	4827303	Minus	104132-104293
	405675	4557087	Plus	70304-70530
10	405708	4156182	Plus	55030-55604
	405897	6758795	Plus	59828-60535
	405932	7767812	Minus	123525-123713
	405943	6758796	Plus	20605-20812
	406087	9123919	Minus	7234-7626
15	406092	9123919	Plus	251370-251797,252168-252882
	406467	9795551	Plus	182212-182958
	406554	7711566	Plus	106956-107121
	406560	7711569	Minus	35162-35292
20	406599	8248616	Plus	10933-11086

TABLE 13A: 465 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES, LIKELY TO ENCODE EXTRACELLULAR OR CELL-SURFACE PROTEINS

Table 13A lists about 465 genes up-regulated in cervical cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 12A, except that the ratio was greater than or equal to 1.7, and the 95th percentile value amongst cervical cancers was greater than or equal 100 units, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 PPDomains: Predicted Protein Domains
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

	Pkey	ExAccn	UnigenelD	PPDomains	Unigene Title	R1
40	425650	NM_001944	Hs.1925	TM,cadherin,Cadherin_C_term	desmoglein 3 (pemphigus vulgaris antigen)	43.6
	418007	M13509	Hs.83169	SS,hemopexin,Peptidase_M10	matrix metalloproteinase 1 (interstitial)	38.9
	439505	W79123	Hs.58561	TM,7tm_1	G protein-coupled receptor 87	28.8
	452240	AI591147	Hs.61232	TM	ESTs	27.0
45	424046	AF027866	Hs.138202	SS,TM,serpin	serine (or cysteine) proteinase inhibitor	24.5
	400289	X07820	Hs.2258	hemopexin,Peptidase_M10	matrix metalloproteinase 10 (stromelysin	20.5
	418345	AJ001696	Hs.241407	SS,TM,serpin	serine proteinase inhibitor 13(P113; se	20.1
	423017	AW178761	Hs.227948	SS,serpin	serine (or cysteine) proteinase inhibitor	19.2
	428227	AA321649	Hs.2248	SS,TM,IL8	small inducible cytokine subfamily B (Cys	15.9
	447164	AF026941	Hs.17518	TM,IBR	Homo sapiens cig5 mRNA, partial sequence	13.8
50	414764	AW013887	Hs.72047	TM	ESTs	12.9
	416661	AA634543	Hs.79440	TM	IGF-II mRNA-binding protein 3	12.7
	427585	D31152	Hs.179729	SS,C1q,Collagen	collagen, type X, alpha 1 (Schmid metaphy	12.6
	406467			TM,ehand	Target Exon	10.5
55	428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 3 (stromelysin 1	10.2
	418882	NM_004996	Hs.89433	TM,ABC_membrane,ABC_tran	ATP-binding cassette, sub-family C (CFTR/	9.4
	419247	S65791	Hs.89764	TM,KH-domain	fragile X mental retardation 1	9.1
	446232	AZ81848	Hs.194691	TM,7tm_3,Ribosomal_L13	retinoic acid induced 3	8.9
	424905	NM_002497	Hs.153704	TM,pkinase	NIMA (never in mitosis gene a)-related ki	8.9
60	422420	U03398	Hs.1524	TM,tubulin,TNF	tumor necrosis factor (ligand) superfamily	8.7
	427821	AA470158	Hs.98202	TM,7tm_1	ESTs	6.9
	436211	AK001581	Hs.334828	Ammonium_transp	hypothetical protein FLJ10719; KIAA1794 p	6.9
	444342	NM_014398	Hs.10887	Lamp	similar to lysosome-associated membrane g	6.8
	422330	D30783	Hs.115263	SS,TM,EGF	epiregulin	6.8
65	447342	AI199268	Hs.19322	SS,lipocalin	Homo sapiens, Similar to RIKEN cDNA 20103	6.8
	407839	AA045144	Hs.161566	TM,cadherin,Cadherin_C_term	ESTs	6.6
	410153	BE311926	Hs.15830	Glycos_transf_2	hypothetical protein FLJ12691	6.5
	414812	X72755	Hs.77367	SS,TM,IL8	monokine induced by gamma Interferon	6.4
	421773	W69233	Hs.112457	SS	ESTs	6.2
70	413385	M34455	Hs.840	TM,IDO	indoleamine-pyrrole 2,3 dioxygenase	5.9
	413753	U17760	Hs.75517	SS,laminin_EGF,laminin_Nterm,adh_short	laminin, beta 3 (nicein (125kd), kafinin	5.8
	432239	X81334	Hs.2936	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 13 (collagenase	5.5
	418563	AK001100	Hs.41690	TM,cadherin	desmocollin 3	5.5
	407366	AF026942		TM,IBR	gh:Homo sapiens cig33 mRNA, partial seque	5.5
75	433091	Y12642	Hs.3185	SS,TM,UPAR_LY6	lymphocyte antigen 6 complex, locus D	5.4
	408536	AW381532	Hs.135188	SS,TM,E1-E2_ATPase,Cation_ATPase_C, N	ESTs	5.4
	420440	NM_002407	Hs.97644	SRCRUteroglobin	mammaglobin 2	5.2
	437044	AL035864	Hs.69517	TM	cDNA for differentially expressed CO16 ge	5.1
	405547			SS,TM,ABC_membrane,ABC_tran,ig	NM_018833"Homo sapiens transporter 2, AT	5.1
80	439223	AW238299	Hs.250618	SS	UL16 binding protein 2	5.1
	426320	W47595	Hs.169300	SS,TM,TGF-beta,TGFb_propeptide	transforming growth factor, beta 2	5.1
	423634	AW959908	Hs.1690	TM	heparin-binding growth factor binding pro	5.0
	426350	NM_003245	Hs.2022	TM,Transglutamin_C,Transglutamin_N,Transglut_core	transglutaminase 3 (E polypeptide, protei	5.0
	409744	AW675258	Hs.56265	TM,metallo, Kelch	Homo sapiens mRNA; cDNA DKFZp586P2321 (fr	4.9

5	444461	R53734	Hs.25978	TM	ESTs, Weakly similar to 2109260A B cell g	4.8
	410361	BE391804	Hs.62661	SS,TM,GBP	guanylate binding protein 1, interferon- γ	4.8
	423673	BE003054	Hs.1695	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 12 (macrophage e	4.8
	450375	AA009647	Hs.8850	TM,disintegrin,Pep_M12B_propep,Repolyisin	a disintegrin and metalloproteinase domai	4.8
	401575	NA		TM	Target Exon	4.6
10	428484	AF104032	Hs.184501	TM	solute carrier family 7 (cationic amino a	4.5
	425071	NM_013989	Hs.154424	SS,TM,T4_deiodinase	deiodinase, iodothyronine, type II	4.4
	431808	M30703	Hs.270833	SS,TM,EGF	amphiregulin (schwannoma-derived growth f	4.3
	434699	AA643687	Hs.149425	TM,Nucleoside_tra2	Homo sapiens cDNA FLJ11980 fis, clone HEM	4.3
	406687	M31126	Hs.272520	SS,Peptidase_M10,hemopexin	pregnancy specific beta-1-glycoprotein 9	4.2
15	404440			TM,MAGE	NM_021048:Homo sapiens melanoma antigen,	4.2
	449228	AJ403107	Hs.148590	TM,PAF-AH,p450	protein related with psoriasis	4.2
	444105	AW189097	Hs.166597	TM,cdherin	ESTs	4.1
	409632	W74001	Hs.55279	SS,serpin	serine (or cysteine) proteinase inhibitor	4.1
	423515	AA327017	Hs.162204	SS,TM,UPAR_LY6	ESTs	4.1
20	423738	AB002134	Hs.132195	SS,TM,trypsin,SEA	airway trypsin-like protease	4.1
	423553	AA405635	Hs.96854	TM	ESTs, Weakly similar to DYLY_HUMAN CYTOPL	4.1
	445537	AJ245671	Hs.12844	TM,ras	EGF-like-domain, multiple 6	4.0
	446989	AK001898	Hs.16740	TM	hypothetical protein FLJ11036	4.0
	428536	AI143139	Hs.2288	TM,efhand,Syndecan	visinin-like 1	3.9
25	413801	M62246	Hs.35406	TM	ESTs, Highly similar to unnamed protein p	3.9
	429441	AJ224172	Hs.204096	Uteroglobulin	lipophilin B (uteroglobulin family member),	3.9
	409501	AF237621	Hs.80828	TM,filamentfilament,C2	keratin 1 (epidermolytic hyperkeratosis)	3.8
	439238	N47305	Hs.46668	TM	ESTs	3.8
	446292	AF081497	Hs.279582	Ammonium_transp	Rh type C glycoprotein	3.8
30	405545			SS,TM,proteasome,Ig,ABC_memb,tranABC_tran,	(MDR1A/P) (TAP2)	3.8
	422938	NM_001809	Hs.1594	TM,thiolase	centromere protein A (17kD)	3.7
	423217	NM_000094	Hs.1640	SS,TM,fn3,vwa,Collagen,Kunitz_BPTI	collagen, type VII, alpha 1 (epidermolys	3.7
	430686	NM_001942	Hs.2633	SS,TM,cdherin,Cadherin_C_term	desmoglein 1	3.7
	444707	AI188613	Hs.41690	TM,cdherin	desmocollin 3	3.7
35	409582	R27430	Hs.271555	TM	ESTs	3.6
	408771	AW732573	Hs.47584	TM,K_tetra,ion_trans	potassium voltage-gated channel, delayed-	3.6
	400441	M15530	Hs.99879	TM,G-alpha	B-cell growth factor 1 (12kD)	3.6
	413278	BE563085	Hs.833	TM,ubiquitinlaminin_G,laminin_EGF,kazal	interferon-stimulated protein, 15 kDa	3.6
	426514	BE616633	Hs.170195	SS,TGFb_propeptide,TGF-beta	bone morphogenetic protein 7 (osteogenic	3.6
40	424927	AW973666	Hs.153850	SS	hypothetical protein C321D2.4	3.6
	408591	AF015224	Hs.46452	SS,TM,Uteroglobulin	mammaglobin 1	3.5
	407756	AA116021	Hs.38260	SS,UCH-1,UCH-2	ubiquitin specific protease 18	3.5
	407137	T97307		TM,GDA1_CD39	gb:ye53h05.s1 Soares fetal liver spleen 1	3.5
	411274	NM_002776	Hs.69423	trypsin	kalikrein 10	3.5
45	400666			SS,hemopexin,Peptidase_M10	NM_002425:Homo sapiens matrix metalloprot	3.5
	412471	M63193	Hs.73946	SS,TM,Glycos_transf_3,Cam_acyltransf	endothelial cell growth factor 1 (platelet	3.4
	450650	T65817	Hs.101257	TM	hypothetical protein MGC3295	3.4
	451778	AI826131	Hs.71243	Ig	ESTs, Weakly similar to zinc finger prote	3.4
	430397	AI924533	Hs.105607	SS,TM	bicarbonate transporter related protein 1	3.4
50	449722	BE280074	Hs.23960	TM,cyclin	cyclin B1	3.4
	422487	AJ010901	Hs.198267	TM,ywd	mucin 4, tracheobronchial	3.4
	449101	AA205847	Hs.23016	SS,TM,7tm_1	G protein-coupled receptor	3.3
	418994	AA296520	Hs.89546	SS,TM,lectin_c,sushi,EGF	selectin E (endothelial adhesion molecule	3.3
	421379	Y15221	Hs.103982	SS,TM,IL8	small inducible cytokine subfamily B (Cys	3.3
55	414774	X02419	Hs.77274	SS,krtlike,trypsin	plasminogen activator, urokinase	3.3
	431958	X63629	Hs.2877	SS,TM,Cadherin_C_term,cadherin	cadherin 3, type 1, P-cadherin (placental	3.3
	418462	BE001596	Hs.85266	SS,TM,Integrin_B,fn3	integrin, beta 4	3.3
	424687	J05070	Hs.151738	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 9 (gelatinase B,	3.3
	401488	NA		SS,TM,trypsin	C4000647*gi4758508[re]NP_004253.1] air	3.2
60	408113	T82427	Hs.194101	TM,7tm_3Ribosomal_L13	Homo sapiens cDNA: FLJ20869 fis, clone AD	3.2
	427359	AW020782	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, clone LN	3.2
	452934	AA581322	Hs.4213	SS,TM,Ig	hypothetical protein MGC16207	3.1
	448988	Y09763	Hs.22785	SS,TM	gamma-aminobutyric acid (GABA) A receptor	3.1
	439750	AL359053	Hs.57664	TM,Integrin_B,Ricin_B_lectinmm	Homo sapiens mRNA full length insert cDNA	3.1
65	414696	AF002020	Hs.76918	SS,TM,Patched	Niemann-Pick disease, type C1	3.1
	435604	AA625279	Hs.25892	TM	uncharacterized bone marrow protein BM040	3.1
	453883	AI638516	Hs.22630	TM,Ets,SAM_PNT	cofactor required for Sp1 transcriptional	3.0
	448733	NM_005629	Hs.187958	SS,TM,SNF,ABC_tran,iodh,pkinase,DSPE,Ribosomal_L	solute carrier family 6 (neurotransmitter	3.0
	444946	AW139205	Hs.156457	SS,TM,abhydrolase	hypothetical protein FLJ22408	3.0
70	437938	AI950087		TM,histone,Ig,MHC_I	gb:wg05c02.x1 NCI_CGAP_Kid12 Homo sapiens	3.0
	424441	X14850	Hs.147097	TM,histone	H2A histone family, member X	3.0
	427061	AB032971	Hs.173392	TM	KIAA1145 protein	3.0
	409703	NM_006187	Hs.56009	SS	2'-5'-oligoadenylate synthetase 3 (100 kD	3.0
	447313	U92981	Hs.18081	TGF-beta	Homo sapiens clone DT1P1B6 mRNA, CAG repe	3.0
75	431070	AW408164	Hs.249184	ABC_tran	transcription factor 19 (SC1)	2.9
	446269	AW263155	Hs.14559	TM	hypothetical protein FLJ10540	2.9
	421190	U95031	Hs.102482	TM,ywd	mucin 5, subtype B, tracheobronchial	2.9
	452732	BE300078	Hs.80449	TM	Homo sapiens, clone IMAGE:3535294, mRNA,	2.9
	443859	NM_013409	Hs.9914	SS,kazal	folistatin	2.9
80	446733	AA863360	Hs.26040	TM,p450	ESTs, Weakly similar to fatty acid omega-	2.9
	449746	AI688594	Hs.176588	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN CYTOCH	2.9
	418844	M62982	Hs.1200	SS,TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase	2.9
	414581	AA256213	Hs.72010	TM,Cam_acyltransf,Choline_kinase,SCO1-SenC	ESTs	2.9
	431629	AU077025	Hs.265827	SS,IRNA_antiSH2,SH3,pkinase	interferon, alpha-inducible protein (clon	2.8
	445873	AA250970	Hs.251946	SS,rm,PABPpkinase,14-3-3,rm	poly(A)-binding protein, cytoplasmic 1-f	2.8
	438113	AI467908	Hs.8882	TM,7tm_1	ESTs	2.8
	410310	J02931	Hs.62192	SS,TM,Tissue_fac	coagulation factor III (thromboplastin, I	2.8

5	411558	AA102670	Hs.70725	SS,TM	gamma-aminobutyric acid (GABA) A receptor	2.8
	413273	U75679	Hs.75257	TM,lg,kinase	stem-loop (histone) binding protein	2.8
	426343	NM_014642	Hs.169387	TM,SCAN7tm_1	KIAA0036 gene product	2.8
	433345	AI681545	Hs.152982	SS	hypothetical protein FLJ13117	2.7
	452234	AW084176	Hs.223296	TM	ESTs, Weakly similar to I38022 hypothetic	2.7
	456181	L36463	Hs.1030	TM,RA,VPS9	ras inhibitor	2.7
	408380	AF123050	Hs.44532	TM,ubiquitin7tm_3,ANF_receptor,sushi	diubiquitin	2.7
	422278	AF072873	Hs.114218	TM,Frizzled,Fz	frizzled (Drosophila) homolog 6	2.7
10	446839	BE091926	Hs.18244	TM	mitotic spindle coiled-coil related prote	2.7
	416250	AA581386	Hs.73452	TM,REJ,PLAT,PKD,WSC,LRRCT,GPSPMP22_Claudin	hypothetical protein MGC10791	2.7
	407287	AI578812		TM,rascadherin	gb:tu59d08.x1 NCI_CGAP_Gas4 Homo sapiens	2.7
	412977	AA125910	Hs.191461	TGF-beta	ESTs	2.7
	400298	AA032279	Hs.61635	TM	six transmembrane epithelial antigen of I	2.7
15	425483	AF231022	Hs.158159	EGF,cadherin,laminin_G	FAT tumor suppressor (Drosophila) homolog	2.7
	430152	AB001325	Hs.234542	SS,TM,MIP	aquaporin 3	2.7
	444006	BE395085	Hs.10086	SS,TM	type I transmembrane protein Fn14	2.7
	418869	AW516565		TM,RasGAP,IQ,WW	gb:qx01d05.x1 Soares_NHCC_cervical_tumor	2.7
	416658	U03272	Hs.79432	SS,TM,EGF,TB	fibrillin 2 (congenital contractual arac	2.6
20	410290	AA402307	Hs.322844	SS,TM,Sema,TIG,Plaxin_repeat	hypothetical protein DKFZp564A176	2.6
	419667	AU077005	Hs.92208	SS,TM,disintegrin,Repolyisin,Pep_M12B_propep	a disintegrin and metalloproteinase domain	2.6
	406671	AA125547	Hs.285754	TM,kinase,Plaxin_repeat,Sema,TIG,LIM	met proto-oncogene (hepatocyte growth fac	2.6
	434444	AI765276	Hs.101257	TM	hypothetical protein MGC3295	2.6
	421817	AF146074	Hs.108660	TM,ABC_tran,ABC_membrane,Rhomboid	ATP-binding cassette, sub-family C (CFTR/	2.6
25	431890	X17033	Hs.271986	vwa,FG-GAP,Integrin_A	integrin, alpha 2 (CD49B, alpha 2 subunit	2.6
	452281	T93500	Hs.28792	TGF-beta,TGFb_propeptide	Homo sapiens cDNA FLJ11041 fis, clone PLA	2.6
	421508	BE302798	Hs.105097	TM,TK	thymidine kinase 1, soluble	2.6
	453331	AI240665	Hs.8895	TM,disintegrin,Pep_M12B_propep,Repolyisin	ESTs	2.6
	447197	R36075		TM,SDF	gb:yh88b01.s1 Soares_placenta Nb2HP Homo	2.5
30	459688	U72671	Hs.151250	SS,TM,lg	intercellular adhesion molecule 5, telenc	2.5
	437412	BE069288	Hs.34744	TM,ABC_tran,ABC_membrane,Rhomboid	Homo sapiens mRNA; cDNA DKFZp547C136 (fro	2.5
	429413	NM_014058	Hs.201877	trypsin	DESC1 protein	2.5
	424420	BE614743	Hs.146688	TM,MAPEG	prostaglandin E synthase	2.5
	427239	BE270447	Hs.174070	TM,UQ_con	ubiquitin carrier protein	2.5
35	407103	AA424881	Hs.256301	TM,cNMP_bindingtrypsin	hypothetical protein MGC13170	2.5
	431130	NM_006103	Hs.2719	SS,TM,wap	epididymis-specific, whey-acidic protein	2.5
	453379	AA035261	Hs.61753	PAN,kringle,trypsin	ESTs	2.5
	421733	AL119671	Hs.1420	SS,TM,lg,kinase	fibroblast growth factor receptor 3 (acho	2.5
	452220	BE158006	Hs.212296	TM,Integrin_A,FG-GAP	ESTs	2.5
40	417975	AA641836	Hs.30085	SS,trypsin	hypothetical protein FLJ23186	2.5
	440381	AA917808	Hs.190495	TM	ESTs	2.5
	441794	AW197794	Hs.253338	TM	ESTs	2.5
	439108	AW163034	Hs.6467	SS,TM	synaptogyrin 3	2.5
	401103	NA		TM,vwd	C120012333g173053611refNP_038652.1 oto	2.4
45	430630	AW269920	Hs.2621	TM,cystatin	cystatin A (stefin A)	2.4
	430129	BE301708	Hs.233955	TM,Glyco_transf_11	hypothetical protein FLJ20401	2.4
	415621	AI648602	Hs.55468	TM,histone,Soc1sugar_tr	ESTs	2.4
	402745			SS,TM,EGF,Idl_recepLb,thyroglobulin_1	NM_002508Homo sapiens nidogen (enactin)	2.4
50	407758	D50915	Hs.38365	SS,TM	KIAA0125 gene product	2.4
	457570	AA579428		TM	gb:nf37c09.s1 NCI_CGAP_Py2 Homo sapiens c	2.4
	429574	BE268321	Hs.208912	SS,TM	hypothetical protein MGC861	2.4
	431211	M86849	Hs.323733	SS,TM,connexin	gap junction protein, beta 2, 26kD (conn	2.4
	452865	AI924046	Hs.119567	SS,TM,PMP22_Claudin	ESTs, Weakly similar to A47582 B-cell gro	2.4
	420511	AF052692	Hs.98485	SS,TM,connexin	gap junction protein, beta 3, 31kD (conn	2.4
55	437897	AA770561	Hs.146170	SS,pro_isomerase	hypothetical protein FLJ22969	2.4
	437846	AA773866	Hs.244569	TM	esophagus cancer-related gene-2	2.4
	418432	M14156	Hs.85112	Insulin	insulin-like growth factor 1 (somatomedin	2.3
	438108	AI471795	Hs.287776	TM	vanilloid receptor-related osmotically ac	2.3
60	453406	AI192987	Hs.61784	kinase,Furin-like,Recep_L_domain	hypothetical protein FLJ14451	2.3
	435542	AA687378	Hs.269533	kinase,RhoGEF,lg,PH,SH3	ESTs	2.3
	434517	AA635690	Hs.337251	TM	hypothetical protein MGC2487	2.3
	431630	NM_002204	Hs.265829	SS,TM,FG-GAP,Integrin_A	integrin, alpha 3 (antigen CD49C, alpha 3	2.3
	422310	AA316622	Hs.98370	SS,TM,ln3,lg,kinase,Ribosomal_L36e,p450	cytochrome P450, subfamily IIS, polypepti	2.3
	441954	AI744935	Hs.8047	TM,Band_7,AAAcdc48_N	Fanconi anemia, complementation group G	2.3
65	416091	AF296370	Hs.283082	SS,TM,Defensin_beta	defensin, beta 3	2.3
	429359	W00482	Hs.2399	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 14 (membrane-lns	2.3
	409402	AF208234	Hs.695	TM,cystatin	cystatin B (stefin B)	2.3
	432284	AA532807	Hs.105822	TM,kinase	ESTs	2.3
	408243	Y00787	Hs.624	SS,TM,IL8	Interleukin 8	2.3
70	423229	AC003965	Hs.125532	SS,trypsin	protease, serine, 26	2.3
	408713	NM_001248	Hs.47042	GDA1_CD39	ectonucleoside triphosphate diphosphohydr	2.3
	440502	AI824113	Hs.78281	RGS,GoLoco,RBD	regulator of G-protein signalling 12	2.3
	429929	AB014583	Hs.226275	TM	KIAA0583 gene product	2.3
	439963	AW247529	Hs.6793	TM,p450Ets	platelet-activating factor acetylhydrolas	2.3
75	428953	AA306510	Hs.194676	SS,TM,TNFR_c6,arf,Stathmin,DEAD	tumor necrosis factor receptor superfamil	2.3
	439398	AA284267	Hs.221504	SS	ESTs	2.2
	440371	BE268550	Hs.80449	TM	Homo sapiens, clone IMAGE:3535294, mRNA,	2.2
	452203	X57522	Hs.158164	SS,TM,ABC_tran,ABC_membrane	transporter 1, ATP-binding cassette, sub-	2.2
	407811	AW190902	Hs.40098	SS	cysteine knot superfamily 1, BMP antagoni	2.2
80	432078	BE314877	Hs.24553	TM	hypothetical protein FLJ12541 similar to	2.2
	429113	D28235	Hs.196384	SS,TM,EGF	prostaglandin-endoperoxide synthase 2 (pr	2.2
	452755	AW138937	Hs.213436	Glyco_transf_29	ESTs, Weakly similar to A34087 hypothetic	2.2
	428434	AW363590	Hs.65551	SS	Homo sapiens, Similar to DNA segment, Chr	2.2
	429922	Z97630	Hs.226117	TM,linker_histone7tm_1	H1 histone family, member 0	2.2

5	417903	NM_002342	Hs.1116	SS,TM,ASC,TNFR_c6	lymphotoxin beta receptor (TNFR superfamily	2.2
	422012	AW403423	Hs.110746	SS,homobox,pou	HCR (a-helix coiled-coil rod homologue)	2.2
	433090	AI720050	Hs.145362	SS,TM	immortalization-upregulated protein	2.2
	417576	AA339449	Hs.82285	TM,AIRS,formyl_transf,GARS	phosphoribosylglycinamide formyltransferase	2.2
	409994	D86864	Hs.57735	IP_transSH2,SH3	acetyl LDL receptor; SREC	2.2
	417433	BE270266	Hs.82128	SS,TM,LRCT,LRNT,LR	5T4 oncofetal trophoblast glycoprotein	2.2
	416763	AI908127	Hs.79748	TM,alpha-amylase7tm_1	solute carrier family 3 (activators of di	2.2
	425999	AW513051	Hs.332981	TM,FAD_binding_2,P53PA,Ribosomal_S2,FAD_bindi	ESTs, Weakly similar to I38022 hypothetical	2.2
10	452799	AI948829	Hs.213786	TM	ESTs	2.2
	414733	BE514535	Hs.77171	TM,MCMHeme_oxygenase	minichromosome maintenance deficient (S.	2.2
	448153	Y10805	Hs.20521	SS,TM,Na_Ca_Ex	HMT1 (hnRNP methyltransferase, S. cerevis	2.2
	428959	AF120274	Hs.194589	SS	artemin	2.2
	443171	BE281128	Hs.9030	SS,TM,7tm_1,rm	TONDU	2.2
	408308	AL033377	Hs.44197	TM,7tm_2	hypothetical protein DKFZp564D0462	2.2
15	409533	AW969543	Hs.21291	TM	mitogen-activated protein kinase kinase k	2.2
	408201	AK000568	Hs.43654	TM	hypothetical protein FLJ20561	2.1
	408996	AI979168	Hs.82226	TM	glycoprotein (transmembrane) nmb	2.1
	417900	BE250127	Hs.82906	TM,WD40,pro_isomerase	CDC20 (cell division cycle 20, S. cerevis	2.1
20	437191	NM_006846	Hs.331555	SS,TM,kazal	serine protease inhibitor, Kazal type, 5	2.1
	412834	R77123	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, clone LN	2.1
	431117	AF003522	Hs.250500	SS,TM,DSL,EGF	deltá (Drosophila)-like 1	2.1
	447674	BE270640	Hs.19192	TM,pkinaseras,arf	cyclin-dependent kinase 2	2.1
	409651	H96643	Hs.283565	bZIPcofilin_ADF,EGF	FOS-like antigen-1	2.1
25	440495	AA887212	Hs.14161	TM,NSFNa_Ca_Ex	hypothetical protein DKFZp434H1930	2.1
	429415	NM_002593	Hs.202097	SS,CUB,NTR,MAM,TIL,TiLa,vwd,EPO_TPO	procollagen C-endopeptidase enhancer	2.1
	421013	M62397	Hs.1345	TM	mutated in colorectal cancers	2.1
	447827	U73727	Hs.19718	SS,TM,Y_phosphatase,fn3,lg,MAM	protein tyrosine phosphatase, receptor ty	2.1
	449224	AW995911	Hs.299883	fn3	hypothetical protein FLJ23399	2.1
	452679	Z42387	Hs.83883	TM	transmembrane, prostate androgen induced	2.1
30	409956	AW103364	Hs.727	SS,TGF-beta,TGFB,propeptide	inhibin, beta A (activin A, activin AB al	2.1
	438580	AA811262	Hs.299202	TM,pkinasesugar_tr	ESTs	2.1
	406400			SS,TM,trypsin	NM_007196Homo sapiens kallikrein 8 (neur	2.1
	424965	AW956282	Hs.144609	TM	Homo sapiens, Similar to RIKEN cDNA 57305	2.1
35	412270	AC005262	Hs.73797	TM,G-alpha	guanine nucleotide binding protein (G pro	2.1
	428471	X57348	Hs.184510	TM,14-3-3	stratifin	2.1
	427375	AL035460	Hs.177536	SS,Zn_carbOpept,hormone5Reprotysin	metallocarboxypeptidase CPX-1	2.1
	416498	U33632	Hs.79351	TM	potassium channel, subfamily K, member 1	2.1
	423453	AW450737	Hs.128791	SS,Grainin,CDP-OH_P_transf	CGI-09 protein	2.1
40	417944	AU077196	Hs.82985	SS,COLFI,Collagen,vwc	collagen, type V, alpha 2	2.1
	424197	AF096834	Hs.142989	SS,TM,CSD	germ cell specific Y-box binding protein	2.1
	446163	AA026880	Hs.25252	TM,fn3	prolactin receptor	2.1
	417331	AW411297	Hs.81972	TM,SH2,PID	SHC (Src homology 2 domain-containing) tr	2.1
	430413	AW842182	Hs.241392	IL8,PX	small inducible cytokine A5 (RANTES)	2.1
45	421685	AF189723	Hs.106778	TM,E1-E2_ATPase,HydrolaseE1-E2_ATPase	ATPase, Ca transporting; type 2C, member	2.1
	407305	AA715284		TM,pkinase,Sema,Plexin_repeat,TIG,LIM	gb:mv35f03r1 NCL CGAP_Br5 Homo sapiens c	2.1
	407792	AI077715	Hs.39384	SS	putative secreted ligand homologous to f	2.0
	418695	AA447014	Hs.193261	SS	hypothetical protein MGC2991	2.0
	439738	BE246502	Hs.9598	TM,RasGAP,IQ,VWV	sema domain, immunoglobulin domain (Ig),	2.0
50	433398	AW843150	Hs.112412	TM,PMP22_Claudin	ESTs	2.0
	456327	H68741	Hs.38774	TM,Glyco_transf_8	ESTs	2.0
	446872	X97058	Hs.16362	TM	pyrimidinergic receptor P2Y, G-protein co	2.0
	419726	U50330	Hs.1274	SS,TM,Atacin,CUB,EGF	bone morphogenetic protein 1	2.0
	410116	AW630671	Hs.58636	SS,TM	squamous cell carcinoma antigen recognize	2.0
55	426500	NM_014638	Hs.170156	TM	KIAA0450 gene product	2.0
	452194	AI694413	Hs.332649	TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfamily 1	2.0
	418140	BE613836	Hs.83551	TM,E1-E2_ATPase	microfibrillar-associated protein 2	2.0
	425856	AF135025	Hs.159679	SS,trypsin	kallikrein 12	2.0
	434346	AA630445	Hs.116773	TM,Fem1c_reduct	ESTs	2.0
60	426274	D38122	Hs.2007	TM,TNF	tumor necrosis factor (ligand) superfamily	2.0
	440008	AW051683	Hs.277686	TM,RhoGEF,FYVE,PH	ESTs	2.0
	424634	NM_003613	Hs.151407	ig,isp_1	cartilage intermediate layer protein, nuc	2.0
	446641	AL049229	Hs.15787	TM,pkinase,rm	Homo sapiens mRNA; cDNA DKFZp564O1016 (fr	2.0
	418851	AA178828	Hs.192435	TM	ESTs	2.0
65	440351	AF030933	Hs.7179	TM,Rad1,Cadherin_C_lem	RAD1 (S. pombe) homolog	2.0
	439496	BE616501	Hs.32343	SS	Homo sapiens, Similar to RIKEN cDNA 11100	2.0
	454197	BE140966		TM,Ammonium_transpkinasin,Ammonium_transp	gb:MR0-HT0065-081199-002-b06 HT0065 Homo	2.0
	433573	AF234887	Hs.57652	TM,7tm_2,GPSIRNA-synt_2b,Seryl_URNA_N	cadherin, EGF LAG seven-pass G-type recep	2.0
	429211	AF052693	Hs.198249	TM,connexin	gap junction protein, beta 5 (connexin 31	2.0
70	420737	L08096	Hs.99899	SS,TM,TNF	tumor necrosis factor (ligand) superfamily	2.0
	455333	AW897851		TM,Glyco_hydro_2	gb:RC1-NN0063-100500-022-c08 NN0063 Homo	2.0
	414784	NM_000344	Hs.288986	SS,TM,BIR	survival of motor neuron 1, telomeric	2.0
	435836	AW292532	Hs.250175	TM,GNS1_SUR4	homolog of yeast long chain polyunsaturat	2.0
	411789	AF245505	Hs.72157	TM,lg,LRCT	DKFZP564I1922 protein	2.0
	441455	AJ271671	Hs.7854	TM,ras,DENN	zinc/ferron regulated transporter-like	2.0
75	426068	AF029778	Hs.166154	SS,TM,DSL,EGF,NUDIX	jagged 2	2.0
	439733	AL365412	Hs.107203	TM,Sm	hypothetical protein from EUROMIMAGE 17593	2.0
	435014	BE560898	Hs.10026	TM,Ribosomal_L17	mitochondrial ribosomal protein L17	1.9
	457819	AA057484	Hs.35406	TM	ESTs, Highly similar to unnamed protein p	1.9
	422737	M26939	Hs.119571	SS,Collagen,COLFI	collagen, type III, alpha 1 (Ehlers-Danlo	1.9
80	431104	AW970859	Hs.313503	Sema,lg	ESTs	1.9
	432210	AI567421	Hs.273330	TM,laminin_G,laminin_EGF,kazatubiquitin	Homo sapiens, clone IMAGE:3544662, mRNA,	1.9
	436511	AA721252	Hs.291502	TM,disintegrin,Reprotysin,Pep_M12B_propep,pkinase,	ESTs	1.9
	419216	AU076718	Hs.164021	SS,IL8	small inducible cytokine subfamily B (Cys	1.9

5	432169	Y00971	Hs.2910	TM,Prbbsyltran	phosphoribosyl pyrophosphate synthetase 2	1.9
	441128	AA570256	Hs.54628	TM,ras	ESTs, Weakly similar to T23273 hypothetical	1.9
	447160	AA330310	Hs.24181	TM	ESTs	1.9
	419138	U48508	Hs.89531	TM,RYDR_ITPR,RyR,SPRY	ryanodine receptor 1 (skeletal)	1.9
	457817	AA247751	Hs.79572	TM,hemopexin,Peptidase_M10	calthepsin D (lysosomal aspartyl protease)	1.9
	431009	BE149762	Hs.48956	SS,TM,connexin	gap junction protein, beta 6 (connexin 30)	1.9
	428957	NM_003881	Hs.194679	SS,TM,vwc,IGFBP,isp_1	WNT1 inducible signaling pathway protein	1.9
	418546	AA224827		TM,vwa,FG-GAP,Integrin_A	gbnc32g04.s1 NCI_CGAP_Pr2 Homo sapiens c	1.9
10	400749			SS,TM,Idl_recept_a,fn3,Idl_recept_Lb	NM_003105:Homo sapiens sorilin-related	1.9
	408369	R38438	Hs.182575	F-protein	solute carrier family 15 (H777) transporters	1.9
	422765	AW409701	Hs.1578	TM,BIR	baculoviral IAP repeat-containing 5 (surv	1.9
	417409	BE272506	Hs.82109	TM,Syndecan	syndecan 1	1.9
	407720	AB037776	Hs.38002	TM,catponin,CH	KIAA1355 protein	1.9
15	418830	BE513731	Hs.88959	TM,CDP-OH_P_transf,MCM	hypothetical protein MGC4816	1.9
	434769	AA648884	Hs.134278	TM,CDP-OH_P_transf,MCM	Homo sapiens cDNA FLJ12676 fis, clone NT2	1.9
	421593	NM_017436	Hs.105956	SS,TM	glutathione S-transferase (GST) pi	1.9
	426054	BE387014	Hs.166146	TM,WH1	Homer, neuronal immediate early gene, 3	1.9
	404604	NA		TM	Target Exon	1.9
20	422753	AI928995	Hs.1575	SS,TM,Sm	small nuclear ribonucleoprotein D3 polype	1.9
	422739	H20106	Hs.119591	SS,ClaL_adaptor_s	adaptor-related protein complex 2, sigma	1.9
	433088	NM_008456	Hs.288215	SS,Prbbsyltran	sialyltransferase	1.9
	419594	AA013051	Hs.91417	TM	topoisomerase (DNA) II binding protein	1.9
	428188	M98447	Hs.22	TM,Transglutamin_C,Transglutamin_N,Transglut_core	transglutaminase 1 (K polypeptide epiderm	1.9
25	428343	AL043021	Hs.12705	TM,Rhomboid,HMG_boxTPR	ESTs	1.9
	429592	AB029041	Hs.209646	Troponin	KIAA1118 protein	1.9
	431620	AA126109	Hs.264981	C2,PH,RasGAP,NTP_transf_2	2'-5'-oligoadenylate synthetase 2 (69-71	1.9
	424670	W61215	Hs.116651	ig	epithelial V-like antigen 1	1.9
	428373	AI751656	Hs.183986	SS,TM,Ig	poliovirus receptor-related 2 (herpesviru	1.9
30	453449	W16752	Hs.32981	SS,Ig,Sema	soma domain, immunoglobulin domain (Ig),	1.9
	432304	AA932188	Hs.69297	TM,Tm_1	ESTs	1.9
	432673	AB028859	Hs.278605	TM,DnaJ,DnaJ_CDnaJ	DnaJ (Hsp40) homolog, subfamily B, member	1.9
	416207	NM_014745	Hs.336433	SS,TM,zf-DHHC	Homo sapiens, clone MGC2908, mRNA, compl	1.9
	408988	AL119844	Hs.49476	TM,Plexin_repeat,Sema,isp_1	Homo sapiens clone TUA8 Cri-du-chat regio	1.9
35	417426	NM_002291	Hs.82124	SS,laminin_EGF,laminin_Nterm	laminin, beta 1	1.9
	443883	AA114212	Hs.9930	SS,TM,serpin,Marek_A	serine (or cysteine) proteinase inhibitor	1.9
	433328	AW298159	Hs.23644	SS,TM	ESTs, Weakly similar to S65824 reverse tr	1.9
	419981	AA897581	Hs.128773	TM,SkI_Sno	ESTs	1.8
	420931	AF044197	Hs.100431	SS,TM,IL8	small inducible cytokine B subfamily (Cys	1.8
40	415023	AA932146	Hs.133494	TM,Ribosomal_S17Ribosomal_L13	Homo sapiens clone TCCCA00164 mRNA seque	1.8
	413644	BE154910	Hs.278793	TM,Glyco_hydro_2	ESTs, Weakly similar to Z195_HUMAN ZINC F	1.8
	449987	AW079749	Hs.184719	TM,ABC_tran,ABC_membraneion_trans	ESTs, Weakly similar to ALU1_HUMAN ALU SU	1.8
	421340	F07783	Hs.1369	SS,sushi	decay accelerating factor for complement	1.8
	417866	AW067903	Hs.82772	SS,TM,Collagen,COL1,TSPN	collagen, type XI, alpha 1	1.8
45	430259	BE550182	Hs.127826	TM,transmembrane4RasGEF,RA	Ra1GEF-like protein 3, mouse homolog	1.8
	432998	AA835948	Hs.153307	TM,SDF	ESTs	1.8
	431671	NM_016937	Hs.267289	TM,NA	polymerase (DNA directed), alpha	1.8
	411773	NM_006799	Hs.72026	trypsin	protease, serine, 21 (trypsin)	1.8
50	425247	NM_006940	Hs.155324	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 11 (stromelysin	1.8
	422976	AL076657	Hs.1600	TM,cpn60_TCP1,Sema	chaperonin containing TCP1, subunit 5 (cp	1.8
	425159	NM_004341	Hs.154868	SS,TM,GATase,OTCase,CPSase_L_chain,Dihydrooro	carbamoyl-phosphate synthetase 2, asparta	1.8
	447776	AI525825	Hs.130181	Ricin_B_lectin	UDP-N-acetyl-alpha-D-galactosamine:polype	1.8
	426908	AW815163	Hs.172851	SS,TM,fusion_gly,Myosin_tailadh_short	arginase, type II	1.8
	408116	AA251393	Hs.289052	TM,Na_Ca_ExCam_acyltransf	Homo sapiens, Similar to RIKEN cDNA 54304	1.8
55	417847	AI521558	Hs.7331	Uteroglobulin	hypothetical protein FLJ22316	1.8
	415791	H09366	Hs.78853	SS,TM,UNG	uracil-DNA glycosylase	1.8
	407903	AI287341	Hs.154029	TM,ubiquitin,laminin_G,laminin_EGF,kazal	bHLH factor Hes4	1.8
	422511	AU076442	Hs.117938	TM,p450	collagen, type XVII, alpha 1	1.8
	414117	W88559	Hs.1787	TM,lon_trans,K_tetra	proteolipid protein 1 (Pelizaeus-Merzbach	1.8
60	426841	AI052358	Hs.193726	TM,esp	ESTs	1.8
	415272	AA164215	Hs.203186	TM,TPR,pkinase,Ig,B56	ESTs	1.8
	426440	BE382756	Hs.169902	TM,sugar_tr,Fork_head	solute carrier family 2 (facilitated gluc	1.8
	419488	AA316241	Hs.90691	FGF	nucleophosmin/nucleoplasmin 3	1.8
	418452	BE379749	Hs.85201	SS,TM,lectin_c	C-type (calcium dependent, carbohydrate-r	1.8
65	431363	M86528	Hs.266902	SS,NGF	neurotrophin 5 (neurotrophin 4/5)	1.8
	440975	AW499914	Hs.7579	SS,TM	hypothetical protein FLJ10402	1.8
	438962	BE046594		TGF-beta,bZIP	gbn41c11.x1 NCI_CGAP_RDF2 Homo sapiens	1.8
	414602	AW630088	Hs.76550	SS	Homo sapiens mRNA; cDNA DKFZp564B1264 (fr	1.8
	418054	NM_002318	Hs.83354	TM,milo_carr,Lysyl_oxidase	lysyl oxidase-like 2	1.8
70	440501	AA897391	Hs.202229	TM,Galactosyl_T	ESTs	1.8
	449309	AW589823	Hs.224189	TM	ESTs	1.8
	421461	AW291023	Hs.97255	TM,Lysyl_oxidase,SCP2,Band_7	ESTs, Weakly similar to A46010 X-linked r	1.8
	412584	X54870	Hs.74085	TM,lectin_c	DNA segment on chromosome 12 (unique) 248	1.8
	441565	AW953575	Hs.303125	TM	p53-induced protein PIGPC1	1.8
75	431837	T9326	Hs.326553	TM,7tm_3_ANF_receptor,sushi	olfactory receptor, family 2, subfamily I	1.8
	436251	BE515065	Hs.296585	SS,Y_phosphataseTIG	nucleolar protein (KKE/D repeat)	1.8
	448633	AA311426	Hs.21635	TM,EGF,laminin_G,fibrinogen_C,F5_F8_type_C,tubulin	tubulin, gamma 1	1.8
	424291	AL120051	Hs.144700	TM,Ephrin,Hist_deacetyl	ephrin-B1	1.8
	415388	AF018081	Hs.78409	SS,TM,TSPN,Collagen	collagen, type XVIII, alpha 1	1.8
	435550	AI224456	Hs.4934	TM,LRR,LRRCT	H.sapiens polyA site DNA	1.8
80	448568	AA149121	Hs.71947	TM,LRRCT	ESTs	1.8
	439246	AA498072	Hs.77783	SS,TM,REJ,PLAT,PKD,WSC,LRRCT,GPSPMP22_Cla	membrane-associated tyrosine- and threon	1.8
	410001	AB041036	Hs.57771	SS,TM,lypsin	kallikrein 11	1.8
	417312	AW888411	Hs.81915	SS,Stathmin	leukemia-associated phosphoprotein p18 (s	1.8

5	444152	AI125694	Hs.149305	TM	hypothetical protein MGC2603	1.8
	453454	AW052008	Hs.8551	TM	PRP4/STKWD splicing factor	1.8
	449320	AB030835	Hs.23476	SS,adenylatekinase	Cip1-interacting zinc finger protein	1.8
	428329	AA426091	Hs.98453	TM,Gal-bind_lectin	ESTs, Moderately similar to R27328.2 [H.s]	1.8
	452875	BE275760	Hs.30928	TM,Apolipoprotein	DNA segment on chromosome 19 (unique) 117	1.8
	444031	BE271513	Hs.25303	TM,Peptidase_M10,hemopexin	hypothetical protein FLJ13154	1.8
	443534	AI076123		TM	gbay92e04.x1 Soares_fetal_liver_spleen_1	1.8
	413313	NM_002047	Hs.75280	TM,WHEP-TRS,7tm_2	glycyl-tRNA synthetase	1.8
10	452874	AK001061	Hs.30925	SS	hypothetical protein FLJ10199	1.8
	453140	AA032238	Hs.170531	TM	ESTs	1.8
	418541	BE243136	Hs.86947	SS,TM,disintegrin,Pep_M12B_propep,Reprolysin	a disintegrin and metalloproteinase domain	1.8
	432925	AA878324	Hs.192734	SS	ESTs	1.8
	453857	AL080235	Hs.35861	TM	DKFZP586E1621 protein	1.8
15	457663	AW371946	Hs.337459	TM	ESTs	1.8
	452873	AK001247	Hs.30922	TM	hypothetical protein FLJ10385	1.8
	436396	AI683487	Hs.152213	SS,wnt	wingless-type MMTV integration site family	1.8
	452835	AK001269	Hs.30738	TM	hypothetical protein FLJ10407	1.7
	459647	R34107	Hs.198287	ig	pregnancy specific beta-1-glycoprotein 11	1.7
20	418245	AA088767	Hs.83883	TM,PEPCK	transmembrane, prostate androgen induced	1.7
	448484	BE613340	Hs.334725	TM	Homo sapiens, Similar to RIKEN cDNA 94300	1.7
	431369	BE184455	Hs.251754	SS,wap	secretory leukocyte protease inhibitor (a	1.7
	434877	AW974792	Hs.292171	TM	ESTs	1.7
	428923	BE047698	Hs.188785	TM	ESTs	1.7
25	402915	NA		TM,HCO3_cotransp	ENSP0000020587~Bicarbonate transporter-	1.7
	420185	AL044056	Hs.158047	TM	ESTs	1.7
	445739	AW136354	Hs.145303	TM	ESTs	1.7
	409435	AI810721	Hs.95424	TM,p450	ESTs	1.7
	408688	AI634522	Hs.152925	TM	KIAA1268 protein	1.7
30	420085	AI741909	Hs.44680	TM	hypothetical protein FLJ20979	1.7
	433933	AI754389	Hs.133494	TM,Ribosomal_S17,Ribosomal_L13	Homo sapiens clone TCCCA00164 mRNA seque	1.7
	430965	AA489732	Hs.154918	hormone_rec,Prog_receptor,zf-C4	ESTs	1.7
	414703	BE243877	Hs.76941	SS,TM,Na_K-ATPaseE2F_TDP	ATPase, Na? transporting, beta 3 polypept	1.7
	423464	NM_016240	Hs.128856	TM,Collagen	CSR1 protein	1.7
35	416737	AF154335	Hs.79691	SS,TM,LIM,PDZsugar_tr,PDZ,LIM	LIM domain protein	1.7
	409012	AL117435	Hs.49725	TM,RhoGEFzf-DHHC,adh_short	DKFZP4341216 protein	1.7
	423804	AW403448	Hs.1706	TM,IRF	interferon-stimulated transcription facto	1.7
	410418	D31382	Hs.63325	SS,TM,trypsin,ldl_recept_a	transmembrane protease, serine 4	1.7
	440028	AW473675	Hs.125843	TM	ESTs, Weakly similar to T17227 hypothetic	1.7
40	457646	AA725650	Hs.112948	TM,SPRY	ESTs	1.7
	445439	BE243084	Hs.12719	SS,TGF-beta	regulator of nonsense transcripts 1	1.7
	420426	AA262045	Hs.36567	TM,Galactosyl_T_2ATP-synt_C	Homo sapiens cDNA FLJ14227 fs, clone NT2	1.7
	431341	AA307211	Hs.251531	TM,proteasome	proteasome (prosome, macropain) subunit,	1.7
45	412338	AA151527	Hs.69485	TM,Sema,Plaxin_repeat,TIG,Plaxin_repeat	hypothetical protein FLJ12436	1.7
	414799	AI752416	Hs.77326	SS,thyroglobulin_1,JGFBP	insulin-like growth factor binding protel	1.7
	452700	AI859390	Hs.288940	TM,DIX,RGS,thioredo	five-span transmembrane protein M83	1.7
	430877	NM_005269	Hs.2693	GST_C,tRNA-synt_1,WHEP-TRS,TGF-beta	glioma-associated oncogene homolog (zinc	1.7
	428624	AI125222	Hs.98712	TM,thioredo,Y_phosphatase,MAMJg,fm3MSP_domain	hypothetical protein DKFZP434H0311	1.7
	444065	AW449415	Hs.10260	TM,ion_trans	Homo sapiens cDNA FLJ11341 fs, clone PLA	1.7
50	416319	AI815601	Hs.79197	SS,TMJg	CD83 antigen (activated B lymphocytes, im	1.7
	429367	AB007867	Hs.278311	Sema,Plaxin_repeat,TIG	plexin B1	1.7
	430425	AA531428	Hs.241412	TM	apolipoprotein L_2	1.7
	441668	AI611973	Hs.127525	TM,Ammonium_transp	ESTs	1.7
	418469	U34879	Hs.85279	SS,TM,adh_short	hydroxysteroid (17-beta) dehydrogenase 1	1.7
55	450835	BE262773	Hs.25584	TM,ArfGap	hypothetical protein FLJ10767	1.7
	418859	AA229558		TM	gbnc15d10.s1 NCL_CGAP_Pr1 Homo sapiens c	1.7
	426304	AA463844	Hs.31339	TMJg,ITAM	fibroblast growth factor 11	1.7
	423635	X85019	Hs.130181	TM,Ricin_B_lectin	UDP-N-acetyl-alpha-D-galactosamine:polype	1.7
	414820	AA371931	Hs.77422	TM,ion_trans,LIM,Synaptophysin	proteolipid protein 2 (colonic epithelium	1.7
60	440654	AW014242	Hs.159998	TM,connexin	ESTs	1.7
	412276	BE262621	Hs.73798	SS,MIF	macrophage migration inhibitory factor (g	1.7
	422087	X58968	Hs.111301	SS,Peptidase_M10,fm2,hemopexin	matrix metalloproteinase 2 (gelatinase A,	1.7
	407151	H25836	Hs.301527	SS,TNF	ESTs, Moderately similar to unknown [H.s]	1.7
	410726	AI623859	Hs.15936	TM,PX	ESTs	1.7
65	452012	AA307703	Hs.279766	TM,kinesin	kinesin family member 4A	1.7
	433627	AF078866	Hs.284296	TM,SURF4,SURF1,DEADlipocalin	Homo sapiens cDNA: FLJ22993 fs, clone KA	1.7
	409220	BE243323	Hs.51233	TM,death,TNFR_c6	tumor necrosis factor receptor superfamily	1.7
	427082	AB037858	Hs.173484	TM,mito_carr	hypothetical protein FLJ10337	1.7
	426410	BE298445	Hs.305890	TM,Bcl-2,BH4	BCL2-like 1	1.7
70	433598	AI762836	Hs.271433	TM,Cytidyltyltransf,SIRZ7tm_2	ESTs, Moderately similar to ALU2_HUMAN AL	1.7
	436495	BE268948	Hs.290874	TM,Armadillo_seg	ESTs, Weakly similar to ALU8_HUMAN ALU SU	1.7
	422032	AA476966	Hs.110857	TM,TFIIS,RNA_POL_M_15K0serpin,hormone_rec,zf-C4	polymerase (RNA) III (DNA directed) polyp	1.7
	429735	AF125304	Hs.212680	SS,TNFR_c6	tumor necrosis factor receptor superfamily	1.7
	427600	AW630918	Hs.179774	TM,Transglutaminin_C,Transglutaminin_N,Transglut_core	proteasome (prosome, macropain) activator	1.7
75	431981	AA664069	Hs.115779	laminin_B,laminin_EGF	ESTs	1.7
	407735	N41744	Hs.19978	TM,Sulfatase	CGI-30 protein	1.7
	420187	AK001714	Hs.95744	TM	hypothetical protein similar to ankyrin r	1.7
	424520	AA101043	Hs.151254	SS,TM,trypsin	kallikrein 7 (chymotryptic, stratum corne	1.7
	430488	D19589	Hs.13453	TM	hypothetical protein FLJ14753	1.7
80	423393	R37772	Hs.21420	TM,thioredoxin kinase	p21-activated protein kinase 6	1.7
	444051	N48373	Hs.10247	SS,Jg		

TABLE 13B

5	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
10	Accession:	Genbank accession numbers	
	Pkey	CAT Number	Accessions
15	408344	105240_1	AA053843 BE162213
	418546	176677_1	AA224827 T59708 T59843 BE156903
20	418859	179717_1	AA229558 AA345492 AA229582
	418869	179863_1	AW516565 AA229762 AA230035
25	437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875
			AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493
30			AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062
			AA282915 AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642
35			AA642789 AA856975 AW505512 AI961530 AW629970 BE612881 AW276997 AW513501 AW512843 AA044209 AW856538 AA180009 AA337499
			AW961101 AA251669 AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996
40			AA293273 AA969759 N75628 N22388 H84729 H50052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531
			H83488 W37181 W78802 R66056 AI002839 R67840 AA300207 AW959581 T63226 F04005
45	438962	467390_1	BE046594 BE046667 AA828585 AI207343
	443534	572957_1	AI076123 AI244834 AI695239
50	447197	711623_1	R36075 AI366546 R36167
	454197	1050392_1	BE140966 BE140961 BE140967 BE141006 BE140985 BE140970 BE141669 BE141653 BE141664 BE141655 BE141661 BE141660 BE140969
55			BE141673 BE141650 BE141674 BE141550 BE141688 AW178241 BE140994 BE141666 BE140998 BE141008 BE140988 BE141011 BE140975
			BE141667 BE141675 BE141657 BE141681 BE141656 BE141672 BE141680 AW178237 BE141012 BE140990 BE141658 BE141648 BE141013
60			BE141668 BE140973 BE141004 BE140863 BE140984 BE141009 AW178232 BE141007 BE141649 AW178293 BE140993 AW178233 BE141646
			BE141005 BE141691 BE141000 BE141652 BE140965 BE141562 BE140960 BE140962 BE141001 BE140978 AW178229 AW178239 BE141671
65			AW178230 BE141547 AW178235 BE141663 BE141549 BE140996 BE141003 AW178236 BE141002 BE141556
			AW897851 AW897852
70	455333	1281044_1	AA579426 AA579436 AA573736
	457570	357443_1	

TABLE 13C

40	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
45	Strand:	Indicates DNA strand from which exons were predicted.		
	NI_position:	Indicates nucleotide positions of predicted exons.		
50	Pkey	Ref	Strand	NI_position
	400666	8118496	Plus	17982-18115,20297-20456
55	400749	7331445	Minus	9162-9293
	401103	8568122	Minus	98330-98449
60	401485	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
	401575	7229804	Minus	76253-76364
65	402745	9212200	Minus	76516-76590
	402915	7406502	Minus	140-276
70	404440	7528051	Plus	80430-81581
	404604	9212537	Minus	72019-72509
75	405545	1054740	Plus	118677-118807,119091-119296,121626-121823
	405547	1054740	Plus	124361-124520,124914-125050
80	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
	406467	9795551	Plus	182212-182958

TABLE 14A: 209 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT TISSUES THAT ARE LIKELY TO ENCODE EITHER ENZYMES OR PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES

Table 14A lists about 209 genes up-regulated in cervical cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 12A, except that the ratio was greater than or equal to 2.0, and the 95th percentile value amongst cervical cancers was greater than or equal 40 units, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modifiable by small molecules (e.g. pkinase, peptidase, phosphatase, ATPase, or ion transporter domains). The predicted protein domains are noted.

70	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
75	UnigeneID:	Unigene number			
	PPDomains:	Predicted Protein Domains			
80	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor to normal adult tissues			
85	Pkey	ExAccn	UnigeneID	PPDomains	R1
	418007	M13509	Hs.83169	SS,hemopexin,Peptidase_M10	38.9
90	439506	W79123	Hs.58561	TM,7tm_1	28.8
	400289	X07820	Hs.2258	hemopexin,Peptidase_M10	20.5
95	415817	U88967	Hs.78867	SS,TM,Y_phosphatase,carb_anhyd	16.4
	416209	AA236776	Hs.79078	TM,HORMA	15.4
100	404996	NM_001333	Hs.87417	Peptidase_C1	13.1
				matrix metalloproteinase 1 (interst	
105				G protein-coupled receptor 87	
				matrix metalloproteinase 10 (stroma	
110				protein tyrosine phosphatase, recep	
				MAD2 (mitotic arrest deficient, yea	
115				CTSL2 Cathepsin L2	

5	428618	AA885360	Hs.160199	pkina	Target CAT	12.7
	429486	AF155827	Hs.203963	helica	hypothetical protein FLJ10339	12.6
	419183	U60699	Hs.89663	p450	cytochrome P450, subfamily XXIV (vi	12.3
	428368	BE440042	Hs.83326	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 3 (stromal	10.2
	420759	T11832	Hs.127797	helica	Homo sapiens cDNA FLJ11381 fis, clo	10.2
	458194	AW383618	Hs.265459	p450	ESTs, Moderately similar to ALU2_HU	9.4
	446232	AI281848	Hs.194691	TM,7tm_3Ribosomal_L13	retinoic acid induced 3	8.9
	424905	NM_002497	Hs.153704	TM,pkina	NIMA (never in mitosis gene a)-rela	8.9
10	452291	AF015592	Hs.28853	TM,pkina	CDC7 (cell division cycle 7, S. cer	8.7
	424086	AI351010	Hs.102267	Lysyl_oxidase	lysyl oxidase	8.3
	425710	AF030880	Hs.159275	TM,Sulfate_transp,STAS	solute carrier family, member 4	7.8
	433133	AB027249	Hs.104741	TM,Collagen,pkina	PDZ-binding kinase; T-cell original	7.4
	447254	NM_004153	Hs.17908	SS,AAA,BAH	origin recognition complex, subunit	7.1-
15	431941	AK000106	Hs.272227	pkina,Furin-like,Recep_L_dom	Homo sapiens cDNA FLJ20099 fis, clo	6.9
	427821	AA470158	Hs.98202	TM,7tm_1	ESTs	6.9
	436211	AK001581	Hs.334828	Ammonium_transp	hypothetical protein FLJ10719; KIAA	6.9
	403471	NA		SS,TM,trypsin	Target Exon	6.7
	410153	BE311926	Hs.15830	Glycos_transf_2	hypothetical protein FLJ12691	6.5
20	457405	AA504860		TM,7tm_2	gb:ab03a10.s1 Stratiogene fetal reti	6.4
	421948	L42583	Hs.334309	filament,HCO3_cotransfilament	keratin 6A	6.3
	439292	AA090421	Hs.5555	TM,AAA,Ferri_reduct	hypothetical protein MGC5347	5.8
	413625	AW451103	Hs.71371	TM,E1-E2_ATPase,Hydrolase	ESTs	5.8
	425695	NM_005401	Hs.159238	TM,Band_41,Y_phosphatase	protein tyrosine phosphatase, non-r	5.7
25	438394	BE379623	Hs.27693	SS,pro_isomerase	peptidylprolyl isomerase (cyclophil	5.6
	432239	X81334	Hs.2936	SS,Peptidase_M10,hemopexin	matrix metalloproteinase 13 (collag	5.5
	408536	AW381532	Hs.135188	SS,TM,E1-E2_ATPase,Cation_ATPa	ESTs	5.4
	432226	AW182766	Hs.273558	Cytidyltransf	phosphate cytidyltransferase 1, c	5.2
	419520	AB009303	Hs.90800	TM,hemopexin,Peptidase_M10	matrix metalloproteinase 16 (membra	5.1
30	426350	NM_003245	Hs.2022	TM,Transglutamin_C,Transglutam	transglutaminase 3 (E polypeptide,	5.0
	421155	H87879	Hs.102267	SS,Lysyl_oxidase,Aldose_epim,E	lysyl oxidase	4.9
	423673	BE003054	Hs.1695	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 12 (macrop	4.8
	450375	AA009647	Hs.8850	TM,disintegrin,Pep_M12B_propep	a disintegrin and metalloproteinase	4.8
	418379	AA218940	Hs.137516	AAA	fdgectin-like 1	4.7
35	457465	AW301344	Hs.122908	Pribosyltran,Sulfatase	DNA replication factor	4.6
	412333	AW937485		TM,7tm_1	gb:QV3-DT0044-221299-045-b09 DT0044	4.6
	450510	AA010056	Hs.242998	DNA_topoisomI,DNA_topoisomIIGF	ESTs	4.6
	436291	BE568452	Hs.5101	abhydrolase	protein regulator of cytokinesis 1	4.6
	446353	AI290919	Hs.153661	HECTpkina	ESTs	4.5
40	435435	T89473	Hs.192328	lipase,PLAT	ESTs	4.5
	425071	NM_013989	Hs.154424	SS,TM,T4_deiodinase	deiodinase, lodothyronine, type II	4.4
	433322	H50621	Hs.134156	TM,ion_transNB-ARC,CARD_mito_c	ESTs, Weakly similar to I38022 hypo	4.4
	408908	BE296227	Hs.25082	TM,pkina	serine/threonine kinase 15	4.4
	444781	NM_014400	Hs.11950	PH_lactamase_B	GPI-anchored metastasis-associated	4.4
45	428479	Y00272	Hs.184572	pkina	cell division cycle 2, G1 to S and	4.2
	406687	M31126	Hs.272620	SS,Peptidase_M10,hemopexin	pregnancy specific beta-1-glycoprot	4.2
	423035	AW449679	Hs.156739	TM,Glyco_transf_8	H.sapiens XG mRNA (clone PEP11)	4.2
	449228	AJ403107	Hs.148590	TM,PAF-AH,p450	protein related with psoriasis	4.2
	423738	AB002134	Hs.132195	SS,TM,trypsin,SEA	airway trypsin-like protease	4.1
50	457030	AI301740	Hs.173381	TM,Dihydrochlorase	dihydropyrimidinase-like 2	4.1
	448995	AI613276	Hs.5662	adenylatekinase	guanine nucleotide binding protein	4.0
	415857	AA866115	Hs.127797	helica	Homo sapiens cDNA FLJ11381 fis, clo	4.0
	438390	AI422017		TM,DSL,7tm_17tm_1	gb:45f12x1 NCI_CGAP_Bm23 Homo s	4.0
	429900	AA460421	Hs.30875	pkina	ESTs	4.0
55	446292	AF081497	Hs.279682	Ammonium_transp	Rh type C glycoprotein	3.8
	422938	NM_001809	Hs.1594	TM,thiolase	centromere protein A (17kD)	3.7
	408771	AW732573	Hs.47584	TM,K_tetra,ion_trans	potassium voltage-gated channel, de	3.6
	424296	AI631874	Hs.155140	pkina	casein kinase 2, alpha 1 polypeptid	3.6
	436246	AW450863	Hs.119931	connexinhormone_rec,zf-C4	ESTs	3.5
60	411274	NM_002776	Hs.69423	trypsin	kallikrein 10	3.5
	400666			SS,hemopexin,Peptidase_M10	NM_002425:Homo sapiens matrix metal	3.5
	426920	AA393351	Hs.132121	PDEase	ESTs	3.5
	412471	M63193	Hs.73946	SS,TM,Glycos_transf_3,Cam_acy	endothelial cell growth factor 1 (p	3.4
	430704	AW813091	Hs.335799	Epimerase	ESTs	3.4
65	455092	BE152428		Sulfatase	gb:CM0-HT0323-151299-126-b04 HT0323	3.4
	453775	NM_002916	Hs.35120	AAA,PI3_P14_kina,PI3Ka,PI3K	replication factor C (activator 1)	3.4
	438993	AA828995		Integrin_B	gb:od77b08.s1 NCI_CGAP_Ov2 Homo sap	3.4
	426572	AB037783	Hs.170623	hormone_rec,zf-C4	hypothetical protein FLJ11183	3.4
	449101	AA205847	Hs.23016	SS,TM,7tm_1	G protein-coupled receptor	3.3
70	427660	AI741320	Hs.114121	hormone_rec,zf-C4	Homo sapiens cDNA: FLJ23228 fis, cl	3.3
	402481			TM,GDI,7tm_1	NM_001821:Homo sapiens choroiderem	3.3
	414774	X02419	Hs.77274	SS,kringle,trypsin	plasminogen activator, urokinase	3.3
	412246	AI160873	Hs.69233	SulfotransferACOX	zinc finger protein	3.3
	418462	BE001596	Hs.85266	SS,TM,Integrin_B,fn3	integrin, beta 4	3.3
75	424687	J05070	Hs.151738	SS,Peptidase_M10,fn2,hemopexin	matrix metalloproteinase 9 (gelatin	3.3
	401486	NA		SS,TM,trypsin	C4000647:gi4758508[ref]NP_004253.	3.2
	408113	T82427	Hs.194101	TM,7tm_3Ribosomal_L13	Homo sapiens cDNA: FLJ20869 fis, cl	3.2
	427359	AW020782	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, cl	3.2
	402337			SS,p450	Target Exon	3.2
80	420930	AW888650		ribonuclease_T2	gb:CM4-NT0007-130500-551-f05 NT0007	3.2
	443426	AF098158	Hs.9329	pkina	chromosome 20 open reading frame 1	3.1
	439750	AL359053	Hs.57664	TM,Integrin_B,Ricin_B_lectinrr	Homo sapiens mRNA full length inser	3.1
	420039	NM_004605	Hs.94581	CARD,SulfotransferDAGKc	sulfotransferase family, cytosolic,	3.0
	448733	NM_005629	Hs.187958	SS,TM,SNF_ABC_tran,iodh,pkina	solute carrier family 6 (neurotrans	3.0

	444946	AW139205	Hs.156457	SS,TM,abhydrolase	hypothetical protein FLJ22408	3.0
	450841	AI741466	Hs.270515	pro_isomerase	ESTs	3.0
	428262	AI651324	Hs.7298	death,pkinase	biphenyl hydrolase-like (serine hyd	3.0
5	435399	AA579463		pkinase	gb:ac50c03.s1 Stratagene hNT neuron	2.9
	446733	AA863360	Hs.26040	TM,p450	ESTs, Weakly similar to fatty acid	2.9
	449746	AI668594	Hs.176588	SS,p450	ESTs, Weakly similar to CP4Y_HUMAN	2.9
	418844	M62982	Hs.1200	SS,TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase	2.9
	414581	AA256213	Hs.72010	TM,Cam_acyltransf,Choline_kin	ESTs	2.9
10	431629	AU077025	Hs.265827	SS,IRNA_antiSH2,SH3,pkinase	interferon, alpha-inducible protein	2.8
	445873	AA250970	Hs.251946	SS,rm,PABPkinase,14-3-3,rm	poly(A)-binding protein, cytoplasmic	2.8
	438113	AI467908	Hs.8882	TM,7tm_1	ESTs	2.8
	422689	AW856665		helicase_C,SNF2_Nhelicase_C	gb:RC3-CT0297-2S0100-013-d03 CT0297	2.8
	439453	BE264974	Hs.5566	SS,AAA	thyroid hormone receptor interactor	2.8
15	413582	AW295647	Hs.71331	carb_anhydrase	hypothetical protein MGC5350	2.8
	410664	NM_006033	Hs.65370	TM,lipase,PLAT	lipase, endothelial	2.8
	456456	AA477609	Hs.89563	FBPase	nuclear cap binding protein subunit	2.8
	413273	U75679	Hs.75257	TM,lip,pkinase	stem-loop (histone) binding protein	2.8
	426343	NM_014642	Hs.169387	TM,SCAN7tm_1	KIAA0036 gene product	2.8
20	403763			TM,7tm_1	NM_001059*Homo sapiens tachykinin	2.7
	408380	AF123050	Hs.44532	TM,ubiquitin7tm_3,ANF_receptor	diubiquitin	2.7
	401230			SS,TM,ion_trans,IQ	NM_014191*Homo sapiens sodium chan	2.7
	418030	BE207573	Hs.83321	SS,TM,Peptidase_S26,Bombesin	neuromedin B	2.7
	445640	AW969626	Hs.31704	TM,alpha-amylase	ESTs, Weakly similar to KIAA0227 [H	2.7
25	432865	AI753709	Hs.152484	TM,ion_transNB-ARC,CARD,WD40,m	ESTs, Weakly similar to I38022 hypo	2.6
	419667	AU077005	Hs.92208	SS,TM,disintegrin,Reprolysin,P	a disintegrin and metalloproteinase	2.6
	406671	AA129547	Hs.285754	TM,pkinase,Plexin_repeat,Sema,	met proto-oncogene (hepatocyte grow	2.6
	412530	AA766268	Hs.266273	abhydrolase	hypothetical protein FLJ13346	2.6
	431890	X17033	Hs.271985	vwa,FG-GAP,integrin_A	Integrin, alpha 2 (CD49B, alpha 2 s	2.6
30	404184	NA		SS,TM,7tm_1	NM_030903*Homo sapiens olfactory r	2.6
	428450	NM_014791	Hs.184339	pkinase,KAI1	KIAA0175 gene product	2.6
	425698	NM_016112	Hs.159241	TM,pkinase,ion_trans	polycystic kidney disease 2-like 1	2.6
	453331	AI240665	Hs.8895	TM,disintegrin,Pep_M12B_propep	ESTs	2.6
	444826	AI674482	Hs.148441	pkinase,SAM	ESTs	2.6
35	414987	AA524394	Hs.294022	connexinhormone_rec,zf-C4,conn	hypothetical protein FLJ14950	2.6
	438746	AI885815	Hs.184727	Ribosomal_S2,transferrin	ESTs	2.5
	429413	NM_014058	Hs.201877	trypsin	DESC1 protein	2.5
	407103	AA424881	Hs.256301	TM,cNMP_bindingtrypsin	hypothetical protein MGC13170	2.5
	453379	AA035261	Hs.61753	PAN,kringle,trypsin	ESTs	2.5
40	421733	AL119671	Hs.1420	SS,TM,lip,pkinase	fibroblast growth factor receptor 3	2.5
	452220	BE158006	Hs.212296	TM,Integrin_A,FG-GAP	ESTs	2.5
	417975	AA641836	Hs.30085	SS,trypsin	hypothetical protein FLJ23186	2.5
	400301	X03535	Hs.1657	TM,Oest_recep,zf-C4,hormone_re	estrogen receptor 1	2.5
	408938	AA059013	Hs.22607	Y_phosphatase	ESTs	2.4
45	411643	AI924519	Hs.192570	DEAD,helicase_C	hypothetical protein FLJ22028	2.4
	446638	AL133063	Hs.15783	TM,pkinase	Homo sapiens mRNA; cDNA DKFZp434P11	2.4
	430129	BE301708	Hs.233955	TM,Glyco_transf_11	hypothetical protein FLJ20401	2.4
	417655	AA780791	Hs.14014	Peptidase_M41,AAA,pkinase	hypothetical protein FLJ14813	2.4
	448005	AW207437	Hs.170378	pkinase	ESTs	2.4
50	423973	AF038461	Hs.136574	TM,lipoxygenase,PLAT	arachidonate 12-lipoxygenase, 12R t	2.4
	437897	AA770561	Hs.146170	SS,pro_isomerase	hypothetical protein FLJ22969	2.4
	425397	J04088	Hs.156346	DNA_topoisomII,DNA_topoisomI/GIF	topoisomerase (DNA) II alpha (170kD	2.4
	432777	AA564991	Hs.269477	alpha-amylase	ESTs	2.4
	421247	BE391727	Hs.102910	TM,IRNA-synt_1,SPRYF5_F8_type_	general transcription factor IIH, p	2.4
55	425465	L18964	Hs.1904	TM,pkinase,DAG_PE-bind,OPR,pld	protein kinase C, iota	2.4
	419281	H96452	Hs.42189	TM,E1-E2,ATPase,HMA,Hydrolase	ESTs	2.4
	434205	AF119861	Hs.283032	SH3,efhand,C2,PH,RhoGEF,AAA,PG	hypothetical protein PRO2015	2.4
	453406	AI192987	Hs.61784	pkinase,Furin-like,Recep_L_dom	hypothetical protein FLJ14451	2.3
	435542	AA687376	Hs.269533	pkinase,RhoGEF,lg,PH,SH3	ESTs	2.3
60	443151	AI827193	Hs.132714	DNA_mis_repair,HATPase_cAcylph	ESTs	2.3
	431630	NM_002204	Hs.265829	SS,TM,FG-GAP,integrin_A	integrin, alpha 3 (antigen CD49C, a	2.3
	422310	AA316622	Hs.98370	SS,TM,fn3,lg,pkinase,Ribosomal	cytochrome P450, subfamily IIS, pol	2.3
	441954	AI744935	Hs.8047	TM,Band_7,AAA,cdc48_N	Fanconi anemia, complementation gro	2.3
	414907	X90725	Hs.77597	SS,TM,pkinase,POLO_box	pto (Drosophila)-like kinase	2.3
65	439810	AL109710	Hs.85568	aconitase,Aconitase_C	EST	2.3
	429359	W00482	Hs.2399	SS,TM,Peptidase_M10,hemopexin	matrix metalloproteinase 14 (membra	2.3
	432284	AA532807	Hs.105822	TM,pkinase	ESTs	2.3
	452947	AW130413		alpha-amylase	gb:ac50f04.x1 NCI_CGAP_Gas4 Homo sa	2.3
70	423229	AC003965	Hs.125532	SS,trypsin	protease, serine, 26	2.3
	453941	U39817	Hs.36820	DEAD,HRDC,helicase_C	Bloom syndrome	2.3
	439963	AW247529	Hs.6793	TM,p450ets	platelet-activating factor acetylth	2.3
	424439	AA579635	Hs.1770	DNA_ligase	ligase I, DNA, ATP-dependent	2.2
	452755	AW138937	Hs.213436	Glyco_transf_29	ESTs, Weakly similar to A34087 hypo	2.2
	429922	Z97630	Hs.226117	TM,linker_histone7tm_1	H1 histone family, member 0	2.2
75	434149	Z43829	Hs.19574	TM,EPH_1bd,fn3,pkinase,SAM	hypothetical protein MGC5469	2.2
	417576	AA339449	Hs.82285	TM,AIRS,formyl_transf,GARS	phosphoribosylglycinamide formyltra	2.2
	409994	D86864	Hs.57735	IP_transSH2,SH3	acetyl LDL receptor; SREC	2.2
	416763	AI908127	Hs.79748	TM,alpha-amylase7tm_1	solute carrier family 3 (activators	2.2
	414733	BE514535	Hs.77171	TM,MCMHeme_oxygenase	minichromosome maintenance deficien	2.2
80	443171	BE281128	Hs.9030	SS,TM,7tm_1,rm	TONDU	2.2
	430637	BE160081	Hs.256290	S_100Peptidase_M16	S100 calcium-binding protein A11 (c	2.2
	452379	U71207	Hs.29279	SS,Hydrolase	eyes absent (Drosophila) homolog 2	2.2
	408308	AL033377	Hs.44197	TM,7tm_2	hypothetical protein DKFZp564D0462	2.2
	417900	BE250127	Hs.82996	TM,WD40,pro_isomerase	CDC20 (cell division cycle 20, S. c	2.1

5	424490	AJ278016	Hs.55565	TM,ptkinase,ank	ankyrin repeat domain 3	2.1
	412834	R77123	Hs.79881	TM,7tm_1	Homo sapiens cDNA: FLJ23006 fis, cl	2.1
	410855	X97795	Hs.66718	SNF2_N_helicase_C	RAD54 (S.cerevisiae)-like	2.1
	418804	AA809632		HATPase_c,HSP90,PHD,zf-C2H2	gb:nz17h04.s1 NCL_CGAP_GCB1 Homo sa	2.1
	447674	BE270640	Hs.19192	TM,ptkinases,arf	cyclin-dependent kinase 2	2.1
	450663	H43540	Hs.25292	SS,TM,RNase_HII	ribonuclease HI, large subunit	2.1
	408805	H69912	Hs.48269	TM,ptkinase	vaccinia related kinase 1	2.1
	429415	NM_002593	Hs.202097	SS,CUB,NTR,MAM,TIL,TILa,vwd,EP	procollagen C-endopeptidase enhance	2.1
10	447827	U73727	Hs.19718	SS,TM,Y_phosphatase,fn3,lg,MAM	protein tyrosine phosphatase, recep	2.1
	428273	AI867228	Hs.303211	Glycos_transf_2	ESTs	2.1
	404274			SS,TM,ptkinase,fn3	NM_002944*:Homo sapiens v-ros avian	2.1
	403133			ptkinase,K_tetra,Band_41,RhoGEF	Target Exon	2.1
	440249	AI246590	Hs.337275	VHL,TatD_DNase	ESTs	2.1
15	438580	AA811262	Hs.299202	TM,ptkinasesugar_tr	ESTs	2.1
	406400			SS,TM,tryptsin	NM_007196:Homo sapiens kallikrein 8	2.1
	427375	AL035460	Hs.177536	SS,Zn_carbOpept,hormone5Reprot	metallocarboxypeptidase CPX-1	2.1
	423453	AW450737	Hs.128791	SS,Granin,CDP-OH_P_transf	CGI-09 protein	2.1
	433716	AA608808	Hs.225118	Acylphosphatase	ESTs	2.1
20	420757	X78592	Hs.99915	TM,hormone_rec,Androgen_recep,	androgen receptor (dihydrotestoster	2.1
	425018	BE245277	Hs.154196	DNase_I,K_tetra	E4F transcription factor 1	2.1
	421685	AF189723	Hs.106778	TM,E1-E2_ATPase,HydrolaseE1-E2	ATPase, Ca transporting, type 2C, m	2.1
	457288	AA521458	Hs.192738	pro_isomerase	ESTs	2.1
	407305	AA715284		TM,ptkinase,Sema,Plexin_repeat,	gb:nv35f03.r1 NCL_CGAP_Br5 Homo sap	2.1
25	456327	H69741	Hs.38774	TM,Glyco_transf_8	ESTs	2.0
	422429	AA310527		ptkinase,RGS,PH,ptkinase,PH,RGS	gb:EST181333 Jurkat T-cells V Homo	2.0
	402974	NM_001501	Hs.129715	GnRHhormone5,hormone4	gonadotrophin-releasing hormone 2	2.0
	458016	AW188099	Hs.131813	ptkinase	ESTs	2.0
	452194	AI694413	Hs.332649	TM,7tm_3,ANF_receptor,sushi	olfactory receptor, family 2, subfa	2.0
30	428028	U52112	Hs.182018	TM,ptkinase,MBD	Interleukin-1 receptor-associated k	2.0
	427747	AW411425	Hs.180655	ptkinase,lipoxygenase,PLATilpox	serine/threonine kinase 12	2.0
	452841	T17431	Hs.65412	TM,DEAD,helicase_C	DEAD/H (Asp-Glu-Ala-Asp/His) box po	2.0
	449539	W80363	Hs.58446	ptkinase,Furin-like,Recep_L_dom	ESTs	2.0
	418140	BE613836	Hs.83551	TM,E1-E2_ATPase	microfibrillar-associated protein 2	2.0
35	430076	AA465115	Hs.318773	AAA,BAH	KIAA1836 protein	2.0
	425749	AW328587	Hs.159448	Ribosomal_L7Ae,LRR,LRRCT,ptkina	surfeit 2	2.0
	425855	AF135025	Hs.159679	SS,tryptsin	kallikrein 12	2.0
	400135	L40027	Hs.118890	ptkinase	glycogen synthase kinase 3 alpha	2.0

40 TABLE 14B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

45	Pkey	CAT number	Accessions
			*
50	412333	1289037_1	AW937485 AW937589 AW937658 AW937654 AW937492
	418804	179138_1	AA809632 AI917245 A1701732 AA228406
	420930	197736_1	AW888650 AW888651 BE149946 BE149948 BE149951 BE149947 AW888649 AA281840 AA281822 AW888652
	422429	216469_1	AA310527 AW952295 Z44865 H06641
	422689	219899_1	AW856665 AA315006 AW954733
	435399	405576_1	AA679463 AW813779 AW813709
55	438390	45662_1	AI422017 AI422945 AI363249 AI423113 AI925592 AI420795 AI208187 AI423279 AI423645 AI424090 AI359637 AL044732 D17003
	438993	467651_1	AA828995 AA834879 AI926361
	452947	939810_1	AW130413 AI932362
	455092	1252971_1	BE152428 AW855572 AW855607
	457405	333127_1	AA504860 AA504911

60 TABLE 14C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

70	Pkey	Ref	Strand	Nt_position
	400566	8118496	Plus	17982-18115,20297-20456
	401230	9929527	Minus	33835-34006,34539-34592,36461-36745,48925-49098,52604-52758
	401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
75	402337	6957691	Plus	4116-4286,16811-16973,17107-17256,19715-20040,22029-22205
	402481	9797406	Plus	87891-88991
	403133	7331427	Plus	38314-38634
	403471	9930559	Minus	85867-85983
	403763	7229888	Minus	43575-43887
80	404184	4581418	Minus	12652-13548
	404274	9885189	Plus	104127-104318
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

TABLE 15A: 752 GENES UP-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT CERVIX

5 Table 15A lists about 752 genes up-regulated in cervical cancer compared to normal adult cervix. These were selected as for Table 12A, except that the ratio was greater than or equal to 7.0, the denominator was the median value for three non-malignant cervical specimens, and the 96th percentile value amongst cervical cancers was greater than or equal 80 units.

	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
10	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of cervical cancer to normal cervix			
15	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homolog of murine	58.3
	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HEMBA1004341	36.2
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cys-X-Cys), mem	35.6
20	421508	NM_004833	Hs.105115	absent in melanoma 2	33.6
	443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit, beta type, 1	32.0
	454390	AB020713	Hs.56966	KIAA0906 protein	30.5
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	30.4
	433226	AW503733	Hs.9414	KIAA1488 protein	30.0
	413503	BE410228	Hs.75410	heat shock 70kD protein 5 (glucose-regulated protein,	29.4
25	411669	BE612676	Hs.303116	stromal cell-derived factor 2-like 1	28.9
	414132	AI801235	Hs.48480	ESTs	28.3
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	28.1
	448569	BE382657	Hs.21486	signal transducer and activator of transcription 1, 9	27.4
	432906	BE265489	Hs.3123	lethal giant larvae (Drosophila) homolog 2	27.2
30	418963	BE304571	Hs.89529	aldo-keto reductase family 1, member A1 (aldehyde red	26.9
	439953	AW247529	Hs.6793	platelet-activating factor acetylhydrolase, isoform I	26.5
	449722	BE280074	Hs.23960	cyclin B1	26.2
	414812	X72755	Hs.77367	monokine induced by gamma interferon	25.3
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	25.1
35	432917	NM_014125	Hs.279812	PRO0327 protein	24.6
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	23.6
	457465	AW301344	Hs.122908	DNA replication factor	23.1
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone COL06049	22.9
40	429083	Y09397	Hs.227817	BCL2-related protein A1	22.9
	401405			Target Exon	22.8
	426272	AW450671	Hs.189284	ESTs	22.7
	424878	H57111	Hs.221132	ESTs	22.6
	412140	AA219691	Hs.73625	RAB6 Interacting, kinesin-like (rakbinesin 6)	22.5
	444371	BE540274	Hs.239	forkhead box M1	22.2
45	418030	BE207573	Hs.83321	neuromedin B	22.0
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, homolog)-	21.6
	400195			Eos Control	21.3
	416795	AI497778	Hs.20509	HBV pX associated protein-8	21.2
	424865	AF011333	Hs.153563	lymphocyte antigen 75	21.0
50	438011	BE466173	Hs.145696	splicing factor (CC1.3)	20.7
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin 1, progelatin	20.3
	436923	AW293704	Hs.122658	ESTs	20.2
	415791	H09366	Hs.78853	uracil-DNA glycosylase	20.0
	448775	AB025237	Hs.388	nudix (nucleoside diphosphate linked moiety X)-type m	19.6
55	435647	AI653240	Hs.49823	ESTs	19.6
	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to gene trap PA	19.5
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	19.5
	428433	AA521410	Hs.41371	ESTs	19.4
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK2-associated	19.3
60	417308	H60720	Hs.81892	KIAA0101 gene product	19.2
	429574	BE268321	Hs.208912	hypothetical protein MGC861	19.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	19.0
	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	19.0
	438899	AF085833	Hs.135624	ESTs	19.0
65	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	18.9
	438598	AI805943	Hs.326067	hypothetical protein MGC5178	18.8
	408908	BE296227	Hs.250822	serine/threonine kinase 15	18.8
	427488	M91401	Hs.178658	RAD23 (S. cerevisiae) homolog B	18.6
	400195			NM_007057*-Homo sapiens ZW10 interactor (ZWINT), tran	18.5
70	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin)	18.4
	410324	AW292539	Hs.30177	ESTs	18.3
	453028	AB006532	Hs.31442	RecQ protein-like 4	18.1
	410608	AI538438	Hs.159087	ESTs	18.1
	432503	AA551196	Hs.188952	ESTs	17.9
75	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	17.7
	430709	R34356		gbyh85d01.s1 Soares placenta Nb2HP Homo sapiens cDNA	17.6
	449962	AA004879	Hs.187820	ESTs	17.3
	425408	AB002375	Hs.156814	KIAA0377 gene product	17.1
	440774	AI420611	Hs.127832	ESTs	16.8
80	408201	AK000568	Hs.43654	hypothetical protein FLJ20561	16.7
	436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypothetical protein [16.7
	426897	AW976570	Hs.97387	ESTs	16.5
	447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypothetical protein F	16.5

5	433159	AB035898	Hs.150587	kinesin-like protein 2	16.3
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	16.3
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptional activation,	16.3
	453941	U39817	Hs.36820	Bloom syndrome	16.1
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	16.0
10	407999	AI126271	Hs.49433	ESTs, Weakly similar to YZ28_HUMAN HYPOTHETICAL PROTE	16.0
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT2RP2006454	15.7
	407720	AB037776	Hs.38002	KIAA1355 protein	15.6
	425316	AA354977	Hs.191565	ESTs, Moderately similar to T14342 NSD1 protein - mou	15.6
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage elastase)	15.5
15	419777	D60134	Hs.270975	ESTs	15.3
	453886	R66282	Hs.20247	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	15.2
	443715	AI583187	Hs.9700	cyclin E1	15.2
	407786	AA687538	Hs.38972	tetraspan 1	15.2
	431910	AK000142	Hs.101774	hypothetical protein FLJ23045	15.2
20	417634	W27202	Hs.82327	glutathione synthetase	15.1
	432692	AW974944	Hs.200577	ESTs	15.1
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cys-Cys), membe	15.1
	427999	AI435128	Hs.181369	ubiquitin fusion degradation 1-like	15.0
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	15.0
25	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clone IFI-6-16)	14.9
	435354	AA678267	Hs.117115	ESTs	14.8
	406836	AW514501	Hs.156110	immunoglobulin kappa constant	14.8
	416109	AI420311	Hs.126550	suppressor of K transport defect 1	14.8
	417933	X02308	Hs.82952	thymidylate synthetase	14.7
30	438970	AA837782	Hs.321058	ESTs	14.7
	409680	W31092	Hs.55847	mitochondrial ribosomal protein 64	14.7
	432401	NM_013330	Hs.274479	NME7	14.6
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	14.5
	420734	AW972872	Hs.293736	ESTs	14.5
35	434256	AI378817	Hs.191847	ESTs	14.5
	418269	AA806113	Hs.189025	ESTs	14.3
	427372	AW960673	Hs.177530	ATP synthase, H transporting, mitochondrial F1 complex	14.3
	427081	AI474533	Hs.170528	ESTs, Moderately similar to ALUC_HUMAN III ALU CLASS	14.2
	420309	AW043537	Hs.21766	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC S	14.2
40	429966	BE081342	Hs.283037	HSPC039 protein	14.2
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-inducible, 67	14.1
	443957	AA521049	Hs.34487	hypothetical protein FLJ23412	14.0
	418803	U50079	Hs.88566	histone deacetylase 1	14.0
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	14.0
45	420139	NM_005357	Hs.95351	lipase, hormone-sensitive	13.9
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), actin binding pr	13.9
	433255	AI274270	Hs.96840	KIAA1527 protein	13.9
	431838	AI097229	Hs.217484	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	13.8
	449801	AA477355	Hs.288300	hypothetical protein FLJ23231	13.8
50	447078	AW885727	Hs.301570	ESTs	13.8
	441240	AA923749	Hs.132442	ESTs	13.8
	439398	AA284267	Hs.221504	ESTs	13.6
	404630			Target Exon	13.6
	408321	AW405882	Hs.44205	cortistatin	13.6
55	426427	M86699	Hs.169840	TTK protein kinase	13.5
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	13.5
	403055			C2002219:gil12737280:ref XP_006682.2 keratin 18 [Ho	13.5
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	13.5
	425261	BE385099	Hs.334727	hypothetical protein MGC3017	13.3
60	439926	AW014875	Hs.137007	ESTs	13.3
	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-associated kinesin	13.2
	451141	AW772713	Hs.247186	ESTs	13.2
	447390	X95384	Hs.18426	translational inhibitor protein p14.5	13.2
	419828	T81422	Hs.14922	ESTs	13.2
65	428147	AW629965	Hs.234983	ESTs, Weakly similar to 2109260A B cell growth factor	13.2
	410068	AI633888	Hs.58435	FYN-binding protein (FYN-120/130)	13.1
	407595	BE350012	Hs.248365	ESTs	13.1
	432721	AL121478	Hs.180532	glucose phosphate isomerase	13.1
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associ	13.0
70	413314	BE081585		gb:QV2-BT0635-210400-156-b07 BT0635 Homo sapiens cDNA	13.0
	430929	AA489166	Hs.156933	ESTs	12.9
	449571	AW016812	Hs.200266	ESTs	12.9
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of the prostate	12.8
	417105	X60992	Hs.81226	CD6 antigen	12.6
75	434263	N34895	Hs.44648	ESTs	12.6
	412059	AA317962	Hs.249721	ESTs, Moderately similar to PC4259 fertilin associate	12.6
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	12.5
	437056	AI147061		gb:ok33a11.s1 Soares_NSIF_F8_SW_OT_PA_P_S1 Homo sapien	12.5
	438768	AI307416	Hs.184675	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY	12.5
80	444478	W07318	Hs.240	M-phase phosphoprotein 1	12.5
	450738	AA010907	Hs.184456	hypothetical protein	12.4
	418205	L21715	Hs.83760	tropomyosin I, skeletal, fast	12.4
	442994	AI026718	Hs.16954	ESTs	12.4
	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone HEP20977	12.4
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	12.4
	435327	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylgl	12.3
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (survivin)	12.3

	410245	C17908	Hs.194125	ESTs	12.3
	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	12.3
	418941	AA452970	Hs.155218	E1B-55kDa-associated protein 5	12.3
5	432325	AW973209	Hs.261782	ESTs	12.3
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	12.3
	418518	U60097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dystonia)	12.2
	449296	AL137257	Hs.23458	Homo sapiens cDNA: FLJ23015 fis, clone LNG00818	12.2
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501	12.2
10	427295	AW291212	Hs.293943	hypothetical protein MGC11266	12.2
	415443	T07353	Hs.7948	ESTs	12.1
	429770	AJ766047	Hs.99736	ESTs	12.1
	428955	AA579297	Hs.26937	brain and nasopharyngeal carcinoma susceptibility pro	12.1
	435244	N77221	Hs.187824	ESTs	12.1
15	432810	AA863400	Hs.23054	ESTs	12.1
	434423	NM_006769	Hs.3844	LIM domain only 4	12.0
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit, beta type, 9	12.0
	459273	AW608906	Hs.334767	hypothetical protein MGC5629	12.0
	419945	AW290975	Hs.118923	ESTs	11.9
20	442159	AW163390	Hs.278554	heterochromatin-like protein 1	11.9
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MAMMA1002566	11.9
	407804	AF228603	Hs.39957	pleckstrin 2 (mouse) homolog	11.8
	401557			Target Exon	11.8
	434408	AJ031771	Hs.132586	ESTs	11.8
25	406747	AJ925153	Hs.217493	annexin A2	11.8
	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein (EGP) (KSA)	11.8
	429412	NM_006235	Hs.2407	POU domain, class 2, associating factor 1	11.8
	445655	AA873830	Hs.167746	B cell linker protein	11.7
	419138	U48508	Hs.89631	ryanodine receptor 1 (skeletal)	11.7
30	427527	AJ809057	Hs.302053	immunoglobulin heavy constant mu	11.7
	432287	AK001057	Hs.274268	Homo sapiens cDNA FLJ10195 fis, clone HEMBA1004771	11.6
	408548	AA055449	Hs.63187	ESTs, Weakly similar to ALUC_HUMAN !!! ALU CLASS C W	11.6
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 kD)	11.6
	447082	T85314	Hs.42644	thioredoxin-like	11.5
35	409931	BE293233	Hs.129771	ESTs	11.4
	426172	AA371307	Hs.125056	ESTs	11.4
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(hnRNP methyltr	11.4
	456880	AW015644	Hs.155005	TEA domain family member 1 (SV40 transcriptional enha	11.4
40	433849	BE465884	Hs.280728	ESTs	11.4
	430519	AF129534	Hs.49210	F-box only protein 4	11.4
	434442	AA737415	Hs.152826	ESTs	11.3
	457205	AJ905780	Hs.198272	Target CAT	11.3
	422713	AA902780	Hs.119325	Huntingtin-interacting protein A	11.3
	443491	AW499665	Hs.9456	SW/SNF related, matrix associated, actin dependent r	11.3
45	424339	BE257148	Hs.145416	endoglycan	11.3
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	11.3
	450208	AJ686945	Hs.272062	ESTs	11.2
	446849	AJ076617	Hs.16251	cleavage and polyadenylation specific factor 3, 73kD	11.2
	424965	AW956282	Hs.144609	Homo sapiens, Similar to RIKEN cDNA 5730578N08 gene,	11.2
50	442737	A8002319	Hs.8663	KIAA0321 protein	11.2
	409113	AJ074897		gb:zm85a05.r1 Stratagene ovarian cancer (937219) Homo	11.2
	415782	AA169345	Hs.123177	ESTs	11.1
	417958	AA767382	Hs.193417	ESTs	11.1
	402539	AW502761	Hs.30909	KIAA0430 gene product	11.0
55	413677	AW503116	Hs.301819	zinc finger protein 146	11.0
	414706	AW340125	Hs.76989	KIAA0097 gene product	11.0
	421632	AA825426	Hs.238832	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	11.0
	438995	AJ277986	Hs.164875	ESTs	11.0
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)	10.9
60	432363	AA534489		gb:mf76g11.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone 3'	10.9
	451655	H85689	Hs.225560	ESTs	10.9
	429237	AA448417	Hs.104990	ESTs	10.9
	427719	AJ393122	Hs.134726	ESTs	10.9
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	10.8
65	410093	AW589558	Hs.296120	ESTs, Weakly similar to KIAA0970 protein [H.sapiens]	10.8
	400080			Eos Control	10.8
	424517	AJ539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643	10.8
	401539			NM_002675:Homo sapiens promyelocytic leukemia (PML),	10.8
	446099	T33096	Hs.17126	hypothetical protein MGC15912	10.7
70	451056	AJ758660	Hs.206132	ESTs	10.7
	409235	AA188827	Hs.7988	ESTs, Weakly similar to I38022 hypothetical protein [10.7
	451730	AF095687	Hs.26937	brain and nasopharyngeal carcinoma susceptibility pro	10.7
	428054	AJ948688	Hs.266619	ESTs	10.6
	441636	AA081846	Hs.7921	Homo sapiens mRNA; cDNA DKFZp566E183 (from clone DKFZ	10.6
75	438654	AJ005270	Hs.123543	ESTs	10.6
	424321	V74048	Hs.1765	lymphocyte-specific protein tyrosine kinase	10.6
	449035	AJ815728	Hs.19980	DNA polymerase epsilon p12 subunit	10.6
	436137	AJ056769	Hs.133512	ESTs	10.6
	417863	AB000450	Hs.82771	vaccinia related kinase 2	10.6
80	439975	AW328081	Hs.6817	inosine triphosphatase (nucleoside triphosphate pyrop	10.6
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen inducible gene	10.6
	454355	AW812535		gb:CM4-ST0182-051099-021-c09 ST0182 Homo sapiens cDNA	10.6
	435542	AA687376	Hs.269533	ESTs	10.6
	431386	AA504359	Hs.110057	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC S	10.5

	416564	AW795793	Hs.175827	Homo sapiens cDNA FLJ12257 fis, clone MAMMA1001501, h	10.5
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT2RM4002390	10.5
	408329	AF155510	Hs.44227	heparanase	10.5
5	410146	AW592655		gb:hi45f12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA c	10.5
	427600	AW630918	Hs.179774	proteasome (prosome, macropain) activator subunit 2 (10.4
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial collagenase)	10.4
	407241	M34516		gb:Human omega light chain protein 14.1 (lg lambda ch	10.4
	435061	AI651474	Hs.163944	ESTs	10.4
10	409653	AW451693	Hs.220826	ESTs	10.4
	428294	AA425488		gb:zw46d02.r1 Soares_total_fetus_Nb2HF8_9w Homo sapie	10.4
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sensitivity prote	10.4
	408809	AW274673	Hs.279706	ESTs, Weakly similar to A47582 B-cell growth factor p	10.4
	410174	AA306007	Hs.59461	DKFZP434C245 protein	10.4
15	424792	U92538	Hs.153138	origin recognition complex, subunit 5 (yeast homolog)	10.3
	422406	AF025441	Hs.116206	Opa-interacting protein 5	10.3
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B, 92kD gelati	10.3
	413809	L25851	Hs.851	integrin, alpha E (antigen CD103, human mucosal lymph	10.3
	413507	BE145360	Hs.190064	ESTs, Weakly similar to I38022 hypothetical protein [10.3
20	448119	H38587	Hs.82295	dedicator of cyto-kinesis 1	10.2
	457288	AA521458	Hs.192738	ESTs	10.2
	402025			NM_021624:Homo sapiens histamine H4 receptor (HRH4),	10.2
	440572	AW183778	Hs.249584	ESTs, Weakly similar to MYSA_HUMAN MYOSIN HEAVY CHAIN	10.2
	453323	AF034102	Hs.32951	solute carrier family 29 (nucleoside transporters), m	10.2
25	443780	NM_012068	Hs.9754	activating transcription factor 5	10.1
	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapiens cDNA 5' en	10.1
	443414	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo	10.1
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolog	10.1
	430848	AW021726		gb:d127e02.y1 Morton Fetal Cochlea Homo sapiens cDNA	10.1
30	422470	AB017919	Hs.117232	peptidyl arginine deiminase, type V	10.1
	449501	AI652924	Hs.231942	ESTs	10.1
	420731	AL042052	Hs.104432	ESTs	10.1
	404345	AA730407	Hs.159156	protocadherin 11	10.1
	400438	AF185611		Target	10.1
35	438170	AI916685	Hs.194601	ESTs	10.1
	432193	AA372264	Hs.273193	hypothetical protein FLJ10706	10.1
	458715	AK000973	Hs.16725	hypothetical protein FLJ10111	10.1
	427766	AA412258	Hs.188817	ESTs	10.1
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	10.0
40	403038			Target Exon	10.0
	434674	AA831879	Hs.136985	ESTs	10.0
	439685	AW956781	Hs.293937	ESTs, Weakly similar to FXD2_HUMAN FORKHEAD BOX PROTE	10.0
	439428	AA835825	Hs.190490	ESTs	10.0
	403310			Target Exon	9.9
45	408392	U28831	Hs.44566	KIAA1641 protein	9.9
	421849	AW410872	Hs.108894	hypothetical protein FLJ20411	9.9
	433384	AI021992	Hs.124244	ESTs	9.9
	433343	BE409809	Hs.301005	purine-rich element binding protein B	9.9
	437267	AW511443	Hs.258110	ESTs	9.9
50	455978	AI310151	Hs.173524	ESTs	9.9
	435851	AA700946	Hs.191933	ESTs	9.9
	452243	AL355715	Hs.28555	programmed cell death 9	9.9
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	9.9
	414001	AI610347	Hs.103812	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY	9.9
55	436669	AA535975	Hs.174308	Homo sapiens, clone IMAGE:3453347, mRNA, partial cds	9.8
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phosphate), member 2	9.8
	417087	AA193193	Hs.188325	Homo sapiens cDNA FLJ11484 fis, clone HEMBA1001835	9.8
	455855	BE147440		gb:RC1-HT0229-080100-015-009 HT0229 Homo sapiens cDNA	9.8
	410390	AA876905	Hs.125286	ESTs	9.8
60	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic acid transpo	9.8
	442660	AW138174	Hs.130651	ESTs	9.8
	436186	BE390717	Hs.5074	similar to S. pombe dim1	9.8
	426773	NM_015556	Hs.172180	KIAA0440 protein	9.8
	413476	U25849	Hs.75393	acid phosphatase 1, soluble	9.7
65	418347	AA216419		gb:nc16e03.s1 NCL_CGAP_Pr1 Homo sapiens cDNA clone si	9.7
	448752	AA593867	Hs.300842	KIAA1608 protein	9.7
	440349	AA884196	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone THYRO1001322	9.7
	431363	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	9.7
	430752	AA485330	Hs.303278	ESTs	9.7
70	436523	BE612990	Hs.5212	single-strand selective monofunctional uracil DNA gly	9.7
	415740	N80486	Hs.39911	Homo sapiens mRNA for FLJ00089 protein, partial cds	9.7
	411930	F06485	Hs.7740	oxysterol binding protein-like 1	9.7
	430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior gradient-2 [H	9.7
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothetical protein [9.6
75	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA1011 protein	9.6
	434957	AF283775	Hs.35380	x 001 protein	9.6
	407292	AA876638		gb:nc45e06.s1 NCL_CGAP_Pr12 Homo sapiens cDNA clone s	9.6
	459109	AW292447	Hs.140821	ESTs	9.6
	457892	AA744389		gb:ny51e10.s1 NCL_CGAP_Pr18 Homo sapiens cDNA clone s	9.6
80	432074	AA525248	Hs.149723	ESTs	9.6
	440463	AI733087	Hs.129994	ESTs	9.6
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	9.6
	445326	AI220072	Hs.165893	ESTs	9.6
	434953	BE049102	Hs.121573	ESTs, Weakly similar to TRHY_HUMAN TRICHOHYALI [H.sap	9.6

	420361	N92054	Hs.194718	zinc finger protein 265	9.6
	415853	H06016	Hs.100855	ESTs	9.6
	429599	AA806106	Hs.123664	ESTs	9.6
5	417037	BE083336	Hs.80976	antigen identified by monoclonal antibody Ki-67	9.6
	449317	AW293413	Hs.132906	19A24 protein	9.6
	436588	AA759233	Hs.126506	ESTs	9.6
	409261	BE315042	Hs.19210	hypothetical protein MGC11308	9.5
	401069			C11000374:gi110764778[gb]AAAGZ2817.1[AF302150_1 (AF30	9.5
10	414065	AW515373	Hs.271249	Homo sapiens cDNA FLJ13580 fis, clone PLACE1008851	9.5
	409902	AI337658	Hs.156351	ESTs	9.5
	432258	AW973078	Hs.293039	ESTs	9.5
	438581	AW977766	Hs.292133	ESTs, Moderately similar to I78885 serine/threonine-s	9.5
	405536			NM_005805:Homo sapiens 26S proteasome-associated pad1	9.5
15	418216	AA662240	Hs.283099	AF15q14 protein	9.5
	434573	AW372340	Hs.159717	ESTs	9.5
	439354	AF086174		gb:Homo sapiens full length insert cDNA clone ZB94A08	9.5
	455410	AW936878		gb:PM2-DT0023-060300-004-a04 DT0023 Homo sapiens cDNA	9.5
	400736			Target Exon	9.5
20	419474	AW968619	Hs.155849	ESTs	9.4
	406464			C17000168:gi7294725[gb]AAF50062.1 (AE003544) CG7547	9.4
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	9.4
	427258	AA400091	Hs.39421	ESTs	9.4
	404680			Target Exon	9.4
25	433840	AA129782	Hs.3576	Homo sapiens mRNA full length insert cDNA clone EURO1	9.4
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	9.4
	457008	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapiens]	9.4
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	9.4
	451846	T65840	Hs.11762	ESTs	9.4
30	419988	W39388	Hs.55336	Homo sapiens, clone MGC17421, mRNA, complete cds	9.4
	402967			Target Exon	9.3
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	9.3
	441075	AA915991	Hs.179214	ets variant gene 3	9.3
	451107	AA235108	Hs.17639	Homo sapiens ubiquitin protein ligase (UBE3B) mRNA, p	9.3
	404649			Target Exon	9.3
35	420897	AW139261	Hs.232280	ESTs	9.3
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	9.3
	420298	AI189510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ S	9.3
	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypothetical protein [9.3
40	420101	AW500529	Hs.95180	KIAA0767 protein	9.3
	428166	AA423849	Hs.79530	M5-14 protein	9.3
	420022	AA256253	Hs.120817	ESTs	9.3
	444020	R92962	Hs.35062	ESTs	9.3
	454765	AW819629		gb:RC5-ST0293-140200-014-H05 ST0293 Homo sapiens cDNA	9.3
45	415021	R54409	Hs.301693	Homo sapiens, clone IMAGE3638994, mRNA, partial cds	9.3
	418606	AA084248	Hs.85339	G protein-coupled receptor 39	9.3
	415009	C75253	Hs.220950	ESTs	9.3
	428845	AL157579	Hs.153610	KIAA0751 gene product	9.3
	433348	AA877996	Hs.126376	ESTs, Weakly similar to JCS314 CDC28/cdc2-like kinase	9.2
50	417881	AI879117		gb:au54g09.y1 Schnelder fetal brain 00004 Homo sapien	9.2
	446354	AW449650	Hs.202249	ESTs	9.2
	427018	AA397538	Hs.136280	Homo sapiens cDNA: FLJ22288 fis, clone HRC04157	9.2
	434410	AA632644		gb:np87b07.s1 NC1_CGAP_Thy1 Homo sapiens cDNA clone s	9.2
	448072	AI459306	Hs.24908	ESTs	9.2
55	457322	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HEP08257	9.2
	424317	AI855032	Hs.26017	ESTs	9.2
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	9.2
	404112	BE302729	Hs.173162	neighbor of COX4	9.2
	433334	AI927208	Hs.231958	matrix metalloproteinase 28	9.1
60	434960	AW374941	Hs.72545	ESTs	9.1
	431658	BE409917	Hs.266935	IRNA selenocysteine associated protein	9.1
	439158	R60323	Hs.193888	ESTs	9.1
	443081	H86858	Hs.132909	ESTs	9.1
	429432	AI678059	Hs.202676	synaptonemal complex protein 2	9.1
65	452706	AW449390	Hs.257150	ESTs, Moderately similar to SUR1_HUMAN SURFEIT LOCUS	9.1
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 gene	9.1
	430780	N95102	Hs.334858	hypothetical protein MGC12250	9.1
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defective, S. cere	9.1
	418379	AA218940	Hs.137516	fidgetin-like 1	9.1
70	431405	AW070895	Hs.252574	ribosomal protein L10a	9.0
	405454			C12000541:gi5729884[ref]NP_006539.1 IGF-II mRNA-bin	9.0
	438362	AA805678	Hs.12326	ESTs	9.0
	401940			Target Exon	9.0
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	9.0
75	442432	BE033589	Hs.38178	hypothetical protein FLJ23468	9.0
	459086	AA021163	Hs.22287	ESTs	9.0
	418653	AI734064	Hs.136212	ESTs	9.0
	444152	AI125694	Hs.149305	hypothetical protein MGC2603	9.0
	437534	AA814471	Hs.291800	ESTs	9.0
80	435074	AI760944	Hs.116937	ESTs	9.0
	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA, complete cds	9.0
	442829	AW263123	Hs.127554	ESTs	9.0
	431675	AA699965	Hs.202375	ESTs	9.0
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	8.9

	420183	W92885	Hs.143408	ESTs	8.9
	421133	AA814971	Hs.257634	ESTs	8.9
	407605	W03512	Hs.6479	hypothetical protein MGC13272	8.9
5	441370	AI242433	Hs.270085	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	8.9
	437966	AW891130	Hs.38173	ESTs	8.9
	426360	AW290981	Hs.211296	ESTs, Weakly similar to 2109260A B cell growth factor	8.8
	448111	AA053486	Hs.20315	interferon-induced protein with tetratricopeptide rep	8.8
	408021	AW137133	Hs.245867	ESTs	8.8
10	429228	AI553633	Hs.337139	ESTs	8.8
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1) mRNA, partial	8.8
	431184	AW970116	Hs.310616	ESTs	8.8
	425219	AF207881	Hs.155185	cytosolic ovarian carcinoma antigen 1	8.8
	439774	AL360257	Hs.213493	Homo sapiens mRNA full length insert cDNA clone EURO1	8.8
15	432573	AA553612	Hs.324696	KIAA1594 protein	8.8
	450881	W80462	Hs.270521	ESTs, Highly similar to ALU2_HUMAN ALU SUBFAMILY SB S	8.8
	437835	AI146771	Hs.158008	ESTs	8.8
	453204	R10799	Hs.191990	ESTs	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
20	408805	H59912	Hs.48269	vaccinia related kinase 1	8.7
	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuolar proton pu	8.7
	422583	AA410506	Hs.27973	KIAA0874 protein	8.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	8.7
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapiens]	8.7
25	454132	AW131759	Hs.248286	ESTs	8.7
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-inducing)	8.7
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolog)-like	8.7
	441525	AW241887	Hs.127728	ESTs	8.7
	459539	AI279186	Hs.211194	gb:qm24a04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone 3'	8.7
30	443148	AI034357	Hs.143897	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX S	8.7
	424255	AI192657	Hs.143897	dysterlin, limb girdle muscular dystrophy 2B (autosom	8.7
	459435	AA320038	Hs.42029	gb:EST22383 Adipose tissue, white II Homo sapiens cDN	8.7
	443117	AI248826	Hs.18851	ESTs	8.6
	457434	AW628192	Hs.198248	hypothetical protein FLJ10875	8.6
35	442505	AW003775	Hs.126711	UDP-Gal4betaGlcNAc beta 1,4-galactosyltransferase, p	8.6
	430901	AA488833	Hs.250618	ESTs, Weakly similar to I38588 reverse transcriptase	8.6
	439223	AW238299	Hs.250618	UL16 binding protein 2	8.6
	417739	Z43995	Hs.155919	gb:HSC1QB121 normalized infant brain cDNA Homo sapien	8.6
	415961	H10983	Hs.137674	ESTs	8.6
40	424042	Y10601	Hs.430	ankyrin-like with transmembrane domains 1	8.6
	451035	AU076785	Hs.121557	plastin 1 (I isoform)	8.6
	447155	AA100605	Hs.10056	ESTs, Weakly similar to DP1_HUMAN POLYPOSIS LOCUS PRO	8.6
	412668	AA456195	Hs.6430	hypothetical protein FLJ14621	8.6
	458042	AW058464	Hs.100292	protein with polyglutamine repeat, calcium (ca2) home	8.6
45	456530	AL049437	Hs.152982	Homo sapiens mRNA; cDNA DKFZp586E1120 (from clone DKF	8.6
	433345	AI681545	Hs.124814	hypothetical protein FLJ13117	8.6
	445006	W91903	Hs.36708	ESTs	8.5
	453922	AF053306	Hs.154443	budding uninhibited by benzimidazoles 1 (yeast homolo	8.5
	455161	BE145900	Hs.241392	gb:MR0-HT0208-221299-204-b12 HT0208 Homo sapiens cDNA	8.5
50	424308	AW975531	Hs.24143	minichromosome maintenance deficient (S. cerevisiae)	8.5
	430413	AW842182	Hs.77807	small inducible cytokine A5 (RANTES)	8.5
	423494	AW504365	Hs.147097	Wiskott-Aldrich syndrome protein interacting protein	8.5
	415018	U49395	Hs.100426	purinergic receptor P2X, ligand-gated ion channel, 5	8.5
	404534		Hs.1262132	C11001758::gij12621132[ref]NP_075243.1] MEGF1 [Rattus	8.5
55	438451	AI081972	Hs.189413	ESTs	8.5
	435176	AA744875	Hs.151973	ESTs	8.5
	443245	AI040955	Hs.9029	hypothetical protein FLJ23511	8.5
	443162	T49951	Hs.272458	DKFZP434G032 protein	8.5
	457478	T15803		protein phosphatase 3 (formerly 2B), catalytic subuni	8.5
60	403839			Target Exon	8.5
	434932	BE613162	Hs.121004	hypothetical protein MGC3036	8.4
	420991	AW504814	Hs.204169	Homo sapiens mRNA for FLJ00111 protein, partial cds	8.4
	457854	BE547674		ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	8.4
	455994	BE179190		gb:RC0-HT0613-210300-032-07 HT0613 Homo sapiens cDNA	8.4
65	402796			Target Exon	8.4
	423426	AW389579	Hs.100426	Homo sapiens ELISC-1 mRNA, partial cds	8.4
	429568	AI088691	Hs.147097	Homo sapiens mRNA; cDNA DKFZp564D0472 (from clone DKF	8.4
	404110		Hs.100426	NM_020245::Homo sapiens tubby super-family protein (T	8.4
70	424441	X14850	Hs.77462	H2A histone family, member X	8.4
	433155	AL037035	Hs.182265	Homo sapiens cervical cancer metastasis-suppressor 1 (B	8.4
	414839	X63692	Hs.83937	DNA (cytosine-5)-methyltransferase 1	8.4
	406867	AA157857	Hs.199890	keratin 19	8.4
	418278	AI088489	Hs.82425	hypothetical protein	8.4
	458696	AW375333	Hs.37078	ESTs	8.4
75	456248	AL035786	Hs.37427	actin related protein 2/3 complex, subunit 5 (16 kD)	8.4
	403152	AA576664	Hs.170810	v-crk avian sarcoma virus CT10 oncogene homolog-like	8.4
	407649	BE066724	Hs.132906	erythrocyte membrane protein band 4.1 (elliptocytosis	8.4
	448387	AI874402	Hs.132141	ESTs	8.4
	433671	AW138797	Hs.122730	19A24 protein	8.4
80	425891	AI041717	Hs.38348	ESTs	8.4
	447347	AA570056	Hs.182625	ESTs, Moderately similar to KIAA1215 protein [H.sapie	8.4
	439079	AF085937		ESTs	8.4
	458115	BE091587		gb:IL2-BT0731-240400-069-H04 BT0731 Homo sapiens cDNA	8.4
	428144	BE269243		VAMP (vesicle-associated membrane protein)-associated	8.4

	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	8.3
	443056	AI457996	Hs.132578	ESTs	8.3
	410391	H17881	Hs.15043	Homo sapiens clone FLB5227 PRO1367 mRNA, complete cds	8.3
5	407989	AW135208	Hs.256092	ESTs	8.3
	410536	N39533		gb:yy27d04.s1 Soares fetal liver spleen 1NFLS Homo sa	8.3
	452273	AI870685	Hs.231022	ESTs	8.3
	454297	AI223335	Hs.50651	Janus kinase 1 (a protein tyrosine kinase)	8.3
	453718	AL119317	Hs.120360	phospholipase A2, group VI (cytosolic, calcium-indepe	8.3
10	401654			NM_007242:Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) b	8.3
	432891	AF161483	Hs.279761	HSPC134 protein	8.3
	419923	AW081455	Hs.120219	ESTs	8.2
	433627	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone KAT11914	8.2
	435452	AA831004	Hs.124874	ESTs	8.2
15	418583	U80908	Hs.87241	hypothetical protein from clones 23549 and 23762	8.2
	440065	W03476	Hs.266331	hypothetical protein MGC4595	8.2
	439752	T78968	Hs.14411	ESTs	8.2
	447983	AW612726	Hs.282113	ESTs, Weakly similar to I38022 hypothetical protein [8.2
	441966	AA568689	Hs.16131	hypothetical protein FLJ12876	8.2
20	408182	AA047854		gb:z49g04.r1 Soares retina N2b4HR Homo sapiens cDNA	8.2
	432180	Y18418	Hs.272822	RuvB (E coli homolog)-like 1	8.2
	435005	BE551650	Hs.158126	Homo sapiens cDNA FLJ13350 fis, clone OVARC1002143	8.2
	414962	AF273304	Hs.235376	XPMC2 protein	8.2
	444476	AF020038	Hs.11223	isocitrate dehydrogenase 1 (NADP), soluble	8.2
25	408175	W29089	Hs.19066	hypothetical protein DKFZp667O2416	8.2
	413940	AI633205	Hs.159914	ESTs, Weakly similar to I78885 serine/threonine-speci	8.2
	437277	AA748016	Hs.123370	ESTs	8.2
	431445	AA505135	Hs.44037	ESTs	8.1
	418927	BE349635	Hs.190284	ESTs	8.1
30	452446	AA086123	Hs.297856	ESTs	8.1
	445380	AI222019	Hs.144838	ESTs	8.1
	421174	AW969058	Hs.291974	ESTs, Moderately similar to A46010 X-linked retinopat	8.1
	444374	AA098441	Hs.11039	hypothetical protein MGC2722	8.1
	417247	N58024		gb:yy63c01.s1 Soares fetal liver spleen 1NFLS Homo sa	8.1
35	438335	AI498421	Hs.243168	ESTs	8.1
	445235	AI564022	Hs.138207	ESTs	8.1
	422585	NM_016186	Hs.118620	protein Z-dependent protease inhibitor precursor	8.1
	442522	AI087038	Hs.146592	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ S	8.1
	430684	AI808979	Hs.293193	ESTs	8.1
40	446442	BE221533	Hs.257858	ESTs	8.1
	441410	AA932689	Hs.233304	ESTs, Weakly similar to I38022 hypothetical protein [8.0
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein product [H.sa	8.0
	449539	W80363	Hs.58446	ESTs	8.0
	406663	U24583	Hs.302063	immunoglobulin heavy constant mu	8.0
45	423767	H18263	Hs.132753	F-box only protein 2	8.0
	450937	R49131	Hs.26267	ATP-dependant interferon response protein 1	8.0
	430977	AA490069	Hs.308676	Homo sapiens cDNA FLJ14302 fis, clone PLACE2000003	8.0
	455677	BE066061	Hs.8867	cysteine-rich, angiogenic inducer, 61	8.0
	436706	AA725808	Hs.194609	ESTs	8.0
50	459407	N92114		gb:za22h11.r1 Soares fetal liver spleen 1NFLS Homo sa	8.0
	444132	AK000452	Hs.10340	hypothetical protein FLJ20445	8.0
	437149	AI686651	Hs.202234	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY SB2	8.0
	418499	AI627392	Hs.302023	hypothetical protein FKSG25	8.0
	411298	AW835858		gb:PMO-LT0017-031299-001-h07 LT0017 Homo sapiens cDNA	8.0
55	432571	AF151054	Hs.278429	hepatocellular carcinoma-associated antigen 59	8.0
	416295	AI064824	Hs.193385	ESTs	8.0
	427485	AF039652	Hs.178655	ribonuclease H1	8.0
	409857	AW501908		gb:UH-BR0p-ajp-c-12-0-ULr1 NIH_MGC_52 Homo sapien	7.9
60	433854	AA610649	Hs.333239	ESTs	7.9
	458080	BE142728		gb:MR0-HT0157-021299-004-d08 HT0157 Homo sapiens cDNA	7.9
	423573	AA328504		gb:EST31993 Embryo, 12 week I Homo sapiens cDNA 5' en	7.9
	404495			C8001441*gi 8923061 ref NP_060114.1 hypothetical pr	7.9
	443135	AI376331	Hs.156103	ESTs	7.9
	448939	BE267795	Hs.22595	hypothetical protein FLJ10537	7.9
65	413283	R78669	Hs.23756	hypothetical protein similar to swine acylneuraminate	7.9
	443987	AW163123	Hs.10071	seven transmembrane protein TM7SF3	7.9
	434197	AA627223		gb:nq63b04.s1 NCL_CGAP_Ov6 Homo sapiens cDNA clone si	7.9
	436882	AW016722	Hs.194976	SH2 domain-containing phosphatase anchor protein 1	7.9
	434502	AW974915	Hs.116550	ESTs	7.9
70	435507	AI143579	Hs.26510	vacuolar protein sorting 33B (yeast homolog)	7.9
	444896	AI201480	Hs.144856	ESTs	7.9
	419320	H96666	Hs.6137	ESTs	7.9
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	7.9
	425569	AA359597	Hs.301701	Homo sapiens cDNA FLJ12073 fis, clone HEMBB1002387	7.9
75	445209	AW294230	Hs.80988	collagen, type VI, alpha 3	7.9
	449193	AI637997	Hs.195653	ESTs	7.9
	447397	BE247676	Hs.18442	E-1 enzyme	7.9
	455037	BE144549		gb:MR0-HT0167-081199-001-a02 HT0167 Homo sapiens cDNA	7.9
	453367	AW732847	Hs.70573	PKC1-1-related HIT protein	7.8
80	439317	AF086127	Hs.50600	ESTs, Weakly similar to T47156 hypothetical protein D	7.8
	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	7.8
	406562			NM_004520:Homo sapiens kinesin heavy chain member 2	7.8
	435192	AK000739	Hs.4835	eukaryotic translation initiation factor 3, subunit 8	7.8
	413500	BE144914		gb:CM3-HT0183-181099-023-b05 HT0183 Homo sapiens cDNA	7.8

	436216	AA380887	Hs.5085	dolichyl-phosphate mannosyltransferase polypeptide 1,	7.8
	418523	AW194757	Hs.266804	ESTs	7.8
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo sapiens cDNA	7.8
5	430146	AW815330		gb:QV0-ST0215-060100-083-a09 ST0215 Homo sapiens cDNA	7.8
	441841	AA971819	Hs.176083	ESTs	7.8
	457677	AA628890	Hs.158701	ESTs	7.8
	421090	BE301870	Hs.101813	solute carrier family 9 (sodium/hydrogen exchanger),	7.8
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-conjugating enzy	7.8
10	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo sapiens cDNA	7.8
	406410			C5000010*:gij10440464 kibj BAB15765.1 (AK024475) FLJ0	7.8
	453579	AI204463	Hs.61857	ESTs	7.8
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogene homolog-lik	7.7
	452139	AA099969	Hs.16331	Homo sapiens cDNA: FLJ21482 fis, clone COL85135	7.7
	405510			ENSP00000233779*:Hypothetical 68.0 kDa protein.	7.7
15	440777	AA994020	Hs.128553	ESTs	7.7
	446424	AW134529	Hs.244647	ESTs	7.7
	448004	AW451477	Hs.257456	ESTs	7.7
	430610	AW821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP S	7.7
20	427080	AW068287	Hs.173466	ras-related C3 botulinum toxin substrate 2 (rho famil	7.7
	451693	BE220445	Hs.279635	ESTs	7.7
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	7.7
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	7.7
	427735	AA916785	Hs.180610	splicing factor protein/glutamine rich (polypyrimidin	7.7
25	425423	NM_005897	Hs.157180	intracellular A particle-promoted polypeptide	7.7
	450663	H43540	Hs.25292	ribonuclease H1, large subunit	7.7
	432585	AA705591	Hs.190209	ESTs	7.7
	402682			Target Exon	7.7
	400247			Eos Control	7.7
30	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	7.7
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp58612022 (from clone DKF	7.7
	405514			ENSP00000241075:TRRAP PROTEIN.	7.7
	412406	AW948172		gb:RC0-MT0013-280300-021-b06 MT0013 Homo sapiens cDNA	7.7
	440226	AA873387	Hs.207330	ESTs	7.7
35	435625	H50654	Hs.113999	ESTs	7.7
	418529	AW005695	Hs.250897	TRK-fused gene	7.6
	407758	D50915	Hs.38365	KIAA0125 gene product	7.6
	447276	AL049795	Hs.17987	hypothetical protein MGC1203	7.6
	449938	AW970612	Hs.172635	Homo sapiens cDNA: FLJ21367 fis, clone COL03051	7.6
40	422893	X98411	Hs.121555	myosin IF	7.6
	451593	AF151879	Hs.26706	CGI-121 protein	7.6
	424148	BE242274	Hs.1741	integrin, beta 7	7.6
	447519	U46258	Hs.339665	ESTs	7.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolog 1	7.6
45	435279	AW930372	Hs.180793	ESTs, Weakly similar to S65657 alpha-1C-adrenergic re	7.6
	426523	S68616	Hs.170222	solute carrier family 9 (sodium/hydrogen exchanger),	7.6
	456926	AB018284	Hs.158688	KIAA0741 gene product	7.6
	416294	D86980	Hs.79170	KIAA0227 protein	7.6
	409206	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo sapiens cDNA	7.6
50	417086	AA194446	Hs.73451	ESTs, Weakly similar to S55024 nebulin, skeletal musc	7.6
	418181	U37012	Hs.83727	cleavage and polyadenylation specific factor 1, 160kD	7.5
	436910	AA926944		gb:om68g01.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone 3'	7.5
	401008			Target Exon	7.5
	413245	BE244334	Hs.75249	ADP-ribosylation factor-like 6 interacting protein	7.5
55	446820	AW295037	Hs.254986	ESTs	7.5
	439279	AI039473	Hs.130636	ESTs	7.5
	426116	AA868729	Hs.144694	ESTs	7.5
	410098	BE326839	Hs.17433	hypothetical protein FLJ20967	7.5
	422326	AI114875	Hs.78592	eukaryotic translation initiation factor 2B, subunit	7.5
60	435513	AW404075	Hs.42785	DC11 protein	7.5
	421629	N80121	Hs.4983	ESTs	7.4
	434663	AA641972	Hs.130058	ESTs	7.4
	452461	N78223	Hs.108106	transcription factor	7.4
	418811	AK001407	Hs.88663	hypothetical protein FLJ10545	7.4
65	405417			CX001144*:gij7242973 dij BAAS2547.1 (AB037730) KIAA1	7.4
	414076	AA467736		gb:nc74e05.s1 NCI_CGAP_P12 Homo sapiens cDNA clone, m	7.4
	435014	BE560898	Hs.10026	mitochondrial ribosomal protein L17	7.4
	449610	AI242042	Hs.14044	ESTs	7.4
	403397			Target Exon	7.4
70	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	7.4
	451336	AB029006	Hs.26334	spastic paraplegia 4 (autosomal dominant; spastin)	7.4
	404914			NM_004046*:Homo sapiens ATP synthase, H+ transporting	7.4
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-activating fact	7.4
	432820	AI554057	Hs.152477	ESTs	7.4
	418978	T85295	Hs.268606	ESTs	7.4
75	446636	AC002563	Hs.15767	citron (rho-interacting, serine/threonine kinase 21)	7.4
	454639	AW811633		gb:RC2-ST0158-091099-011-405 ST0158 Homo sapiens cDNA	7.4
	434522	AF189259	Hs.283081	gamma-aminobutyric acid (GABA) receptor, theta	7.4
	458235	AW297043	Hs.255604	ESTs, Weakly similar to A47234 homeobox protein H6 [H	7.4
	441043	AA913422	Hs.192104	ESTs	7.4
80	422838	AA524065	Hs.93670	Homo sapiens cDNA: FLJ22664 fis, clone HSI08202	7.3
	455096	AW855718		gb:RC1-CT0279-070100-021-a06 CT0279 Homo sapiens cDNA	7.3
	442307	AW027690	Hs.90037	ESTs	7.3
	425453	AW374284	Hs.297215	Homo sapiens chromosome 19, cosmid R26894	7.3

5	455327	AW896238	Hs.334805	Homo sapiens cDNA FLJ14604 fis, clone NT2RP1000363, m	7.3
	420982	AW576160	Hs.100729	KIAA0692 protein	7.3
	424563	AA446932	Hs.151428	ret finger protein 2	7.3
	417125	AW181998	Hs.81248	CUG triplet repeat, RNA-binding protein 1	7.3
	453902	BE502341	Hs.3402	ESTs	7.3
10	445842	A343510	Hs.176992	ESTs	7.3
	454128	AL031259	Hs.41639	programmed cell death 2	7.3
	427011	BE302729	Hs.173162	neighbor of COX4	7.3
	450872	A1742594		gb:wg55h05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapien	7.3
	451512	AI800236	Hs.207080	ESTs	7.3
15	405708	AI282759		gb:qt84a01.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone I	7.3
	432576	AW157424	Hs.165954	ESTs, Weakly similar to I38022 hypothetical protein [7.3
	459304	AW005809	Hs.281076	ESTs, Weakly similar to CHD4_HUMAN CHROMODOMAIN HELIC	7.3
	401375			NM_020999*:Homo sapiens neurogenin 3 (NEUROG3), mRNA	7.3
	413258	BE075114		gb:PM1-BT0585-110200-003-c11 BT0585 Homo sapiens cDNA	7.3
20	406016			Target Exon	7.3
	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	7.3
	422742	AA316117	Hs.337128	ESTs	7.3
	440031	BE045970	Hs.244746	ESTs	7.3
	429389	AA454779	Hs.201441	Homo sapiens cDNA FLJ11079 fis, clone PLACE1005111	7.3
25	449656	AA002008	Hs.188633	ESTs	7.3
	444310	AI140432	Hs.175936	ESTs	7.3
	459274	AA382590	Hs.170980	KIAA0948 protein	7.3
	425404	BE048060	Hs.133494	Homo sapiens clone TCCCA00164 mRNA sequence	7.3
	431150	T63857		gb:yc16e01.s1 Stratagene lung (937210) Homo sapiens c	7.3
30	443217	NM_001545	Hs.9078	immature colon carcinoma transcript 1	7.2
	413405	AW022253	Hs.215976	ESTs	7.2
	447653	BE327277	Hs.161145	ESTs	7.2
	414704	NM_014757	Hs.76986	mastermind (Drosophila), homolog of	7.2
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibitor, clade B (o	7.2
35	409188	AW363284	Hs.32553	ESTs	7.2
	453493	AL039478	Hs.304447	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.2
	456111	AK000150	Hs.78185	MAX-like bHLHZIP protein	7.2
	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	7.2
	446364	AB006624	Hs.14912	KIAA0286 protein	7.2
40	432215	AJ076609	Hs.2934	ribonucleotide reductase M1 polypeptide	7.2
	436943	AA773838	Hs.5353	caspase 10, apoptosis-related cysteine protease	7.2
	446336	AW815036	Hs.151251	ESTs	7.2
	418469	U34879	Hs.85279	hydroxysteroid (17-beta) dehydrogenase 1	7.2
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	7.2
45	429065	AI753247	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT2RP3002304	7.2
	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polypeptide 1	7.2
	416450	AA180467		gb:zcp14g08.s1 Stratagene fetal retina 937202 Homo sap	7.2
	443714	AB033015	Hs.23941	KIAA1189 protein	7.2
	455447	AW947507		gb:RCO-MT0002-140300-011-a12 MT0002 Homo sapiens cDNA	7.2
50	437154	AI023133	Hs.10739	ESTs	7.2
	423059	AW378445	Hs.123080	Homo sapiens unknown protein mRNA, partial cds	7.2
	419092	J05581	Hs.89603	mucln 1, transmembrane	7.2
	426736	AA431615	Hs.130722	ESTs	7.2
	417748	Z43011	Hs.21169	ESTs	7.2
55	434748	AI862604	Hs.211884	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.2
	438929	AW195515	Hs.253177	ESTs	7.2
	452061	AI074259	Hs.469	succinate dehydrogenase complex, subunit A, flavoprot	7.1
	446416	AV658299	Hs.163959	ESTs	7.1
	415023	AA932146	Hs.133494	Homo sapiens clone TCCCA00164 mRNA sequence	7.1
60	434766	AA742222	Hs.120634	ESTs	7.1
	432566	AW439330	Hs.256889	ESTs, Weakly similar to 2109260A B cell growth factor	7.1
	420252	AW270404	Hs.193161	ESTs	7.1
	435403	AA779987	Hs.269658	ESTs	7.1
	430151	AW958203		gb:EST380398 MAGE resequences, MAGJ Homo sapiens cDNA	7.1
65	427908	AA417272	Hs.24122	ESTs	7.1
	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitter transporter	7.1
	400098			Eos Control	7.1
	412647	AW975090		gb:EST387196 MAGE resequences, MAGN Homo sapiens cDNA	7.1
	437234	AI472213	Hs.247711	hypothetical protein FLJ20557	7.1
70	453366	AW958751	Hs.28921	zinc finger protein	7.1
	425803	AI825204	Hs.211408	ESTs	7.1
	447383	N24231		gb:yn22a11.r1 Soares melanocyte 2NblHM Homo sapiens cD	7.1
	423864	BE275607	Hs.1708	chaperonin containing TCP1, subunit 3 (gamma)	7.1
	450799	AW407504		gb:UI-HF-BMD-adk-g-12-0-UI.r1 NIH_MGC_38 Homo sapiens	7.1
75	409592	BE280951	Hs.55058	EH-domain containing 4	7.1
	453945	NM_005171	Hs.36908	activating transcription factor 1	7.1
	425196	AL037815	Hs.155097	carbonic anhydrase II	7.0
	439778	AL109729	Hs.99364	putative transmembrane protein	7.0
	417662	R07478	Hs.269845	ESTs	7.0
80	438087	AI863770	Hs.190422	ESTs	7.0
	452724	R84810	Hs.30464	cyclin E2	7.0
	448633	AA311426	Hs.21635	tubulin, gamma 1	7.0
	433154	AA578526	Hs.160994	ESTs	7.0
	440094	AI651558	Hs.270372	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SE	7.0
	409253	H91200	Hs.52002	CD5 antigen-like (scavenger receptor cysteine rich fa	7.0
	431270	BE046609		gb:hna41e11.x1 NCI_CGAP_RDF2 Homo sapiens cDNA clone 3	7.0
	407629	AA649242	Hs.62632	ESTs	7.0

5	408296	AL117452	Hs.44155	DKFZP586G1517 protein	7.0
	445439	BE243084	Hs.12719	regulator of nonsense transcripts 1	7.0
	427106	AA398193	Hs.97584	ESTs	7.0
	408623	AW811978	Hs.254037	ESTs	7.0
	426561	AA381437		gb:EST94514 Activated T-cells I Homo sapiens cDNA 5'	7.0
	408492	AA555217	Hs.183684	eukaryotic translation initiation factor 4 gamma, 2	7.0
	428894	AA437066	Hs.271736	ESTs	7.0
	419102	AA234098	Hs.42424	ESTs, Weakly similar to 2004399A chromosomal protein	7.0
10	429087	AA446019	Hs.104967	ESTs	7.0
	422684	BE561617	Hs.119192	H2A histone family, member Z	7.0
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase kinase 5	7.0
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-82 protein [H.	7.0
	443599	AI079559	Hs.134125	ESTs	7.0
15	400715			ENSP00000237081*:KJAA1217 PROTEIN (FRAGMENT).	7.0
	446514	AW449233	Hs.150847	ESTs	7.0
	413992	W26276	Hs.136075	RNA, U2 small nuclear	7.0
	402442			Target Exon	7.0
	419497	NM_006410	Hs.90753	Tat-interacting protein (30kD)	7.0
20	439575	W79259		gb:zd75c06.r1 Soares_fetal_heart_NbHH19W Homo sapiens	7.0
	407027	U63312		gb:Human cosmid LL12NC01-242E1, ETV6 gene, exons 1B a	7.0

Table 15B

25	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
30	Pkey	CAT Number	Accessions
	408182	104479_1	AA047854 AA057506 AA053841
	409113	110079_2	AA074897 AA113914 AA064871 AA079329 AA071309 AA084710 AA129030 AA075042 AA074794 AA071453 AA078803 AA148628 AA122204 AA074159 AA126185 AA079117 AA127089 AA070912 AA079280 AA131372 AA078833 AA071087 AA076131 AA071047 AA079401 AA083070 AA102076 AA115163 AA074198 AA134725 AA113889 AA121103 AA075041 AA065148 AA071310 AA101144 AA079659 AA078931 AA079209 AA070928 AA068994 AA069817 AA076187 AA069053 AA131489 AA071308 AA063317 AA070156 AA071430 AA076056 AA075684 AA070053 AA126283 AA126078 AA075895 AA079208 AA074583 AA071086 AA079623 AA070627 AA078802 AA076622 AA065051 AA079143 AA071110 AA079434 AA148748 AA079230 AA085188 AA074485 AA070680 AA076151 AA083166 AA085118 AA079450 AA085044 AA120938 AA079200 AA100188 AA081472 AA122355 AA129031 AA085362 AA069220 AA070940 AA075968 AA074563 AA084027 AA115929
35			
40	409206	1108161_1	AW364844 AW364847 AW937534 AW937593 AW937659
	409857	1156298_1	AW501908 AW502959 AW502540
	410146	1178974_1	AW592655 R05927 R06916
	410536	1207322_1	N39533 AW753094 AW753093
	411298	1237955_1	AW835858 AW835836 AW835823 AW835834 AW835831 AW835832 AW835843 AW835816 AW835833 AW835815 AW835849 AW835835 AW835848 AW835851 AW835852 AW835862 AW835855 AW835825 AW835847 AW835838
45	412406	1293055_1	AW948172 AW948178 AW948169 AW948176 AW948191 AW948192 AW948186 AW948184 AW948187 AW948188 AW948189 AW948181 AW948177 AW948171 AW948183 AW948173
	412647	1317604_1	AW975090 N44182
	413258	1355998_1	BE075114 BE075283 BE075118
	413314	1360034_1	BE081585 BE081717 BE081663 BE081794 BE081659
50	413500	1373933_1	BE144914 BE394989
	414076	141490_1	AA467736 AA135210 AW968166 AA467804
	416450	159551_1	AA180467 AA449184 AA464831 AA505048
	417247	1660859_1	N58024 T58194 T11693 N64222 T05848
	417739	1696198_1	Z43995 R12357 R34740
55	417881	170544_1	AI879117 AW161351 Z45755 BE003661 AA206949 AA476541
	418347	174149_1	AA216419 F03238 AA229517
	422429	216469_1	AA310527 AW952295 Z44865 H06641
	423573	229714_1	AA328504 AA327783 AW952370
60	426561	269158_1	AA381437 AA628833 AW407275
	428294	289365_1	AA425488 AA496895 F23221
	430146	313562_1	AW815330 AW968170 AI732687 AI732725 AA468343 AA467817 AW063961
	430151	313668_1	AW968203 AI732757 AA470353 AA468025 AA468479 AI734151
	430709	322338_1	R34356 AW969880 AA484613
	430848	324821_1	AW021726 AA487752 AA488085
65	431150	328626_1	T63857 AW971220 AA493469 T63699
	431270	330676_1	BE046609 BE046118 AA501504
	432363	345469_1	AA534489 AW970240 AW970323
	434197	381655_1	AA627223 AA643443 AA650619 AA643463 AA643453 AA643439 AA643438 AW802964 AW821595 AW821594 AA643431 AA643432 AW827513
70	434407	385744_1	AW815333 AW815409 AA632563
	434410	385798_1	AA632644 AA635376 AA664188
	436910	429182_1	AA926944 AA767974 AA737237
	437056	432262_1	AI147061 AA743380 AA765223 AW976398 AI803927
	439354	47146_1	AF086174 W31796 W04694
	439575	47400_1	W79259 AF086396 W73927
75	444314	600667_1	AI140497 AW749525 AW749626 AW749644
	447197	711623_1	R36075 AI366546 R36167
	447383	71990_1	N24231 BE617964 N36313
	450799	847242_1	AW407504 W31274 AI738877
80	450872	849959_1	AI742594 AI761397 R31198 AI819332 R31257
	454355	1130264_1	AW812535 AW812536 AW390307
	454639	1227728_1	AW811633 AW811652 AW811898
	454765	1233905_1	AW819629 AW854320

5	455037 455096 455161 455410	1249783_1 1253078_1 1256167_1 1268380_1	BE144549 AW851677 AW851643 AW851711 AW851719 AW855718 AW855740 AW855748 BE145900 AW859906 BE145895 BE145831 BE145914 BE145820 BE145817 BE145890 BE145908 AW936678 AW936637 AW936682 AW936685 AW936817 AW936811 AW936762 AW936653 AW936815 AW936812 AW936683 AW936822 AW936823 AW936821 AW936732 AW936730 AW936781 AW947507 AW947509 AW947791 BE008335 BE147440 BE147708 BE147563 BE147456 BE179190 BE179206 BE179182 BE179185 BE179186 BE179194 AA744389 AA744270 AA744284 AA744299 AA745380 AA744337 AA846905 AA847698 BE142728 AA834047 AW937124 BE091587 BE091730 BE091577 BE091655 BE091729 BE091640 BE091578 BE091727 BE091803 BE091660 BE091721 BE088255 BE076582 AW992312 BE008791 BE082385 BE083504 BE083466 AW997967 AW997991 BE166595 AW843686 AW844334 BE079091 AW603391 BE081427 BE079514 BE184580 BE009962 BE008722 AW579912 AW860561 AW890184 AW795276 AW850410 AW850411 AW610330 AW860564 AW860578 AW862519 BE073924 BE008687 BE073657 BE073921 AW274106 BE011060 AW268120 AI335067 AW793748 AW997736 BE080117 AW867987 AI547161 AW847767 AW393586 AW579444 BE083334 AI547158 AW799863 AA585179 AW992792 AW882215 BE011913 AW997894 AI547159 AW992772 AW581178 AA092247 AW843916 BE079190 AW878478 BE083648 BE066454 AI469937 AW393594 AW579899 AW939276 BE173265 AW878631 AW878638 AW992802 BE079913 AA633638 AW369008 BE076590 AW843456 AW992791 BE173247 AW843921 AW843333 AW878334 BE090235 BE078240 BE066325 AW603276 BE169310 AW817299 BE091641 BE000160 AW898164 AW994624 AW998391 AW862797 AW899438 AW750667 AW939685 AW940017 AI200402 BE167391 AW939318 AW799837 AW939953 AW939681 BE078188 AA490599 BE076595 AW297451 BE076544 AW803372 BE081223 AW939237 BE084239 AI174202 BE077804 BE078028 AA512912 AI124808 AI147524 AI884882 AW939962 AW939254 BE171687 AW998400 AW998348 AW998353 AW998268 AW998303 AW998302 AW998299 AA502748 BE077882 AW998295 BE090238 AW604655 AI423051 BE093093 AW579913 AW606384 BE006143 BE170415 AW998054 BE084608 AW992779 BE088111 AW610555 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BE094328 BE001336 AW868170 BE074119 AW884149 BE091734 BE008744 AI540867 BE185808 BE080193 BE185858 AA476398 BE081040 BE074724 BE085426 BE074725 AW988297 AW867606 BE185798 AW898734 BE076369 BE081672 BE088178 AA610264 BE088118 AA284217 AW578085 BE074518 BE001359 BE001328 AW820227 AW686196 AW868190 AW904548 BE008526 BE012037 BE079361 BE005870 AW867804 AW878433 BE008751 BE005875 BE008748 BE093440 BE183050 AA506676 BE001329 BE008803 BE080123 BE008041 AW994688 AW994675 AW994760 AW994691 AW994681 BE080189 BE080112 AW868173 AI768000 AW883094 AW868179 BE080201 AW665449 BE067473 BE008746 BE184053 BE076437 BE076376 BE076402 AA480395 BE082436 BE184134 BE185224 BE085428 BE006682 AW688181 AW998358 AW866102 BE083507 BE077974 BE008835 BE093439 BE076108 AI416987 BE008788 BE069909 BE093441 BE185502 BE183053 AW750669 BE011812 BE008672 BE081684 BE093445 AW868184 BE081839 BE008797 AW842067 BE008678 BE008670 BE551820 AW838974 BE081637 BE046696 BE008673 BE010328 BE083250 BE089614 BE082052 BE081424 BE001678 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AW838884 AW053806 AW063837 AW878479 BE078815 BE008802 AW992789 BE007925 AW802204 BE011825 BE092130 BE184059 BE079087 BE150568 BE185497 BE078808 AW83761 AW842295 BE161523 AA484796 AA480390 AW994667 BE073205 AW607316 BE083201 AW802265 AW578700 BE078715 AW860403 AW897456 AW996558 AW890602 AW860413 AA425412 BE008364 BE150438 AW602606 AI435236 AA574285 AI823745 AA501773 AI002587 AW832749 BE185491 AW996489 BE001442 AW946425 BE001586 AI524864 BE085556 AW867549 AW604038 BE079632 AI752160 AW998398 AW883904 AW882376 AW467098 BE080116 AW839384 AW883995 AA420955 BE074091 AW996348 AW860625 AW860633 AW946513 BE083485 AW860412 AW602207 BE075407 AW838972 AW607023 AW602201 AW799772 AW862452 AW862451 BE505041 BE161537 AW602206 AW860404 AW860555 BE007843 AW860632 AW862457 AW998019 AW860405 BE092062 AW603921 BE183386 AW868194 BE075664 BE078184 AI541202 AI204949 BE092451 AW603111 AA484587 AA484402 AW998675 AW896064 BE069923 AW867965 BE069919 BE092069 AA807842 AW605500 AW605501 BE085409 AA506738 BE080080 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BE182345 BE182373 BE008401 AA84441 BE182362 BE182372 BE008414 BE078186 BE009165 BE010266 BE009162 BE009167 BE011006 BE073335 BE182370 AW750556 BE182347 BE011000 AA484576 BE092982 BE183897 BE092973 AA573037 AW882317 BE081832 AA478471 AA551613 BE182366 AW838886 AW026827 BE008413 AW896605 AA503558 AA776622 BE084825 AA502971 BE081842 BE010628 AW802218 AI888924 AW867986 BE081144 AW577492 AI241060 AW802041 AW802005 BE011244 BE087051 AA984758 AA452597 AW992786 AW797500 BE077829 BE008042 AW881760 BE093516 AW802084 AW369007 BE185123 BE087775 AW801018 BE093443 AW867978 AW843271 BE173850 AW997859 BE010620 AW992516 AW843908 BE083200 BE164675 BE074340 AW880289 BE075433 BE008456 AW946438 BE066570 BE093547 AA508107 AW867992 BE076239 BE183881 AW817422 BE087717 AW899147 BE010608 AW992295 AA436737 BE075412 BE093011 AW581656 BE089629 BE080756 BE150494 AW930320 AW883102 BE076370 BE000625 BE166095 AW867979 BE182159 AW577501 AW577488 AW577491 BE010637 BE069910 BE093295 BE005243 AI620783 AW992550 AW890590 AW577496 AW577504 AW842725 AW842666 AW864691 AW997722 AW842662 BE009233 BE087809 BE083196 AA287768 AW939691 AW815631 BE001453 AW841903 BE077613 AW577500 BE081479 AW992558 BE011065 AW843187 AW867990 AW898296 BE074339 AA501697 AW749997 BE076249 AW867991 BE085718 AW994607 BE010578 BE075436 AW386825 AA484667 BE081144 AW577492 AW997932 AW899089 AW842706 AW890727 AW843175 BE075428 AW843155 AW842679 AW842708 BE095915 AW842721 AW438792 AI251478 BE069911 BE067054 BE079889 BE075453 BE069927 AA491920 BE170606 BE182305 BE080052 AW84306 BE011075 BE075369 AA525261 AW391518 BE079202 AA658195 BE076138 AW799901 AA438359 AW992510 BE011810 AA508724 BE075488 BE075561 AA258982 BE078726 BE069914 AA213699 BE075376 AA484500 AW809999 BE077872 AA503571 AW884724 AW880124 AW868454 AW577502 AW577489 AW799829 AW992545 BE075806 AW994608 BE350368 AA557836 BE077682 AW844660 AW883431 BE085872 AW838887 AW843890 AW868404 AA578417 BE074115 AW842680 AW277193 AW890728 AW605111 BE093940 AW890710 BE085560 AW868180 AW896778 BE089925 BE011054 BE075965 AW842668 AW868310 BE011071 BE075429 AW843152 AW905848 BE075397 AW842762 BE075402 BE077950 AW837810 BE079998 BE183965
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BE075431 AW815917 AW998359 AW799883 AW603782 AA557480 AW841444 BE075915 AA548034 AW843393 AW391559 BE083265 AW939721
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 AW603765 AW843919 AW578235 BE184139 AW997742 BE183923 BE084210 AW802033 AW748724 AW939018 AW997459 AW842742 AA213697
 BE182308 BE011078 AW607702 AW882623 BE080016 AW580994 BE076531 AA443462 AW607407 AW883382 AW939399 AW605627 AW844615
 AW939724 AW815931 AW883765 AA287421 BE075626 AW946171 AW841445 AW797994 AW815957 AA683300 AW369004 BE075368 BE081560
 AW605626 AW939398 AA507280 AA506317 AW841230 AW992519 AA465332 AA425246 BE090234 BE090236 AA483259 AA451961 AA535566
 AA506406 AA888571 AA503568 AA507130 AA532944 AA501672 BE168634 AA492022 AA507662 AW842286 AA494226 AA776038 AA442419
 AW579900 BE171816 AA863055 AA491916 AA447490 AA461423 AA434543 AA243279 AW997466 AW603740 BE000295 AA658571

TABLE 15C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400715	8118885	Minus	80151-80297
400736	8118985	Plus	143447-143851
401008	8117391	Minus	81421-81551,82364-82512,82862-82938
401069	3927852	Minus	45682-45831
401375	7417809	Minus	6121-6766
401405	7768126	Minus	69276-69452,69548-69958
401539	8072433	Minus	62028-62608
401557	8099856	Minus	112785-112924
401654	9097132	Minus	64695-64797
401940	3738108	Plus	153460-153592
402025	7547159	Plus	173835-173998
402442	9796503	Plus	141714-141842,142010-142122
402682	8138477	Minus	147522-147795
402796	3646083	Minus	6126-6265,6416-6689
402967	5360987	Minus	33518-34546
403038	7717439	Minus	290021-290284
403055	8748904	Minus	109532-110225
403310	8139936	Minus	183883-184026
403397	9438368	Minus	84481-84655
403839	4176355	Plus	21201-22223
404110	9212839	Minus	18344-18510
404495	8151634	Minus	59449-60477
404534	8247909	Minus	147853-148086
404630	9796665	Plus	74495-74715
404649	9796926	Minus	100027-100399
404680	9797204	Minus	159810-159979,160213-160321,161023-161304,162862-163140,164490-164644,166404-166530,166936-167083,167392-167522
404914	7341760	Plus	92603-92827
405417	4753290	Minus	50704-51499
405454	7656675	Plus	133807-134053
405510	7630909	Minus	101028-101174
405514	9454624	Plus	35953-36151
405536	9795661	Plus	164091-164162,164397-164516,166720-166790,167785-167935
406016	8272661	Plus	41341-41940
406410	9256394	Minus	115806-116104
406464	9789674	Plus	72161-72562
406562	7711584	Plus	37316-37426

TABLE 16A: 200 GENES DOWN-REGULATED IN CERVICAL CANCER COMPARED TO NORMAL ADULT CERVIX

Table 16A shows 200 genes down-regulated in cervical cancer compared to normal adult cervix. These were selected as for Table 15A, except that the numerator and denominator were switched, the median value amongst normal cervixes was greater than or equal 40 units, and the ratio was greater than or equal to 3.0 (i.e. 3-fold down-regulated in tumor vs. normal cervix).

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of cervical cancer to normal cervix

Pkey	ExAccn	UnigenelD	Unigene Title	R1
453596	AA441838	Hs.62905	hypothetical protein FLJ14834	18.1
443912	R37257	Hs.184780	ESTs	16.8
420923	AF097021	Hs.273321	differentially expressed in hematopoietic lineages	13.6
414422	AA147224	Hs.337232	Homeo box A13	13.1
420058	AK001423	Hs.94694	Homo sapiens cDNA FLJ10561 fis, clone NT2RP2002672	12.9
412639	AW961284	Hs.296235	ESTs	12.4

	418934	AA296520	Hs.89546	selectin E (endothelial adhesion molecule 1)	12.4
	407938	AA905097	Hs.85050	phospholamban	11.3
	410544	AJ446543	Hs.95511	ESTs	11.3
5	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-adrenergic rece	11.1
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 protein [H.sapiens]	11.0
	420674	NM_000055	Hs.1327	butyrylcholinesterase	10.9
	453060	AW294092	Hs.21594	hypothetical protein MGC15754	10.6
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to hypoxia induci	10.5
10	452106	AJ141031	Hs.21342	ESTs	9.5
	428780	AJ478578	Hs.50536	ESTs	9.5
	431706	AJ816086	Hs.296341	adenylyl cyclase-associated protein 2	9.2
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PLACE1002968	9.0
	430468	NM_004673	Hs.241519	angiotensin-like 1	9.0
15	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chain	8.7
	448944	AB014505	Hs.22599	atrophin-1 interacting protein 1; activin receptor inte	8.6
	401486	NA		C40006477:gi 4758508 ref NP_004253.1 airway trypsin-li	8.4
	417511	AL049176	Hs.82223	chordin-like	8.3
	429900	AA460421	Hs.30875	ESTs	8.2
20	411908	L27943	Hs.72924	cytidine deaminase	8.0
	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiesterase	8.0
	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from clone DKFZp	8.0
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	8.0
	421666	AL035250	Hs.1408	endothelin 3	7.9
25	450164	AJ239923	Hs.30098	ESTs	7.9
	412642	BE244598	Hs.809	hepatocyte growth factor (hepatopoietin A; scatter factor	7.7
	425608	AA360486	Hs.92448	ESTs	7.6
	442748	AI016713	Hs.135787	ESTs	7.3
	415672	N53097	Hs.193579	ESTs	7.2
30	414175	AJ308876	Hs.103849	hypothetical protein DKFZp761D112	7.2
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	7.0
	424634	NM_003613	Hs.151407	cartilage intermediate layer protein, nucleotide pyroph	6.7
	414214	D49958	Hs.75819	glycoprotein M6A	6.5
	436637	AJ783629	Hs.25766	ESTs	6.5
35	408621	AJ970672	Hs.46638	chromosome 11 open reading frame 8	6.5
	432101	AI918950	Hs.123642	EphA3	6.3
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA, complete cds	6.3
	424153	AA451737	Hs.141496	MAGE-like 2	6.3
	420228	R25023	Hs.12369	ESTs	6.2
40	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myotilin)	6.1
	444931	AV652066	Hs.75113	general transcription factor IIA	6.1
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HEMBA1002970	6.1
	425849	AJ000512	Hs.296323	serum/glucocorticoid regulated kinase	6.1
	410425	BE278367	Hs.63510	KIAA0141 gene product	6.0
45	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	6.0
	424973	X92521	Hs.154057	matrix metalloproteinase 19	6.0
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like 1	5.9
	429414	AJ783656	Hs.202096	empty spiracles (Drosophila) homolog 2	5.9
	440594	AW445167	Hs.126036	ESTs	5.9
50	452768	AW069459	Hs.61539	ESTs	5.9
	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 protein [H.sapiens]	5.9
	448533	AL119710	Hs.21365	nucleosome assembly protein 1-like 3	5.9
	425010	T16837	Hs.4241	ESTs	5.9
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.8
55	437980	R50393	Hs.278436	KIAA1474 protein	5.8
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	5.7
	404097	NA		C50002427:gi 9369379 gb AAFB7128.1 AC006434_24 (AC00643	5.7
	422546	AB007969	Hs.301478	KIAA0500 protein	5.7
	445872	AI681573	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HEMBB1001458	5.7
60	429999	AJ761902	Hs.99597	ESTs	5.6
	453354	W55946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HEMBB1002492	5.6
	442082	R41823	Hs.7413	ESTs	5.5
	452073	AA625150	Hs.82098	ESTs	5.4
	430032	AW936136	Hs.99610	ESTs	5.4
65	408767	AA057279	Hs.211928	ESTs	5.4
	433234	AB040928	Hs.65366	KIAA1495 protein	5.3
	431708	AI698136	Hs.108873	ESTs	5.3
	421200	AA284811	Hs.264433	ESTs	5.2
	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HEMBA1001008	5.2
70	409643	AW450866	Hs.257359	ESTs	5.1
	416676	AW392022	Hs.79507	KIAA0582 protein	5.1
	420357	U94333	Hs.97199	complement component C1q receptor	5.0
	417355	D13168	Hs.82002	endothelin receptor type B	5.0
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone COL05674	5.0
75	430965	AA489732	Hs.154918	ESTs	4.9
	419658	XD4430	Hs.93913	interleukin 6 (interferon, beta 2)	4.9
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	4.8
	404485	NA		Target Exon	4.8
80	429594	AK001128	Hs.210297	Homo sapiens cDNA FLJ10266 fis, clone HEMBB1001024	4.8
	417692	R09338	Hs.50724	Homo sapiens cDNA FLJ10934 fis, clone OVARC1000540	4.8
	432304	AA932186	Hs.69297	ESTs	4.7
	430895	U66581	Hs.248121	G protein-coupled receptor 22	4.7
	448851	AI582207	Hs.177166	ESTs	4.7
	405523			C80014097:gi 7441226 pir S31212 collagen alpha 1(XIV)	4.7

	450656	AA010539	Hs.18912	ESTs	4.6
	422942	AF054839	Hs.122540	tetraspan 2	4.6
	401479	T49304	Hs.110850	Rag C protein	4.6
5	444192	AW469413	Hs.151145	ESTs	4.6
	439648	AW780192	Hs.267596	ESTs	4.5
	410378	R23324	Hs.41693	DnaI (Hsp40) homolog, subfamily B, member 4	4.5
	444702	AJ220122	Hs.326560	hypothetical protein MGC2780	4.5
	410909	AW898161	Hs.53112	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX	4.5
10	452249	BE394412	Hs.202095	empty spiracles (Drosophila) homolog 2	4.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	4.5
	411037	BE145915	Hs.99472	ESTs	4.4
	442803	AI675298	Hs.199917	ESTs	4.4
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulatory, type II, be	4.4
15	400628	NA		C10001871*:gij1705533[sp]P32018[CA1E_CHICK COLLAGEN ALP	4.3
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage serine esterase	4.3
	437110	AL049240	Hs.144995	ESTs	4.2
	410646	W79408	Hs.50745	ESTs	4.2
	456304	AI820973		gbnc21c02.y5 NCL_CGAP_Pr1 Homo sapiens cDNA clone, mRN	4.2
20	401270			Target Exon	4.2
	419447	BE092696	Hs.75928	ESTs	4.2
	414807	AI738816	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)	4.2
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	4.2
	434469	AA634806		gbab28c02.r1 Stratagene lung (937210) Homo sapiens cDN	4.1
25	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATION FACTOR	4.1
	418947	W52990	Hs.22860	ESTs	4.1
	416434	AW163045	Hs.79334	nuclear factor, Interleukin 3 regulated	4.0
	454736	BE184348		gb:CMO-HT0576-010500-355-e11 HT0676 Homo sapiens cDNA,	4.0
	407945	X69208	Hs.606	ATPase, Cu transporting, alpha polypeptide (Menkes synd	4.0
30	447499	AW262580	Hs.147674	protocadherin beta 16	4.0
	430686	NM_001942	Hs.2633	desmoglein 1	4.0
	409882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7 (cardiovascula	3.9
	419047	AW952771	Hs.90043	ESTs	3.9
	414272	AI651603	Hs.46988	ESTs	3.9
35	443808	AW377736	Hs.12420	ESTs	3.9
	426883	H21520	Hs.35088	ESTs	3.9
	410659	AJ080175	Hs.68826	ESTs	3.9
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	3.9
	432181	AA527650	Hs.156037	ESTs	3.9
40	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	3.8
	453296	AA034413	Hs.62560	ESTs	3.8
	400878	NA		Target Exon	3.8
	401103	NA		C12001233:gij7305361[ref]NP_038652.1 otogelin [Mus mus	3.8
	436670	AI690021	Hs.201536	ESTs	3.7
45	432251	AW972993	Hs.232165	polycythemia rubra vara 1; cell surface receptor	3.7
	408793	BE258371	Hs.254660	ESTs	3.7
	419093	AJ804054	Hs.112885	spinal cord-derived growth factor-B	3.7
	434844	AF157116	Hs.22350	hypothetical protein LOC56757	3.7
	450776	NM_007250	Hs.320861	Kruppel-like factor 8	3.7
50	437140	AA312799	Hs.283689	activator of CREM in testis	3.6
	418421	R58620	Hs.85050	phospholamban	3.6
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOTHETICAL PROTEIN	3.6
	417194	NS3793		ghyz07a01.r1 Soares_multiple_sclerosis_2nbHMSF Homo sa	3.6
	443567	AI077540	Hs.134090	ESTs	3.6
55	451879	AJ821030		ghyb52f11.y5 Stratagene ovary (937217) Homo sapiens cD	3.6
	421013	M52397	Hs.1345	mutated in colorectal cancers	3.5
	451896	AF196304	Hs.27197	SUMO-1-specific protease	3.5
	413237	AI468574	Hs.171965	ESTs	3.5
	424636	AA453734	Hs.10198	ESTs	3.5
60	432660	AI288430	Hs.64004	ESTs	3.5
	414581	AL079440	Hs.74002	nuclear receptor coactivator 1	3.5
	400802	NA		Target Exon	3.5
	430015	AW768399	Hs.112157	ESTs	3.5
	451978	AW813747	Hs.27371	Homo sapiens mRNA; cDNA DKFZp566J123 (from clone DKFZp5	3.5
65	449088	AI654048	Hs.196556	ESTs	3.5
	425113	AI936992	Hs.154658	plackstrin and Sec7 domain protein	3.5
	458459	AI124553	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone COL09609	3.5
	420249	BE262895	Hs.276916	nuclear receptor subfamily 1, group D, member 1	3.5
	401159	NA		Target Exon	3.5
70	442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQ	3.5
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5 [H.sapiens]	3.4
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC FINGER PROTEIN	3.4
	423587	AA328074	Hs.284256	hypothetical protein FLJ14033 similar to hypoxia induci	3.4
	443178	AI631241	Hs.47312	ESTs	3.4
75	430694	AA810624	Hs.30936	ESTs, Weakly similar to H2BH_HUMAN HISTONE H2B H [H.sap	3.4
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Drosophila) homol	3.4
	437950	U79244	Hs.112642	ESTs	3.3
	419368	AI753518	Hs.209464	KIAA1604 protein	3.3
	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	3.3
80	451398	AJ793124	Hs.144479	ESTs	3.3
	452814	AI092790	Hs.334703	hypothetical protein FLJ14529	3.3
	407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, expressed in pro	3.3
	412295	AW088826	Hs.117176	poly(A)-binding protein, nuclear 1	3.3
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	3.3

444216	D25303	Hs.222	integrin, alpha 9	3.3
418771	AA807881	Hs.25329	ESTs	3.3
433036	AA574091	Hs.105964	ESTs	3.2
404584			Target Exon	3.2
404195			NM_015718*:Homo sapiens NADPH oxidase 3 (NOX3), mRNA. V	3.2
428819	AL135623	Hs.193914	KIAA0575 gene product	3.2
425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
420833	R47948	Hs.188732	ESTs	3.1
413156	AA127133		gbzl87e03.r1 Stratagene colon (937204) Homo sapiens cD	3.1
413607	T64741		gb:yc48f11.r1 Stratagene liver (937224) Homo sapiens cD	3.1
443960	AI093577	Hs.255416	hypothetical protein FLJ21986	3.1
428790	AF023456	Hs.193558	protein phosphatase, EF hand calcium-binding domain 2	3.1
434520	AA205273	Hs.177011	hypothetical protein	3.1
432247	AA531287	Hs.105805	ESTs	3.1
429303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-adrenergic rece	3.1
439734	AC005013	Hs.149	cAMP response element-binding protein CRE-BPa	3.1
433546	AI075877	Hs.125461	hypothetical protein FLJ11539	3.0
430317	AB020645	Hs.239189	glutaminase	3.0
425130	AA448208	Hs.99163	ESTs	3.0
444195	AB002351	Hs.10587	KIAA0353 protein	3.0
409007	AL122107	Hs.49599	Homo sapiens mRNA; cDNA DKFZp434G0827 (from clone DKFZp	3.0
453773	AL133761		gb:DKFZp761C1413_r1 761 (synonym: hamy2) Homo sapiens c	3.0
442974	AI025670	Hs.109308	ESTs, Weakly similar to leucine-rich glioma-inactivated	3.0
446936	H10207	Hs.47314	ESTs	3.0
454086	AW885909	Hs.6975	PRO1073 protein	3.0
420271	AI954365	Hs.42892	ESTs	3.0
435545	AA687415	Hs.28107	ESTs	3.0
445175	AV652851	Hs.20255	ESTs	3.0

30 TABLE 16B

35 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
413156	135116_1	AA127133 AA384396 AW958912 T72119
413607	1379911_1	T64741 BE158393 BE152805
417194	1657323_1	N53793 N53716 N53739
434469	387447_1	AA634806 C18732 AA729161 AA729860
451879	888642_1	AI821030 T47126 AI821318
453773	980699_1	AL133761 AL133767
454736	1232235_1	BE184348 AW817453 BE011068
456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101

50 TABLE 16C

55 Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400628	3818355	Plus	41851-41984
400802	8567867	Minus	174571-174856
400878	9864757	Plus	31493-32842
401103	8568122	Minus	98330-98449
401159	6067118	Minus	3180-3953
401270	9797168	Minus	141659-141813
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
404097	7770701	Plus	55512-55781
404195	3805917	Minus	39186-39332
404485	8096921	Plus	75166-75264,124036-124232
404584	9857511	Plus	138651-139153
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217

70

TABLE 17A: 605 genes upregulated in testicular cancer relative to normal body tissues

75 Table 17A lists about 605 genes upregulated in cervical cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion transporter). Certain predicted protein domains are noted.

80

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar accession number, GenBank accession number
UniGeneID: UniGene number
PredProt.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M,

likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1 95th percentile of cervical cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UnigenelD; Unigene Title; Pred.Prod.Domains; R1

- 408522; AI541214; Hs.46320; Small proline-rich protein SPRK [human, ; none; Cornifin; 33.942
 422168; AA586894; Hs.112408; S100 calcium-binding protein A7 (psoriasis; ehand, S_100; TM=M;SS=N; 33.05
 424098; AF077374; Hs.139322; small proline-rich protein 3; Cornifin; TM=M;SS=N; 32.856
 422158; L10343; Hs.112341; protease inhibitor 3, skin-derived (SKAL; wap; TM=M;SS=Y; 29.604
 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR_LY6, toxin, Activin_recp; TM=M;SS=Y; 27.95054945
 421948; L42583; Hs.334309; keratin 6A; filament, RhoGAP, DUF286, bZIP, Tropomyosin, tubulin, DUF164, TBCA, Collagen; TM=M;SS=N; 26.778
 446292; AF081497; Hs.279682; Rh type C glycoprotein; Arumonium_transp, FecCD; TM=Y;SS=M; 26.1133829
 407242; M18728; ; gbHuman nonspecific crossreacting anti; ig; TM=M;SS=M; 23.382
 424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2, hemopexin, Peptidase_M10; 22.522
 412719; AWO16610; Hs.816; ESTs; none, none; 21.198
 406690; M29540; Hs.220529; carcinoembryonic antigen-related cell ad; ig; TM=M;SS=M; 20.028
 402075; ; ENSP00000251056; Plasma membrane calcium; none; 19.038
 431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placenta; cadherin, Cadherin_C_term; TM=Y;SS=M; 17.92061281
 412471; M63193; Hs.73946; endothelial cell growth factor 1 (plate; Glycos_transf_3, Glycos_trans_3N; TM=M;SS=M; 17.8978979
 417308; H60720; Hs.81892; KIAA0101 gene product; none; TM=M;SS=N; 17.08333333
 429259; AA420450; Hs.380088; Plakophilin; none, none; 17.08235294
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; 16.91568628
 439926; AWO14875; Hs.137007; ESTs; none, none; 16.69
 419693; AA133749; Hs.301350; FYD domain-containing ion transport reg; ATP1G1, PLM, MAT8; TM=Y;SS=M; 16.365
 413753; U17760; Hs.75517; laminin, beta 3 (nicotin (125kD), kalinin; laminin_EGF, laminin_Nterm; 15.75294118
 413278; BE563085; Hs.833; Interferon-stimulated protein, 15 kDa; ubiquitin; 15.48600509
 401781; ; Target Exon; filament; TM=M;SS=N; 15.43568831
 420440; NM_002407; Hs.97644; mammaglobin 2; Uteroglobulin; 15.394
 441633; AW958544; Hs.112242; normal mucosa of esophagus specific 1; none; TM=M;SS=M; 15.12264151
 452240; AI591147; Hs.61232; ESTs; none, none; 14.63
 428957; NM_003881; Hs.194679; WNT1 Inducible signaling pathway protein; tsp_1, wvc, IGFBP; TM=M;SS=M; 14.49772727
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2; TM=M;SS=N; 14.4389313
 432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fis, clone PL; none, none; 14.00909091
 400289; X07820; Hs.2258; matrix metalloproteinase 10 (stromelysin; hemopexin, Peptidase_M10, Astacin; 13.824
 414812; X72755; Hs.77357; monokine induced by gamma interferon; IL8; TM=M;SS=Y; 13.7754386
 421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz, NTR; 13.74595843
 400284; ; NM_000125; Homo sapiens estrogen receptor; hormone_rec, zf-C4, Oest_recep; TM=M;SS=M; 13.31578947
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cy; IL8; TM=M;SS=Y; 13.05294118
 411274; NM_002776; Hs.69423; kallikrein 10; trypsin; TM=M;SS=N; 13.038
 405687; M31126; Hs.352054; matrix metalloproteinase 11 (stromelysin; hemopexin, Peptidase_M10; 13.00311527
 427666; AI791495; Hs.180142; calmodulin-like skin protein (CLSP); ehand; TM=M;SS=N; 12.79
 400301; X03635; Hs.1657; estrogen receptor 1; F-box, hormone_rec, zf-C4, Oest_recep, adh_zinc, ketoacyl-synt, pp-binding, Acyl_transf, Thioesterase, ketoacyl-synt, CAAA, E7, RFX_DNA_binding; TM=M;SS=N; 12.472
 410001; AB041036; Hs.57771; kallikrein 11; trypsin; TM=M;SS=M; 12.47
 422310; AA316522; Hs.98370; cytochrome P450, subfamily IIS, polypept; none, pkinase, fn3, lgr; 12.28597122
 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin; TM=M;SS=N; 12.13379205
 437044; AL035864; Hs.69517; differentially expressed in Fanconi's an; none; TM=M;SS=M; 12.04945055
 418462; BE001696; Hs.85266; Integrin, beta 4; fn3, Integrin_B, Calx-beta, EGF; TM=M;SS=M; 11.95538462
 443859; NM_013409; Hs.9914; folistatin; kazax; 11.95467422
 426350; NM_003245; Hs.2022; transglutaminase 3 (E polypeptide, prote; Transglutamin_N, Transglutamin_C, Transglut_core; TM=M;SS=N; 11.61
 408243; Y00787; Hs.624; interleukin 8; IL8, IL8; TM=M;SS=N; 11.564
 444781; NM_014400; Hs.11950; GPI-anchored metastasis-associated prote; UPAR_LY6, lactamase_B; 11.55285714
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DOT, PI3_P14_kinase, FAT, FATC, BoIA, RUN; TM=M;SS=N; 11.47956989
 418663; AK001100; Hs.41690; desmocollin 3; cadherin, Cadherin_C_term; none; 11.456
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; none; 11.45352113
 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolys; Kunitz, BPTI, fn3, vwa, Collagen, beta-lactamase; TM=M;SS=M; 11.32234432
 426970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabox, 7tm_3; TM=Y;SS=M; 11.28686327
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none, none; 11.076
 451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg; TM=M;SS=N; 11.0381579
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; amk; 11
 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage; hemopexin, Peptidase_M10; TM=M;SS=M; 11
 425071; NM_013989; Hs.154424; deiodinase, lodothyronine, type II; T4_deiodinase; TM=M;SS=Y; 10.93859649
 437938; AI950087; Hs.369628; gb-wq05c02x1 NCI_CGAP_Kid12 Homo sapien; none, none; 10.78084516
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none; TM=M;SS=Y; 10.74825175
 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_HUMAN DEATH; none, none; 10.542
 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC; none; 10.49638462
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none; TM=M;SS=Y; 10.48210736
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A recepto; Neur_chan_LBD, Neur_chan_membr; TM=Y;SS=M; 10.26714286
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran, SMC_N, SMC_C, DUF164; none; 10.142
 421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN, HIN; TM=M;SS=N; 10.1
 418641; BE243136; Hs.86947; a disintegrin and metalloproteinase doma; disintegrin, Reprolysin, Pep_M12B_propep, EGF; TM=Y;SS=M; 10.072
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB, DNA_topoisolV, HATPase_c; 9.996353636
 414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibitor; serpin; 9.986825397
 421506; BE307296; Hs.105097; thymidine kinase 1, soluble; TK; TM=M;SS=N; 9.888888889
 407786; AA687538; Hs.38972; tetraspan 1; transmembrane4; TM=Y;SS=M; 9.876056338
 424441; X14850; Hs.147097; H2A histone family, member X; histone, CBFD_NFYB_HMF; 9.851635514
 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec, zf-C4; none; 9.840720222
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kin; SAM_PNT; none; 9.823170732
 408000; L11690; Hs.198689; bullous pemphigoid antigen 1 (230/240kD); ehand, spectrin, GAS2, SH3, Plectin, RA_Xylose_isom, FED, bZIP, Tropomyosin, Myc-LZ, Mdh_C, CHAIP3; TM=M;SS=N; 9.812

- 409893; AW247090; Hs.57101; minichromosome maintenance deficient (S; MCM,aldo_ket_red;TM=M;SS=N; 9.787878788
- 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank;TM=M;SS=N; 9.637037037
- 425559; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgaris antigen; cadherin;TM=M;SS=M; 9.596
- 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevisiae; WD40;TM=M;SS=N; 9.558
- 444946; AW139205; Hs.155457; hypothetical protein FLJ22408; aldehyde dehydrogenase 2;TM=Y;SS=M; 9.55
- 421481; AW391972; Hs.104696; KIAA1324 protein; none;TM=M;SS=M; 9.529085873
- 408591; AF015224; Hs.46452; mamaglobin 1; Uteroglobulin;TM=M;SS=M; 9.506
- 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen;TM=M;SS=M; 9.477961433
- 444006; BE395085; Hs.334762; type I transmembrane protein Fn14; ldl_recept_a,PKD,MHC_J;TM=M;SS=Y; 9.415151515
- 413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8; 9.408
- 424364; AW383228; Hs.163834; ESTs, Weakly similar to G01763 atrophin; ras;TM=M;SS=N; 9.36
- 429002; AW248439; Hs.2340; junction plakoglobin; Armadillo_seg;TM=M;SS=N; 9.315693431
- 412379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8;TM=M;SS=Y; 9.31
- 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member; aldedh;TM=M;SS=M; 9.29
- 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member; aldedh; 9.264
- 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK;TM=M;SS=Y; 9.241561181
- 445033; AF652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 9.207272727
- 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;SS=N; 9.195167286
- 432223; AW238299; Hs.250618; UL16 binding protein 2; ldl_recept_a,PKD,MHC_J;TM=M;SS=Y; 9.108
- 428758; AA433988; Hs.98502; CA125 antigen; mucin 16; SEA;TM=Y;SS=N; 9.028
- 421777; BE562088; Hs.108196; HSPC037 protein; none;TM=M;SS=N; 9.004
- 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A receptor; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 9.001095491
- 418959; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M;SS=N; 8.942
- 455601; AL368680; Hs.816; SRY (sex determining region Y)-box 2; HMG_box; 8.87
- 429211; AF052693; Hs.198249; gap junction protein, beta 5 (connexin 3; connexin;TM=Y;SS=M; 8.77131783
- 456906; AF117646; Hs.156637; Cas-Br-M (murine) ectropic retroviral tr; zfc3HC4,Cbl_N2,Cbl_N3;TM=M;SS=N; 8.738
- 430397; AJ924533; Hs.105607; bicarbonate transporter related protein; HCO3_cotransp;TM=Y;SS=N; 8.736
- 417034; NM_006163; Hs.80962; neurotensin; none; 8.592
- 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl_2;TM=M;SS=N; 8.536
- 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fs, clone A; 7tm_3;none; 8.49
- 439295; AL133916; Hs.47860; hypothetical protein FLJ20093; ig,ptkinase,LRRLRRNT,LRRCIT;none; 8.460655738
- 409420; Z15008; Hs.54451; laminin, gamma 2 (nicotin (100kD), kalinin; laminin_B,laminin_EGF; 8.414
- 438746; AB85815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin,Guanylate_kin,PDZ,SH3; 8.376205788
- 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1;TM=Y;SS=M; 8.37
- 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 8.364
- 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPc_Y_phosphatase,Ribosomal_S3_N;TM=M;SS=N; 8.266
- 417771; AA804698; Hs.82547; retinoic acid receptor responder (lazarus; none;none; 8.248314607
- 431620; AA126109; Hs.264981; 2'-5'-oligoadenylate synthetase 2 (69-71; NTP_transf_2;TM=M;SS=N; 8.156
- 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha,arf;TM=M;SS=N; 8.142857143
- 448733; NM_005029; Hs.187958; solute carrier family 6 (neurotransmitter; SNF;TM=Y;SS=N; 8.137559809
- 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6,ET,PLA2_inh; 8.043478261
- 424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; DNA_ligase; 8.038194444
- 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase,DSPc;TM=M;SS=N; 8.024752475
- 453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1); none;TM=Y;SS=M; 8
- 424046; AF027866; Hs.138202; serine (or cysteine) proteinase inhibitor; serpin;TM=M;SS=N; 7.982
- 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 7.973684211
- 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fs, clone PL; HLH,death,TNFR_c6,Acyl-CoA_hydro; 7.892
- 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; IQ;TM=M;SS=N; 7.824
- 452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC_tran,ABC_membrane,SRP54,Thymidylate_kin;TM=Y;SS=M; 7.823874755
- 431630; NM_002044; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha; FG-GAP,Rhbd_glycop,Integrin_A;TM=Y;SS=M; 7.758985201
- 432874; W94322; Hs.279551; melanoma inhibitory activity; SH3;TM=M;SS=Y; 7.75887574
- 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoatE;TM=M;SS=N; 7.757751938
- 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig,Rhbd_glycop;TM=Y;SS=M; 7.624
- 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormona_rec,zf-C4;none; 7.605660377
- 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase;TM=M;SS=N; 7.578
- 430280; AA361256; Hs.237868; interleukin 7 receptor; fn3;none; 7.476
- 429299; AJ620463; Hs.347408; hypothetical protein MGC13102; none;TM=Y;SS=N; 7.442528736
- 441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3;none; 7.442495127
- 446163; A020680; Hs.25252; prolactin receptor; none;NA/NA; 7.436781609
- 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,trypsin,plant_thionins; 7.435897436
- 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like,ptkinase,Recep_L_domain,YLP;none; 7.398360656
- 432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 7.394039735
- 431890; X17033; Hs.271986; Integrin, alpha 2 (CD49B, alpha 2 subunit; vwa,Integrin_A,FG-GAP;TM=Y;SS=M; 7.383419689
- 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none;none; 7.382
- 436972; AA284679; Hs.25640; claudin 3; PMP22_Claudin;TM=Y;SS=M; 7.327160494
- 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;SS=N; 7.316
- 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT_bind,STAT_prot;TM=M;SS=N; 7.315412186
- 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,ptkinase;TM=M;SS=N; 7.2984375
- 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevisiae; CDC45;TM=M;SS=N; 7.28
- 451253; HA8299; Hs.26126; claudin 10; PMP22_Claudin,Peptidase_M1,K_tetra;TM=Y;SS=M; 7.256802721
- 416819; U77735; Hs.80205; pim-2 oncogene; pkinase; 7.234455959
- 421817; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 7.162534435
- 451035; AU076785; Hs.430; plasmin 1 (I isoform); ethand,CH,Adaplin_N; 7.145454546
- 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1;TM=Y;SS=M; 7.126
- 414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1;TM=Y;SS=M; 7.122413793
- 425003; AF119048; Hs.154149; apurinic/apyrimidinic endonuclease(APEX; Tropotin,Exo_endo_phos,IQ;TM=M;SS=N; 7.106719368
- 430890; X54232; Hs.2699; glypican 1; Glypican;TM=M;SS=M; 7.088937093
- 407792; AJ077715; Hs.39384; putative secreted ligand homologous to f; none;TM=M;SS=Y; 7.052
- 428514; BE616633; Hs.170195; bone morphogenetic protein 7 (osteogenic; TGF-beta,TGFb_propeptide; 7.042
- 431241; AA496799; Hs.36958; ESTs; SH2,RasGEF;none; 7.03
- 437139; W73685; Hs.118513; ESTs, Weakly similar to RTA RAT PROBABLE; 7tm_1;TM=Y;SS=M; 7.03
- 420311; AW445044; Hs.38207; Human DNA sequence from clone RP4-53015; none;none; 7.026
- 439979; AW600291; Hs.6823; hypothetical protein FLJ10430; none;TM=M;SS=N; 7.008

- 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr: SH3,PX;TM=M;SS=N; 6.991626794
 416250; AA581386; Hs.73452; Kremen 2; kringle, CUB, WSC;; 6.972
 430770; AA765694; Hs.123296; ESTs; none, none; 6.95
 5 418869; AW516565; ; gbxq01d05.x1 Soares_NHCEc_cervical_tumo; none, RasGAP, WW, IQ; 6.948
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily; 60s_ribosomal, Ribosomal_L10, TNFR_c6, DEAD;; 6.914
 418283; S79895; Hs.83942; cathepsin K (pseudosclerosis); Peptidase_C1; 6.876190476
 419667; AU077005; Hs.92208; a disintegrin and metalloproteinase domain; disintegrin, Reprolysin, Pep_M12B_propep; TM=M;SS=M; 6.862970711
 421143; AB024536; Hs.102171; immunoglobulin superfamily containing Ig; Ig_LRR, LRRNT, LRRCT; TM=M;SS=M; 6.849056604
 456181; L36463; Hs.1030; ras inhibitor; RA, SH2, VPS9; TM=M;SS=N; 6.762
 10 436856; AJ469355; Hs.127310; ESTs; pkinase, rrm; TM=M;SS=N; 6.721428571
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none; TM=Y;SS=M; 6.720348837
 439750; AL359053; Hs.57654; Homo sapiens mRNA full length insert cDN; IMPDH_C, IMPDH_N, CBS, integrin_B, Rdn_B, lectin; 6.717307692
 450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2; TM=Y;SS=M; 6.715240642
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg, UQ_con, none; 6.688194444
 15 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema, PSI, Integrin_B; TM=Y;SS=N; 6.670553936
 426385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2, SH3; 6.652921348
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM, PDZ, pkinase; 6.653713299
 425289; AW139342; Hs.155530; Interferon, gamma-inducible protein 16; PAAD_DAPIN, HIN; 6.652671756
 426500; NM_014638; Hs.170156; KIAA0450 gene product; C2, PI-PLC-Y; TM=M;SS=N; 6.639555172
 20 438113; AA67908; Hs.8882; ESTs; 7tm_1, none; 6.6
 444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog); act; PH, none; 6.6
 408482; NM_000676; Hs.45743; adenosine A2b receptor; 7tm_1; TM=Y;SS=M; 6.548148148
 410290; XA132307; Hs.322844; hypothetical protein DKFZp564A176; Sema, PSI, TIG, integrin_B; TM=Y;SS=M; 6.532763533
 25 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA; TM=Y;SS=N; 6.526951673
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glc; sugar_tr; TM=Y;SS=M; 6.512704174
 420039; NM_004605; Hs.376147; sulfotransferase family, cytosolic, 2B; ; Sulfotransfer; 6.496
 423031; AI278995; Hs.374579; ESTs; none, none; 6.447658402
 421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; Ion_trans, K_tetra, asp; 6.426666667
 30 433933; AJ754389; Hs.355397; Homo sapiens clone TCCIA00164 mRNA sequ; none; NA;NA; 6.4
 435094; AI560129; Hs.289008; EST; none, none; 6.312
 432106; N58323; Hs.269098; ESTs, Weakly similar to RETROVIRUS-RELAT; SH3, PDZ, Guanylate_kin, none; 6.276556777
 427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8, SHMT, MIF, GST_C, EF1G, domain, GST_N, S1, Fz, Fritzed, catrefuculin, 7tm_2, rrm, PAP_assoc; TM=Y;SS=M; 6.272727273
 35 435232; NM_001262; Hs.4854; cyclin-dependent kinase inhibitor 2C (p1; ank; TM=M;SS=N; 6.269720102
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 6.219081272
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-assoc; kinesin; TM=M;SS=N; 6.19
 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD, helicase_C, CARD; TM=M;SS=N; 6.188888889
 449230; BE613348; Hs.355392; melanoma cell adhesion molecule; ig_isodh, Ribosomal_L6, F-box; TM=Y;SS=M; 6.188046647
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-I; AAA, NB-ARC, PAAD_DAPIN; NA;NA; 6.15503876
 40 450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta, TGFb_propeptide; 6.152
 432314; AA533447; Hs.285173; ESTs; Xlink, none; 6.123040752
 418844; M62982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase, PLAT; TM=M;SS=N; 6.12
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (act; ig, pkinase; TM=Y;SS=M; 6.095758355
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial; mito_carr; TM=M;SS=N; 6.089164786
 45 452683; AJ089576; Hs.374574; progesterone membrane binding protein; homeobox, none; 6.06284153
 445637; AJ245671; Hs.12844; EGF-like domain, multiple 6; EGF, MAM; 6.05513308
 444309; U83236; Hs.10803; calcium and Integrin binding protein (DN; ethand; 6.04015544
 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD, helicase_C, rrm, Ndr, Cys_knot, TIL, vwa, vwc, vwd, IQ, Rila, abhydrolase, TGF-beta, DUF139, TPR, DSPc, lsp_1, Ribosomal_S21, rvp; TM=M;SS=N; 6.009562842
 50 438108; AJ471795; Hs.287776; vanilloid receptor-related osmotically a; ank, Ion_trans; TM=Y;SS=N; 6.004
 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none; TM=Y;SS=M; 5.984536083
 405484; ; C3002124; gij12737280; refXP_006682.2; lc; none; 5.978964401
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal_L37ae, pkinase, POLO_box, tRNA-synt_1b, dynam, dynamin_2, GED, bZIP, M; 5.978431373
 55 419216; AU076718; Hs.164021; small inducible cytokine subfamily B (Cy; IL8; 5.976
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese, DSPc_Y, phosphatase; TM=M;SS=N; 5.969387755
 411756; BE294350; Hs.71891; discoidin domain receptor family, member; pkinase_F5_F8_type_C; TM=Y;SS=M; 5.95184136
 424291; AL120051; Hs.144700; ephrin-B1; Ephrin; TM=Y;SS=M; 5.951550388
 453459; BE047032; Hs.257789; ESTs; none, none; 5.95
 56373; BE247706; Hs.86693; membrane-spanning 4-domains, subfamily A; none; TM=Y;SS=N; 5.938
 60 429359; W00482; Hs.2399; matrix metalloproteinase 14 (membrane-in; hemopexin, Peptidase_M10; TM=M;SS=M; 5.917857143
 414703; BE243877; Hs.380063; ATPase, Na? transporting, beta 3 polypep; Na_K-ATPase; TM=Y;SS=M; 5.910455487
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked mot; NUDIX; TM=M;SS=M; 5.901865793
 452239; AW379378; Hs.356289; protein tyrosine phosphatase, receptor t; none, none; 5.868362832
 418345; AJ001696; Hs.241407; serine (or cysteine) proteinase inhibitor; serpin; TM=Y;SS=M; 5.842
 65 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 11; Euk_porin; TM=M;SS=M; 5.816363636
 439625; AF086453; Hs.58611; ESTs; Fork_head, glycolytic_enzy, Na_sulph_symp; 5.811594203
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none, none; 5.81
 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR; TM=M;SS=N; 5.806
 415198; AW009480; Hs.943; natural killer cell transcript 4; none; TM=M;SS=N; 5.804137931
 70 431941; AK000106; Hs.272277; Homo sapiens cDNA FLJ20099 fs, clone CO; pkinase, Furin-like, Recep_L_domain, none; 5.8
 457001; J03258; Hs.2062; vitamin D (1,25-dihydroxyvitamin D3) re; hormone_rec, zf-C4, Metallothio_5; TM=M;SS=N; 5.794
 439335; AA742697; Hs.62492; NM_052863; Homo sapiens secretogloblin, fa; none; 5.778568808
 439248; AA498072; Hs.351474; membrane-associated tyrosine- and threon; ank, pkinase, UPF0073; 5.763492064
 452461; N78223; Hs.108108; transcription factor; zf-C3HC4, ubiquitin, PHD, YDG_SRA; TM=M;SS=N; 5.728
 75 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS; 5.714634146
 424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 fs, clone MA; SH2, STAT, STAT_bind, STAT_prol, none; 5.701666667
 419055; M89957; Hs.89575; CD79B antigen (immunoglobulin-associated; ig, ITAM; TM=Y;SS=M; 5.692
 432269; NM_002447; Hs.2942; macrophage stimulating 1 receptor (c-met; pkinase, Sema, PSI, TIG, A4_EXTRA; TM=M;SS=M; 5.686
 452698; AJ826645; Hs.211534; ESTs; ArfGap, PH, ank, Guanylate_kin, PDZ, SH3; 5.683673469
 80 411030; BE387193; Hs.67896; 7-60 protein; none; TM=M;SS=N; 5.676767677
 447131; NM_004585; Hs.17466; retinoic acid receptor responder (lazarar; none; TM=Y;SS=N; 5.672977625
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1; TM=Y;SS=M; 5.666
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; pkb; TM=M;SS=N; 5.655616943

- 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase; TM=M; SS=N; 5.6485623
 415010; NM_004203; Hs.77783; membrane-associated tyrosine- and threon; ank.pkinase; UPF0073; 5.648
 452690; A1536070; Hs.15085; ESTs; pou,homeobox,lig_chan_ANF_receptor; 5.646
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2,SH3.pkinase; TM=M; SS=N; 5.642405063
 5 418703; NM_014448; Hs.87435; Rho guanine exchange factor (GEF) 16; SH3,PH,RhoGEF,Bima_VP3; TM=M; SS=N; 5.636
 426108; AA622037; Hs.166468; programmed cell death 5; DUF122; TM=M; SS=N; 5.635087719
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank.pkinase; TM=M; SS=N; 5.620930233
 432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catal; Metallophos; TM=M; SS=N; 5.608352145
 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related ; SH2,SH3.pkinase; TM=M; SS=N; 5.596052632
 10 430696; AA531276; Hs.59509; ESTs; pkinase,PP2C; none; 5.575112108
 435017; AA336522; Hs.12854; angiotensin II, type I receptor-associat; none; TM=Y; SS=M; 5.556910569
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrola; PAF-AH_Ib,Lipase_GDSL; TM=M; SS=N; 5.556195965
 415012; NM_004383; Hs.77793; c-src tyrosine kinase; SH2,SH3.pkinase; TM=M; SS=N; 5.555421687
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese; 5.549751244
 15 413969; X14034; Hs.75648; phosphodiase C, gamma 2 (phosphodiylin; SH2,SH3,C2,PH,PI-PLC-Y,PI-PLC-X,PDGF; 5.541366907
 406621; X57809; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA; TM=M; SS=N; 5.54076087
 417700; M36542; Hs.1101; POU domain, class 2, transcription factor; homeobox,pou; TM=M; SS=N; 5.536
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none; TM=M; SS=N; 5.52661597
 436576; A458213; Hs.77542; ESTs; 7tm_1,DnaI; 5.52638191
 20 425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind.pkinase_C,OPR; TM=M; SS=N; 5.519672131
 412276; BE286261; Hs.73798; macrophage migration inhibitory factor (MIF,sugar_tr; none; 5.516453382
 417433; BE270266; Hs.82128; ST4 oncofetal trophoblast glycoprotein; LRR,LRRNT,LRRCT; TM=Y; SS=M; 5.514964789
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor t; fn3,Ig_Y_phosphatase,MAM; TM=Y; SS=M; 5.494202899
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane; TM=Y; SS=M; 5.471947195
 25 410608; A1538438; Hs.159087; ESTs; ubiquitin,Integrin_B,UBA; none; 5.465384615
 448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin; TM=M; SS=N; 5.460076046
 408716; A1567839; Hs.151714; Homo sapiens mRNA for KIAA1769 protein; ; UvrD-helicase,RNB,Run1; TM=M; SS=N; 5.450413223
 426410; BE288446; Hs.305890; BCL2-like 1; Bcl-2,BH4; none; 5.444806195
 457819; AA057484; Hs.35406; FLJ20522 Hypothetical protein FLJ20522; none; none; 5.444281525
 30 422597; BE245809; Hs.118634; ATP-binding cassette, sub-family B (MDR); ABC_tran,ABC_membrane,PRK; TM=Y; SS=N; 5.437931035
 429191; AF065215; Hs.198161; phosphodiase A2, group IVB (cytosolic); C2,PLA2_B_jmI; TM=M; SS=N; 5.4375
 448961; AW265634; Hs.133100; ESTs; pkinase,Furin-like,Recep_L_domain; none; 5.435211268
 409012; AL117435; Hs.49725; DKFZP434I216 protein; PH,RhoGEF; TM=M; SS=M; 5.433333333
 35 443466; BE243123; Hs.321045; IKK-related kinase epsilon; Inducible Ik; pkinase,RIO1; TM=M; SS=N; 5.429657795
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C; none; 5.423322684
 423189; M59371; Hs.171596; EphA2; fn3.pkinase,SAM,EPH_Ibd; TM=Y; SS=M; 5.421621622
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisi; pkinase; TM=M; SS=N; 5.412
 432527; AW975028; Hs.102754; ESTs; none; none; 5.40625
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2; TM=Y; SS=M; 5.405504587
 400024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3; TM=M; SS=N; 5.396
 434467; BE652368; Hs.231853; Homo sapiens cDNA FLJ13445 fis, clone PL; 7tm_1; none; 5.391472868
 438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ; 5.389250814
 439670; AF088076; Hs.59507; ESTs, Weakly similar to AC004858 3 U1 sm; none; none; 5.382
 437016; AF076916; Hs.5398; guanine monophosphate synthetase; PHD,SET,zf-
 45 CXXC,EGF,ank,notch,WW,FCH,GATase,GMP_synth_C,Oodudin,YEATS,metal1ho,EB,heme_1,ROCC1,ZZ,FeThRed_A,ENTH,Band_41,HECT; TM=M; SS=N; 5.373937677
 424848; A1263231; Hs.327090; EST; SH3,PDZ,Guanylate_kin; none; 5.36
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phos; MORN,sugar_tr; TM=Y; SS=M; 5.359711223
 405532; ; C15000305.gi3805122[gb]AAC69198.1 [AF0]; ras; TM=M; SS=N; 5.349226804
 50 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated; ig,ITAM,Zn_clus; TM=Y; SS=M; 5.346153846
 453143; AA382234; Hs.356289; protein tyrosine phosphatase, receptor t; serpin; 5.333667335
 423973; AF038461; Hs.136574; arachidonate 12-lipoxygenase, 12R type; lipoxygenase,PLAT; TM=M; SS=N; 5.33
 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0462; none; none; 5.328
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig; TM=Y; SS=M; 5.318
 55 427337; Z48223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; ig; TM=Y; SS=M; 5.309638554
 410165; BE560228; Hs.71869; apoptosis-associated speck-like protein; PAAD_DAPIN,CARD; TM=M; SS=N; 5.293560606
 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-t; fn3_Y_phosphatase,carb_anhydrase; TM=Y; SS=M; 5.28
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none,spectrin,SH3,PH,CH; 5.278947368
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC; TM=Y; SS=N; 5.274746193
 60 416207; NM_014745; Hs.79077; Homo sapiens, clone MGC-2908, mRNA, comp; none; TM=Y; SS=M; 5.272222222
 415117; AF120499; Hs.78016; polynucleotide kinase 3'-phosphatase; Viral_helicase1; TM=M; SS=N; 5.27
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3,RhoGAP,FCH; TM=M; SS=N; 5.251865672
 409430; R21945; Hs.348735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese; none; 5.248
 431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4; TM=Y; SS=M; 5.232
 65 422017; NM_003877; Hs.110776; STAT induced STAT inhibitor-2; SH2; 5.212418301
 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none; 5.209259259
 421502; AF111856; Hs.105039; solute carrier family 34 (sodium phosphat; Ribosomal_L20,Na_PL_cotrans; TM=Y; SS=N; 5.202
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 14; Exo_endo_phos,SH2; TM=M; SS=N; 5.19979716
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (f; ABC_tran,GTP_EFTU,ABC_membrane; none; 5.199074074
 70 416602; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; EGF,vwc,TSPN; 5.198224852
 429556; AW139399; Hs.314807; ESTs; none; TM=M; SS=N; 5.192439853
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; myosin_head,IQ,zf-MYND; TM=M; SS=M; 5.190251572
 400517; ; tengsin; none; TM=M; SS=N; 5.18
 413436; AF238083; Hs.68061; sphingosine kinase 1; DAGIC; TM=M; SS=N; 5.172881356
 75 423527; A1206955; Hs.105861; hypothetical protein FLJ13824; none; TM=M; SS=N; 5.165060241
 419130; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ion_trans,SPRY,RYDR_ITPR,RyR,MIR; TM=Y; SS=N; 5.156976744
 437809; AL137723; Hs.58555; Homo sapiens mRNA; cDNA DKFZp434D0818 (f; none; none; 5.154676259
 452089; AB028949; Hs.183994; KIAA1026 protein; Metallophos; TM=M; SS=N; 5.152360515
 409340; BE174629; Hs.321130; hypothetical protein MGC2771;
 80 aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BclA,RUN; TM=M; SS=N; 5.144859813
 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequ; K_latra,DUF51; none; 5.142
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3,PH,WW,RhoGAP; 5.141534392
 434808; AF155108; Hs.256150; NY-REN-41 antigen; none; TM=M; SS=N; 5.14
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome; TM=M; SS=N; 5.13968254

- 431685; AW296135; Hs.267659; var 3 oncogene; CH1,DAG_PE-bind,PH,RhoGEF,SH2,SH3,DC1;TM=M;SS=N; 5.129476584
- 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase,pkinase_C,HR1;TM=M;SS=N; 5.121527778
- 433573; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G-type rec; 7tm_2EGF,cadherin,EGF,laminin_G,Trypan_glycop,GPS,HRM;TM=Y;SS=M; 5.107438017
- 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras,ABC_tran,ar;TM=M;SS=M; 5.10251046
- 5 419493; AF001212; Hs.90744; proteasome (prosome, macropain) 26S subu; CDK5_activator,PCI,none; 5.095194085
- 411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor; ; inositol_P,lg;TM=M;SS=N; 5.092
- 435243; AW292886; Hs.348932; hypothetical protein dJ434014.3; IRF,none; 5.092
- 434417; AL110157; Hs.3843; Homo sapiens mRNA; cDNA DKFZp586F2224 (f, DSPc,none; 5.091922006
- 10 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3,TPR;TM=M;SS=N; 5.088932806
- 418629; BE247560; Hs.86859; growth factor receptor-bound protein 7; SH2,PH,RA; 5.032840237
- 420030; BE503994; Hs.146233; KIAA0418 gene product; SH3,none; 5.080645161
- 444065; AW449415; Hs.10260; Homo sapiens cDNA FLJ11341 fis, clone PL; SH3; 5.063953488
- 421677; H64092; Hs.38282; ESTs; A1pp,Armadillo_seg,IBB; 5.056
- 15 411165; NM_000169; Hs.69089; galactosylase, alpha; Melibiase; 5.054133858
- 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 5.054
- 423883; AF250238; Hs.134514; ATP-binding cassette, sub-family A (ABC1; ABC_tran,photoRC,SRP54,Ca_channel_B,Pterin_4a;TM=Y;SS=M; 5.051724138
- 421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3_P4_kinase,PI3Ka;TM=M;SS=N; 5.051282051
- 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,fn3,Y_phosphatase;TM=M;SS=N; 5.047311828
- 20 410026; A912061; Hs.55016; hypothetical protein FLJ21935; none,none; 5.04674221
- 426395; BE151985; Hs.355669; hypothetical protein FLJ23316; pkinase,none; 5.040298508
- 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 5.039039039
- 444895; A674383; Hs.22891; solute carrier family 7 (cationic amino; ASC,death,TNFR_c6; 5.037151703
- 413472; BE242870; Hs.75379; solute carrier family 1 (glial high aff; SDF;TM=Y;SS=M; 5.034
- 25 445272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3,HS1_rep;TM=M;SS=N; 5.03030303
- 410772; BE275297; Hs.194685; Homo sapiens clone 24675 mRNA sequence; Topoisom_bac,Toprim; 5.027985075
- 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase; pkinase,CNH;TM=M;SS=N; 5.014652015
- 415166; NM_003652; Hs.78068; carboxypeptidase Z; Zn_carbOpept,Dioxygenase,Fz; 5.012269939
- 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans;TM=Y;SS=M; 5.001811594
- 30 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase; 4.997983871
- 430024; A1808780; Hs.227730; Integrin, alpha 6; integrin_A,FG-GAP;TM=Y;SS=M; 4.994871795
- 409220; BE243323; Hs.51233; tumor necrosis factor receptor superfam; TNFR_c6,death,Lipoprotein_5,TIL;TM=Y;SS=M; 4.987135506
- 423804; AW403448; Hs.1706; Interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;SS=N; 4.985185185
- 423011; NM_000683; Hs.123022; adrenergic, alpha-2C-, receptor, 7tm_1;TM=Y;SS=M; 4.984
- 35 419577; L36531; Hs.91296; integrin, alpha 8; Integrin_A,FG-GAP;TM=Y;SS=N; 4.968
- 402328; ; Target Exon; pkinase;TM=M;SS=N; 4.96728972
- 421242; AW161386; Hs.13561; hypothetical protein MGC4692; none;NA;NA; 4.966334165
- 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 4.964491363
- 414203; BE262170; Hs.78629; ATPase, Na? transporting, beta 1 polypep; none,none; 4.961956522
- 40 409592; R27430; Hs.271565; ESTs; none,Neur_chan_LBD,Neur_chan_memb; 4.946
- 451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M;SS=N; 4.943181818
- 453449; W16752; Hs.32981; sema domain, immunoglobulin domain (Ig); ig,Sema,PSI; 4.930508475
- 425233; Z17861; Hs.155218; E1B-55kDa-associated protein 5; SPRY,SAP,pkinase,fn3,lg; 4.925347222
- 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin,Peptidase_M10; 4.92
- 422282; AF019225; Hs.114309; apolipoprotein L; MotA_ExcB;TM=Y;SS=M; 4.912181303
- 45 442572; A1001922; Hs.135121; hypothetical protein FLJ22415; none,HSP70; 4.910224439
- 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.909972289
- 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 4.904
- 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M;SS=N; 4.897338403
- 411770; NM_014278; Hs.71992; heat shock protein (hsp110 family); HSP70;TM=M;SS=N; 4.894
- 50 446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein c; 7tm_1;TM=Y;SS=M; 4.886
- 423198; M81933; Hs.1634; cell division cycle 25A; Rhodanes;none; 4.884
- 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none; 4.876379691
- 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevi; NusG; 4.876117497
- 427792; M63928; Hs.180841; tumor necrosis factor receptor superfam; SRP14,TNFR_c6; 4.873684211
- 55 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,Ig,Neuregulin;TM=M;SS=N; 4.872641509
- 421541; NM_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, poly; pkinase,pkinase_C;TM=M;SS=N; 4.869318182
- 429619; AL120751; Hs.211568; eukaryotic translation initiation factor; none,none; 4.868073879
- 458873; AW150717; Hs.345728; STAT induced STAT inhibitor 3; none,none; 4.861538462
- 437669; A1358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA; none,pkinase,pkinase_C; 4.854651163
- 60 405545; ; Target Exon; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 4.85
- 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 4.848387097
- 424263; M77640; Hs.1757; L1 cell adhesion molecule (hydrocephalus; fn3,lg,IRK;TM=Y;SS=M; 4.846153846
- 425421; L11669; Hs.157145; tetracycline transporter-like protein; sugar_tr;TM=Y;SS=M; 4.843694494
- 421267; BE314724; Hs.103081; ribosomal protein S6 kinase, 70kD, poly; pkinase,pkinase_C;TM=M;SS=N; 4.842532468
- 65 418736; T18979; Hs.87908; Snf2-related CBP activator protein; helicase_C,AT_hook,SNF2_N;TM=M;SS=N; 4.842
- 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2,none; 4.841071429
- 417331; AW411297; Hs.81972; SHC (Src homology 2 domain-containing) t; SH2,PID,zf-C2H2,SCAN,AMP-binding,KRAB;TM=M;SS=N; 4.839464883
- 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none,SDF,sugar_tr; 4.837837838
- 434521; NM_002267; Hs.3888; karyopherin alpha 3 (importin alpha 4); Armadillo_seg,IBB;TM=M;SS=N; 4.833333333
- 70 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;SS=N; 4.821666667
- 453082; H18835; Hs.31603; hypothetical protein FLJ20041; ion_trans;TM=Y;SS=M; 4.820936639
- 417949; AL049795; Hs.83004; interleukin 14; none,Armadillo_seg,IBB,WD40; 4.81443299
- 439569; AW602166; Hs.222399; CEGP1 protein; EGF,TNFR_c6,granulin,CUB,Keratin_B2,TIL;TM=M;SS=M; 4.81
- 75 432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C;TM=M;SS=N; 4.805063291
- 432194; AL040801; Hs.273219; breast cancer anti-estrogen resistance 1; SH3; 4.803191489
- 431472; AK001023; Hs.256549; nucleotide binding protein 2 (E.coli Min; fer4_NiifH,ParaAPS_kinase,AraA_ATPase;TM=M;SS=N; 4.800930099
- 450690; AA296696; Hs.333418; FYD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 4.795480881
- 448950; AF288687; Hs.9275; CG1-152 protein; E1-E2_ATPase,Hydrolase;TM=Y;SS=N; 4.776923077
- 427681; AB018263; Hs.284232; tumor necrosis factor receptor superfam; death,TNFR_c6,PH,Xlink,RhoGEF,Metallothio_5;TM=M;SS=M; 4.772196262
- 80 432827; Z68128; Hs.3109; Rho GTPase activating protein 4; FCH,RhoGAP,SH3;TM=M;SS=N; 4.760115607
- 433376; A1249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20; 4.751162791
- 419981; AA897581; Hs.128773; ESTs; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 4.748
- 431657; A1345227; Hs.105448; ESTs, Weakly similar to B34087 hypothet; pkinase,PA28_alpha,PA28_beta,Cu_amine_oxid,Cu_amine_oxidN2,Cu_amine_oxidN3; 4.746

- 412958; BE391579; Hs.75087; Fas-activated serine/threonine kinase; none; 4.736781609
- 414443; AU077268; Hs.76144; platelet-derived growth factor receptor; ig; pkinase; TM=Y; SS=N; 4.733
- 419250; AW770185; Hs.356066; U5 snRNP-specific protein, 116 kD; 7tm_1,BAH,zf-CXXC,DNA_methylase; 4.725454546
- 417903; NM_002342; Hs.1116; lympholaxin beta receptor (TNFR superfam; TNFR_c6; TM=M; SS=M; 4.718858132
- 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK_CoaE; 4.718836565
- 426059; BE292842; Hs.166120; interferon regulatory factor 7; IRF; 4.718543046
- 414788; X78342; Hs.77313; cyclin-dependent kinase (CDC2-like) 10; pkinase; TM=M; SS=N; 4.708
- 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC; TM=Y; SS=M; 4.707920792
- 448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase; DCX; TM=M; SS=N; 4.707671958
- 407143; C14076; Hs.332329; EST; none; TM=Y; SS=M; 4.682675815
- 428582; BE336699; Hs.185055; BENE protein; none; TM=Y; SS=M; 4.681818182
- 408806; AW847814; Hs.75608; Homo sapiens cDNA: FLJ21532 fis, clone C; SH3,PDZ,Guanylate_kin,none; 4.680440771
- 448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec; MP; TM=M; SS=M; 4.679841897
- 418836; AI655499; Hs.161712; ESTs; pkinase; Activin_rec; PDZ,ZU5,death; 4.679180887
- 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; ig,kringle,pkinase,Fz; TM=Y; SS=M; 4.675342466
- 414665; AA160873; Hs.356307; serum amyloid A1; zf-C2H2,BTB,K_tetra,none; 4.67447496
- 449843; R85337; Hs.24030; solute carrier family 31 (copper transpor; none; TM=Y; SS=M; 4.673701299
- 428245; AF151048; Hs.183180; anaphase promoting complex subunit 11 (y; none; 4.656756757
- 417088; MS4915; Hs.81170; pim-1 oncogene; pkinase; TM=M; SS=N; 4.656190476
- 420340; NM_000734; Hs.97087; CD32 antigen, zeta polypeptide (IT13 com; ITAM; TM=M; SS=M; 4.65
- 425966; NM_001761; Hs.1973; cyclin F; cyclin,F-box,cyclin_C; TM=M; SS=N; 4.644
- 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain; ig,abhydrolase; 4.640384615
- 430603; AA148164; Hs.247280; HBV associated factor; zf-C3HC4,zf-RanBP,pkinase; 4.630653266
- 419273; BE271180; Hs.293490; ESTs, Weakly similar to I38022 hypothet; none,none; 4.628
- 453380; AI803166; Hs.135121; ESTs, Weakly similar to I38022 hypothet; HSP70,none; 4.619047619
- 459399; BE407712; Hs.153998; creatine kinase, mitochondrial 1 (ubiqu; none,none; 4.618577075
- 412970; AB026438; Hs.177534; dual specificity phosphatase 10; Rhodanese,DSPc; 4.616
- 433577; AW007080; Hs.284192; ESTs; none,none; 4.614
- 444838; AV651680; Hs.208558; ESTs; integrin_A,FG-GAP,none; 4.612149533
- 408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+pep; PTR2; TM=Y; SS=N; 4.602
- 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate_kin; 4.596875
- 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22_Claudin,none; 4.587931035
- 433083; AL042759; Hs.191762; ESTs; SH3,PX; TM=M; SS=N; 4.586
- 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor; ; ig; TM=Y; SS=M; 4.58557047
- 412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C; MARCKS; 4.579087049
- 422009; AJ742845; Hs.110713; DEK oncogene (DNA binding); SAP; 4.576347305
- 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none,lectin_c; 4.57312253
- 414561; AI064813; Hs.195155; Homo sapiens amino acid transport system; Aa_trans; TM=Y; SS=N; 4.573015873
- 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Foscclin,ABC_tran,ABC_membrane,GTP_EFTU; TM=M; SS=M; 4.570526316
- 459053; AI807052; Hs.97792; ESTs; none,7tm_2,GPS; 4.569230769
- 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys,ig,FAD_Synth,ldh,ldh_C,pkinase; 4.566195373
- 439975; AB323081; Hs.6817; inosine triphosphatase (nucleoside triph; Ham1p_like; TM=M; SS=N; 4.56056338
- 416178; AB08527; Hs.192822; serologically defined breast cancer ant; none; TM=M; SS=N; 4.558
- 408051; AI623351; Hs.172148; ESTs; PH,RhoGAP,none; 4.552307692
- 421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; ethand,ldl_recept_a; 4.547761194
- 439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein; 7tm_1,LRR; TM=Y; SS=N; 4.547169811
- 426201; AW182814; Hs.128499; ESTs; SH3,none; 4.541666667
- 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; SS=N; 4.536
- 445229; BE276013; Hs.343828; Homo sapiens mRNA for FLJ00086 protein; ; G-alpha; TM=M; SS=N; 4.530588235
- 413109; AW389845; Hs.110855; ESTs; PHO4,none; 4.529761905
- 426125; X87241; Hs.166994; FAT tumor suppressor (Drosophila) homolog; EGF_catherin,laminin_G; TM=Y; SS=M; 4.529710145
- 402330; ; Target Exon; pkinase,none; 4.528070175
- 439238; I47305; Hs.302161; EDG-8 (endothelial differentiation, sph; 7tm_1; TM=Y; SS=M; 4.524
- 433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE_p10,ICE_p20; 4.523715415
- 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenas; CBS,IMPDH_C,IMPDH_N,NPD; TM=M; SS=N; 4.522900763
- 431429; AF072813; Hs.252831; reticulon 3; Reticulon,Fz,ig,kringle,pkinase; TM=Y; SS=N; 4.512
- 424078; AB006625; Hs.139033; paternally expressed 3; zf-C2H2,KRAB,none; 4.512
- 420602; AF060877; Hs.99236; regulator of G-protein signalling 20; RGS; TM=M; SS=N; 4.51
- 449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm_1; TM=Y; SS=M; 4.506
- 408157; AA047685; Hs.62946; ESTs; none,pkinase; 4.504
- 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT; TM=M; SS=Y; 4.50215208
- 431326; AW970580; Hs.198689; KIAA0728 protein; none,none; 4.501
- 428072; BE258602; Hs.182366; heat shock protein 75; HATPase_c,HSP90; TM=M; SS=N; 4.48828125
- 415149; X12451; Hs.78056; cathepsin L; Peptidase_C1; 4.484375
- 421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypept; p450; TM=Y; SS=M; 4.48
- 445143; U29171; Hs.378918; casein kinase 1, delta; zf-C3HC4,Filamin,zf-B_box,NHL,pkinase,zf-MZ; TM=M; SS=N; 4.478092784
- 421071; AJ311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen; none; TM=Y; SS=M; 4.477337111
- 410590; BE615216; Hs.64745; chloride intracellular channel 3; none; TM=M; SS=N; 4.476
- 438774; AA431620; Hs.379034; hypothetical protein MGC2745; none,none; 4.474874372
- 410726; AI623859; Hs.15936; ESTs; pkinase,pro_isomerase,none; 4.47
- 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory su; CDK5_activator,none; 4.468
- 426485; NM_006207; Hs.170040; platelet-derived growth factor receptor; ig; 4.464944649
- 433646; AA603319; Hs.155195; ESTs; pou,homeobox,lg_chan,ANF_receptor; 4.458
- 410293; AK000047; Hs.61960; hypothetical protein; K_tetra; TM=M; SS=N; 4.453020134
- 453464; AI884911; Hs.32989; receptor (calcitonin) activity modifying; none; TM=Y; SS=N; 4.448198198
- 410583; AW770280; Hs.36258; ESTs, Moderately similar to JCS238 galac; SH3,PDZ,Guanylate_kin,none; 4.446927374
- 441455; AJ271671; Hs.7854; zincron regulated transporter-like; Zip; TM=Y; SS=M; 4.445010183
- 453064; BE40334; Hs.89463; potassium large conductance calcium-act; none,none; 4.436480187
- 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase,ICE_p10,ICE_p20; TM=M; SS=M; 4.433411215
- 411825; AK000334; Hs.352415; solute carrier family 39 (zinc transport; SNF,Zip; TM=Y; SS=N; 4.432765152
- 428376; AF119565; Hs.184011; pyrophosphatase (inorganic); Pyrophosphatase; TM=M; SS=N; 4.428571429
- 429592; AB029041; Hs.209646; KIAA1118 protein; Tropoin,Exo_endo_phos,IQ; TM=M; SS=N; 4.428
- 419344; U94905; Hs.277445; diacylglycerol kinase, zeta (104kD); ank,DAGKa,DAGKc,DAG_FE-bind; TM=M; SS=N; 4.426229508

- 427138; N77624; Hs.173717; phosphatidic acid phosphatase type 2B; PAP2; none; 4.4234375
 414496; W73853; Hs.355424; ESTs; pkinase.F5_F8_type_C.adh_short; none; 4.42114094
 429432; A1678059; Hs.202676; synaptonemal complex protein 2; none; TM=M;SS=N; 4.42
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone; TM=M;SS=N; 4.419207317
 446700; AW206257; Hs.156326; Human DNA sequence from clone RP11-145L2; none; TM=M;SS=N; 4.418181818
 435411; AW444619; Hs.138211; ESTs; none; pkinase; 4.414
 414581; AA256213; Hs.72010; ESTs; none; Cam_acyltransf.Choline_kinase.SCO1-SenC.Glycos_transf_3.Glycos_trans_3N; 4.41
 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domain; death.DED; 4.408523909
 442259; A1690269; Hs.201345; ESTs; Acetyltransf.RhoGAP.FCH.SH3.Kelch.fn3; 4.406
 415860; D56051; Hs.78888; diazepam binding inhibitor (GABA receptor; ACBP; TM=M;SS=N; 4.404678363
 434419; AL040506; Hs.296938; dual specificity phosphatase 7; DSPc; TM=M;SS=N; 4.404
 404440; ; NM_021048; Homo sapiens melanoma antigen; MAGE; TM=M;SS=N; 4.4
 435542; AA887376; Hs.351226; ESTs; SH3.ig.pkinase.PH.spectrin.RhoGEF; none; 4.394
 413367; NM_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar_tr; TM=Y;SS=N; 4.39028777
 435732; AF229178; Hs.123138; leucine rich repeat and death domain con; none; none; 4.38490566
 427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone L: 7tm_1; none; 4.382129278
 425749; AW328587; Hs.159448; surfactant 2; none; 4.382
 41874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase; TM=Y;SS=N; 4.381422925
 414808; D14694; Hs.77329; phosphatidylserine synthase 1; PSS; TM=Y;SS=M; 4.380681818
 431837; T79326; Hs.331967; olfactory receptor, family 2, subfamily 1; none; 7tm_3.sushi.ANF_receptor; 4.376
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypept; Sm.pkinase; 4.370247934
 434876; AF160477; Hs.61450; Ig superfamily receptor LNIR; ig.Rhbd_glycop; TM=Y;SS=M; 4.37
 430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion_trans; TM=Y;SS=M; 4.367777777
 403912; ; C5000394; gi|12737280|ref|XP_006682.2|; none; TM=M;SS=N; 4.367684478
 426268; AF083420; Hs.168913; serine/threonine kinase 24 (Sta20, yeast; pkinase; 4.366348449
 434263; N34895; Hs.79187; ESTs; ig; none; 4.358527132
 404760; ; Target Exon; cadherin; TM=M;SS=M; 4.356
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase; TM=M;SS=N; 4.35472973
 420757; X78592; Hs.99915; androgen receptor (dihydrotestosterone r; hormone_rec.zf-C4.Androgen_recep; TM=M;SS=N; 4.354
 426812; AF105365; Hs.172613; solute carrier family 12 (potassium/chlor; none; TM=Y;SS=N; 4.353244838
 431674; AA089901; Hs.301642; G-protein coupled receptor; none; GCV_H; 4.35
 431886; L77964; Hs.271980; mitogen-activated protein kinase 6; pkinase; TM=M;SS=N; 4.347893916
 447719; BE387402; Hs.19333; hypothetical protein FLJ10349; adenylatekinase.ATP-bind; TM=M;SS=N; 4.346007605
 424837; BE276113; Hs.333034; N-acetyltransferase, homolog of S. cerev; Acetyltransf; TM=M;SS=N; 4.344
 449437; A1702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone K; none; none; 4.334722222
 411768; NM_013371; Hs.71979; interleukin 19; IL10; 4.322
 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase_2; TM=M;SS=N; 4.320359281
 425964; AW889928; Hs.9071; progesterone membrane binding protein; homeobox; none; 4.318867925
 450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; rrm; TM=M;SS=N; 4.316573557
 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase; 4.316
 400290; H18836; Hs.31608; hypothetical protein FLJ20041; none; Cys_knot; 4.314728582
 438899; AF085833; Hs.135624; ESTs; none; P13_P14_kinase.P13Ka.P13K_C2.P13K_rbd.P13K_p85B; 4.314084507
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos; TM=M;SS=M; 4.312121212
 419607; R52557; Hs.91579; Homo sapiens clone Z3783 mRNA sequence; IMP4; TM=M;SS=N; 4.304407714
 421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo_seg.HEAT; TM=M;SS=N; 4.304
 430017; AA263172; Hs.35; protein tyrosine phosphatase, non-recept; Y_phosphatase; TM=M;SS=M; 4.302
 447224; BE617125; Hs.142076; gb:501441664F1 NIH_MGC_65 Homo sapiens c; none; NA; NA; 4.302
 425424; NM_004954; Hs.157199; ELKL motif kinase; pkinase.UBA.KA1; TM=M;SS=N; 4.301639344
 454042; H22570; Hs.47860; hypothetical protein FLJ20093; ig.pkinase.LRR.LRRNT.LRRCT; none; 4.30141844
 446143; BE245342; Hs.306079; sec51 homolog; NUDDX.secY.E1 dehydrog.transket_pyr; TM=Y;SS=M; 4.300872093
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2_HUMAN ALU S; none; rrm; 4.292620865
 432562; BE531048; Hs.278422; DKFZP586G1122 protein; zf-C2H2; TM=M;SS=N; 4.290258449
 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none; TM=M;SS=M; 4.288405797
 421921; H83363; Hs.355993; translocase of inner mitochondrial membr; zf-Tim10_DOP.ethand.CH.spectrin.serpin; TM=M;SS=N; 4.284
 448564; AL044962; Hs.21453; inositol 1,4,5-bisphosphate 3-kinase C; IPK; 4.28057554
 453941; U99817; Hs.36820; Bloom syndrome; DEAD.helicase_C.HRDC; TM=M;SS=N; 4.28
 437712; X04588; Hs.85844; neurotrophic tyrosine kinase, receptor, ; Tropomyosin.pkinase.LRR.LRRCT.Hydantolnase_B.Hydantolnase_A; TM=M;SS=N; 4.277477478
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF.laminin_Nterm.Integrin_B; 4.276162791
 450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyros; none; none; 4.273927393
 438012; AA393254; Hs.43619; ESTs; Armadillo_seg; none; 4.273134328
 409619; AK001015; Hs.55220; BCL2-associated athanogene 2; BAG; TM=M;SS=N; 4.273109244
 418529; AW005695; Hs.250897; TRK-fused gene; Band_41.ERM.pkinase.LRR.LRRCT.MAM.Nucleoplasmn.Tropomyosin.OPR.filament.lZIP.G-gamma.M.OUF164; TM=M;SS=N; 4.272123894
 415214; A1445236; Hs.125124; EphB2; fn3.pkinase.SAM.EPH_fbd; TM=Y;SS=M; 4.268
 438233; W52448; Hs.56147; ESTs; Neur_chan_LBD.Neur_chan_memb.MAGE; 4.26284585
 429019; AA443280; Hs.279907; myosin IIIA; myosin_head.pkinase.PRK.IQ; TM=M;SS=N; 4.262
 424959; NM_005781; Hs.153937; activated p21cdc42hs kinase; ldn.lhn_C.SH3.pkinase.UBA; TM=M;SS=N; 4.258695652
 453655; AW990427; Hs.342874; transforming growth factor, beta receptor; zona_pellucida; none; 4.257208766
 417414; AA434589; Hs.367676; dUTP pyrophosphatase; dUTPase.KRAB; 4.251785714
 453905; NM_002314; Hs.36566; LIM domain kinase 1; pkinase.LIM.PDZ.zf-PARP; TM=M;SS=N; 4.249116608
 424232; AB015982; Hs.143460; protein kinase C, nu; pkinase.DAG_PE-bind.PH; TM=M;SS=N; 4.247692308
 404883; ; ENSP00000216009; Sodium-glucose cotranspo; SSF; TM=Y;SS=M; 4.242424242
 412507; L36645; Hs.73964; EphA4; fn3.pkinase.SAM.EPH_fbd; TM=Y;SS=M; 4.239265714
 411089; AA456454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none; none; 4.237313433
 436957; AA902488; Hs.122952; ESTs; none; DAGKc.DAGKa.RA.DAG_PE-bind; 4.236
 452568; AA805634; Hs.300870; Homo sapiens mRNA; cDNA DKFZp547M072 (fr, P13_P14_kinase; TM=M;SS=M; 4.23537415
 433535; AF111106; Hs.3382; protein phosphatase 4, regulatory subunit; HEAT; TM=M;SS=N; 4.234793187
 432728; NM_005979; Hs.278721; HLA class II region expressed gene KE4; Zip.flg_chan; TM=Y;SS=M; 4.234545455
 416350; AF188625; Hs.189507; phospholipase A2, group IID; phospho; TM=M;SS=Y; 4.234
 409533; AW989543; Hs.144609; mitogen-activated protein kinase kinase ; Pepidase_C48; none; 4.230666667
 427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C; none; 4.228009259
 403362; ; NM_001615; Homo sapiens actin, gamma 2, ; actin; 4.22688478
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen.COLFI.TSPN.laminin_G.CorA; 4.226388889

428897; AJ245719; Hs.194385; hypothetical protein FLJ20234; SH2; TM=M; SS=N; 4.224731183
 425771; BE561776; Hs.159494; Bruton agammaglobulinemia tyrosine kinase; SH2, SH3, pkinase, PH, BTK; TM=M; SS=N; 4.223584211
 418566; C21220; Hs.321717; hypothetical protein FLJ10875; zf-C2H2, BTB, K_tetra, 7tm_1; 4.222807018
 454098; W27953; Hs.217493; Plakophilin; none, none; 4.22
 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); pkinase, FHA, DnaJ; TM=M; SS=N; 4.21875
 419223; X60111; Hs.1244; CD9 antigen (p24); transmembrane4; TM=Y; SS=M; 4.217130215
 436756; Z18364; Hs.198298; v-src avian sarcoma (Schmidt-Ruppin A-2); none, none; 4.216
 450167; AA446404; Hs.24563; NTF2-related export protein 1; NTF2; TM=M; SS=N; 4.215163934
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; efhand; 4.212041885
 432539; AL138169; Hs.278378; karyopherin beta 2b, transportin; none, DS, UPF0139, Glyco_hydro_38; 4.207407407
 416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; KH-domain, rrm; TM=M; SS=N; 4.206
 432284; AA532807; Hs.287740; ESTs; pkinase, none; 4.205454546
 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase, RIO1; TM=M; SS=N; 4.204142012
 450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypotheli; ABC_tran, ABC_membrane, Ig_MHC_II_beta, SRP54, proteasome, ABC_membrane, ABC_tran; 4.202572347
 412817; AL037159; Hs.74619; proteasome (prosome, macropain) 26S subunit; PC_rep; TM=M; SS=N; 4.202061856
 425394; AA356730; Hs.323949; kangxi 1 (suppression of tumorigenicity); transmembrane4, none; 4.195014663
 449335; AW150717; Hs.345728; STAT induced STAT inhibitor 3; SH2; TM=M; SS=N; 4.192248062
 415023; AA932146; Hs.355397; Homo sapiens clone TCCCA00164 mRNA sequ; none; NA; NA; 4.192
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none; TM=M; SS=Y; 4.191878981
 445330; R52656; Hs.21691; ESTs; 7tm_1, none; 4.189922481
 430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX, EXS; TM=Y; SS=N; 4.188333333
 434633; AJ189587; Hs.120915; ESTs; SH3, PH, RhoGAP, none; 4.187106918
 452908; AB001451; Hs.30965; neuronal Shc adaptor homolog; SH2, PID, Zn_carboxypept; TM=M; SS=N; 4.186885246
 439318; AW837046; Hs.6527; G protein-coupled receptor 56; 7tm_2, Cyt_c, asm, GPS; TM=Y; SS=M; 3.930957684
 432201; AJ538613; Hs.298241; Transmembrane protease, serine 3; trypsin, TM=Y; SS=M; 3.893103448
 428969; AF120274; Hs.194689; artemin; TGF-beta; 3.884030418
 444633; AF111713; Hs.12284; junctional adhesion molecule 1; ig; TM=Y; SS=M; 3.831669044
 432305; M62402; Hs.274313; insulin-like growth factor binding prote; thyroglobulin_1, JGFBP, A2M_N; TM=M; SS=N; 3.742996346
 405547; ; NM_018833; Homo sapiens transporter 2, A; ABC_tran, SRP54, ABC_membrane; TM=Y; SS=M; 3.676
 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none; TM=M; SS=Y; 3.634
 426427; M86699; Hs.169840; TTK protein kinase; pkinase; 3.562
 427585; D31152; Hs.179729; collagen, type X, alpha 1 (Schmid metaph; C1q, Collagen; 3.49
 405546; ; NM_018833; Homo sapiens transporter 2, A; ABC_tran, SRP54, ABC_membrane; TM=Y; SS=M; 3.422661871
 439820; AL360204; Hs.283853; Homo sapiens mRNA full length insert cDNA; none, none; 3.402
 404210; ; NM_005936; Homo sapiens myeloid/lymphoid; FHA, PDZ, RA, DIL; TM=M; SS=N; 3.368807339
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 90kD, polyr; pkinase, pkinase_C; 3.213402062
 418678; NM_001327; Hs.87225; cancer/testis antigen (NY-ESO-1); none; TM=M; SS=N; 3.084
 451106; BE382701; Hs.25960; N-MYC oncogene; HLH, Myc_N_term; TM=M; SS=N; 1.55

TABLE 17B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
418869	12789_14	AA229762 AA230035

TABLE 17C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402075	8117407	Plus	121907-122035, 122804-122921, 124019-12416
401781	7249190	Minus	83215-83435, 83531-83656, 83740-83901, 8423
405484	5922025	Plus	199214-199579, 199672-199920, 200262-20049
405932	7767812	Minus	123525-123713
400517	9796686	Minus	49996-50346
402328	4464283	Minus	13758-13922, 14558-14752
405545	1054740	Plus	118677-118807, 119091-119296, 121626-12182
402330	4464283	Minus	15325-15380, 15484-15588, 15842-15915
404440	7528051	Plus	80430-81581
403912	7710730	Minus	72000-72290, 72431-72700, 72929-73199
404760	7767724	Plus	223266-223352, 224472-224585
404883	5101762	Minus	94626-94730, 96998-97059
403362	8571772	Plus	64099-64260
405547	1054740	Plus	124361-124520, 124914-125050
405546	1054740	Plus	124010-124183
404210	5006246	Plus	169926-170121

Table 18A: 194 Up-Regulated Genes in Uterine Cancer Versus Normal Adult Tissues

Table 18A lists about 194 genes up-regulated in uterine cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip array such that the ratio of "average" uterine cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" uterine cancer level was set to the 2nd highest amongst uterine cancers. The "average" normal adult tissue level was set to the 90th percentile value amongst non-malignant tissues. In order to remove gene-specific background

levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

5	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor vs. normal tissue			
10	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	449034	AI624049		gbts41a09x1 NCI_CGAP_U11 Homo sapiens cDNA	55.7
	435094	AI550129	Hs.277523	EST	45.2
	438817	AI023799	Hs.163242	ESTs	42.6
15	421478	AI683243	Hs.97258	ESTs	35.2
	452638	U65011	Hs.30743	Preferentially expressed antigen in melanoma	27.3
	450451	AW591528	Hs.202072	ESTs	26.0
	428153	AW513143	Hs.98367	hypothetical protein FLJ22252	24.8
	428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49) (HG38)	24.2
20	438993	AA828995	Hs.52620	integrin, beta 8	16.7
	436775	AA731111	Hs.291891	ESTs	14.3
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDNA cto	13.5
	441377	BE218239	Hs.202656	ESTs	13.5
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromolysin 2)	12.3
25	400292	AA250737	Hs.72472	BMPRII; bone morphogenetic protein receptor II	10.7
	403899			predicted exon	10.1
	442438	AA959598		gbts26b03.s1 NCI_CGAP_Kd5 Homo sapiens cDNA	10.0
	447350	AI375572	Hs.1939	HER4 (c-erb-B4)	9.8
	453964	AI961486	Hs.12744	ESTs	9.7
30	443830	AI142095	Hs.143273	ESTs	9.1
	459325	AW088369	Hs.282184	ESTs	9.0
	415245	N59650	Hs.27252	ESTs	8.9
	446608	N75217	Hs.257846	ESTs	8.9
	426635	BE395109	Hs.129327	ESTs	8.8
35	433426	H69125	Hs.133525	ESTs	8.7
	437960	AI669586	Hs.222194	ESTs	8.5
	441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin 2b [H]	8.3
	440048	AA897461	Hs.158469	ESTs, Weakly similar to envelope protein [Hs]	7.3
40	447835	AW591623	Hs.164129	ESTs	7.2
	440870	AI687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clone THYRO10	7.1
	412925	AI089319	Hs.179243	ESTs	7.0
	408562	AA436323	Hs.31141	Roundabout homolog 2 transmembrane receptor (robo2)	7.0
	429272	W25140	Hs.110567	ESTs	6.9
45	453197	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAM	6.3
	437938	AI950087		ESTs, Weakly similar to Gag-Pol polyprotein	6.2
	420610	AI683183	Hs.99348	distal-less homeo box 5	6.2
	448672	AI955511	Hs.225106	ESTs	6.1
	452461	N78223	Hs.108106	transcription factor	6.1
50	413335	AI613318	Hs.48442	ESTs	6.1
	449611	AI970394	Hs.197075	ESTs	6.0
	449260	AA741180	Hs.29679	ESTs	6.0
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkinesin6)	6.0
	443715	AI583187	Hs.9700	cyclin E1	6.0
55	432113	AA935065	Hs.152385	ESTs	5.9
	424834	AI001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT2RP20	5.7
	410658	AW105231	Hs.192035	ESTs	5.7
	426465	AI758948		gbcty16f07.x1 NCI_CGAP_UI3 Homo sapiens cDNA	5.7
	446704	AI337228	Hs.197083	ESTs	5.5
60	419503	AA243642	Hs.137422	ESTs	5.5
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane glyco	5.4
	436076	AI193277	Hs.120954	ESTs	5.4
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	5.3
	445258	AI635931	Hs.147613	ESTs	5.3
65	440901	AA909358	Hs.128612	ESTs	5.3
	434636	AA083764	Hs.241334	ESTs	5.3
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone LNG020	5.2
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	5.2
	459583	AI907673		gbclL-BT152-080399-004 BT152 Homo sapiens cDN	5.2
70	436787	AA908554	Hs.192756	ESTs	5.2
	400301	X03635	Hs.1657	Estrogen receptor 1	5.1
	428771	AB028992	Hs.193143	KIAA1069 protein	5.1
	444929	AI685841	Hs.161354	ESTs	5.0
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	5.0
75	405609			predicted exon	5.0
	410102	AW248508	Hs.279727	ESTs	5.0
	433283	BE041135	Hs.175622	ESTs	4.8
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	4.8
	410247	AF181721	Hs.61345	RU2S	4.7
80	422589	AA312735	Hs.179725	ESTs	4.7
	452771	T05477		gb:EST03366 Fetal brain, Stratagene (ca193620	4.7
	407275	AI364186		gb:qxw34h07.x1 NCI_CGAP_U14 Homo sapiens cDNA	4.7
	420440	NM_002407	Hs.97644	mammaglobin 2	4.6
	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens cDNA	4.6

5	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate polypept	4.6
	424115	AA335497	Hs.293955	ESTs	4.6
	414245	BE148072	Hs.75850	WAS protein family, member 1	4.6
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR motif,	4.5
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	4.5
10	447048	AW393080	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone LNG076	4.4
	458861	AI630223		PHD finger DNA binding protein isoform 1 (int)	4.4
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PLACE20	4.3
	420149	AA255920	Hs.88095	ESTs	4.3
	433479	AW511459	Hs.249972	ESTs	4.3
15	449416	AI651016	Hs.246311	ESTs	4.3
	457551	AW821319	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, clone HEP106	4.3
	450109	AI539295	Hs.17967	ESTs	4.3
	436954	AA740151	Hs.130425	ESTs	4.3
	415511	AI732617	Hs.182362	ESTs	4.3
20	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT2RM40	4.3
	406411			predicted exon	4.2
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, homolog)	4.2
	416456	H57052	Hs.176626	hypothetical protein EDAG-1	4.2
	454692	AW813350		gb:MR3-ST0192-100100-024-g07	4.1
25	452249	BE394412	Hs.61252	ESTs	4.1
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	4.1
	449765	N92293	Hs.206832	EST, Moderately similar to ALU8_HUMAN ALU SUB	4.1
	434988	AI418055	Hs.161160	ESTs	4.1
	423515	AA327017	Hs.162204	ESTs	4.0
30	435407	AI149774	Hs.117178	ESTs	4.0
	440886	AW511032	Hs.190516	ESTs	4.0
	444783	AK001468	Hs.62180	ESTs	4.0
	452039	AI922988	Hs.172510	ESTs	4.0
	407300	AA102616	Hs.120769	Homo sapiens cDNA FLJ20463 fis, clone KAT0614	4.0
35	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HUMAN TRANSC	4.0
	449433	AI672096	Hs.9012	ESTs	3.9
	419335	AW560146	Hs.284137	Homo sapiens cDNA FLJ12888 fis, clone NT2RP20	3.9
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp58611518	3.9
	453096	AW294631	Hs.11325	ESTs	3.9
40	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone HEP010	3.9
	445034	AW293376	Hs.160323	ESTs	3.8
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	3.8
	422219	AW978073		gb:EST390182 MAGE resequences	3.8
	440304	BE159984	Hs.125396	ESTs	3.8
45	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228	3.8
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK	3.8
	400250			predicted exon	3.8
	428227	AA321649	Hs.2248	INTERFERON-GAMMA INDUCED PROTEIN	3.8
	420092	AA814043	Hs.88045	ESTs	3.8
50	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 TFPI2	3.8
	437212	AI765021	Hs.210775	ESTs	3.8
	409867	AW502161		gb:U1-HF-BR0p-ajr-g-12-0-U1r1 NIH_MGC_52	3.7
	421477	AI904743	Hs.104650	hypothetical protein FLJ10292	3.7
	427119	AW880562	Hs.114574	ESTs	3.7
55	458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234	3.7
	434539	AW748078	Hs.214410	ESTs	3.7
	424717	H03754	Hs.152213	wingless-type MMTV integration site family	3.7
	412078	X69699	Hs.73149	paired box gene 8 (PAX-8)	3.7
	447342	AI199268	Hs.19322	ESTs; Weakly similar to IIII ALU SUBFAMILY J	3.7
60	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affinity)	3.7
	446619	AI076643	Hs.313	secreted phosphoprotein 1 (osteopontin)	3.7
	453891	AK037751	Hs.36353	Homo sapiens mRNA full length insert cDNA clo	3.7
	443613	AI079356		gb:oz39b09.s1 Soares_NHMPu_S1 Homo sapiens c	3.6
	441285	NM_002374	Hs.167	microtubule-associated protein 2	3.6
65	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblastoma c	3.6
	417847	AI521558	Hs.288312	Homo sapiens cDNA: FLJ22316 fis, clone HRC052	3.6
	441484	AA935481	Hs.58972	ESTs	3.6
	415802	AA169515	Hs.6006	ESTs	3.6
	448112	AW245919	Hs.301018	ESTs	3.6
70	428330	L22624	Hs.2256	matrix metalloproteinase 7 (matrilysin)	3.6
	402606			predicted exon	3.6
	407905	AW103655	Hs.252905	ESTs	3.6
	424917	AI636208	Hs.96901	Homo sapiens cDNA: FLJ23049 fis, clone LNG025	3.6
	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular matrix p	3.6
75	451842	AI820539	Hs.267087	ESTs, Moderately similar to ALU4_HUMAN ALU SU	3.6
	455666	BE065813		gb:RC2-BT0318-110100-012-a08 BT0318 Homo sapi	3.6
	431731	BE266322	Hs.211374	ESTs, Weakly similar to SP49_HUMAN SPLICOSOM	3.6
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 retinal sh	3.6
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein produ	3.6
80	406030			predicted exon	3.5
	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA Libr	3.5
	430481	AA479678	Hs.203269	ESTs, Moderately similar to ALU8_HUMAN ALU SU	3.5
	437641	AA811452	Hs.291911	ESTs	3.5
	415211	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFACE PROTEIN	3.4
	443450	N66045	Hs.133529	ESTs	3.4
	457438	NM_014053	Hs.270694	FLVCR protein	3.4
	451254	AI571016	Hs.172967	ESTs	3.4

5	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HEMB810	3.4
	427778	AA412323	Hs.105323	ESTs	3.3
	435031	AI632091	Hs.116877	ESTs	3.3
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequence.	3.3
	417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-187J11 on c	3.3
	431548	AI834273	Hs.9711	Homo sapiens cDNA FLJ13018 fis, clone NT2RP30	3.2
	432415	T16971	Hs.289014	ESTs	3.2
	423126	AA322245	Hs.290165	ESTs	3.2
10	433420	AI674093	Hs.293961	ESTs	3.2
	435174	AA687378	Hs.194624	ESTs	3.2
	444743	AA045648	Hs.11817	nrdix (nucleoside diphosphate linked molety X	3.2
	452588	AA889120	Hs.110637	Homeo box A10	3.2
	427304	AA761526	Hs.163853	ESTs	3.2
15	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232 (from cl	3.1
	417728	AW138437	Hs.24790	KIAA1573 protein	3.1
	419356	AI656166	Hs.7331	ESTs	3.1
	458627	AW088642	Hs.97984	ESTs; Weakly similar to WASP-family protein [3.1
	435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrolase 1	3.1
20	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone COL054	3.1
	405174			predicted exon	3.1
	403776			predicted exon	3.1
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfamily, m	3.1
	431255	AA497043	Hs.115685	ESTs	3.1
25	442353	BE379594	Hs.49136	ESTs	3.1
	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (formerl	3.1
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	3.1
	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapiens cDNA c	3.1
	406400			kallikrein 8 (neurosin/ovasin)	3.0
30	439949	AW979197	Hs.292073	ESTs	3.0
	430704	AW813091		gb:RC3-ST0186-240400-111-d07 ST0186 Homo sapi	3.0
	401517			predicted exon	3.0
	417830	AW504786	Hs.132808	epithelial cell transforming sequence 2 oncog	3.0
	435267	N23797	Hs.110114	ESTs	3.0
35	426384	AI472078		ESTs	3.0
	422797	AB033064	Hs.120908	KIAA1238 protein	3.0
	428832	AA578229		gb:nl22b12.s1 NCI_CGAP_HSC1 Homo sapiens cDNA	3.0
	449722	BE280074	Hs.23960	cyclin B1	3.0
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A	3.0
40	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapi	3.0

TABLE 18B

45	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
	Pkey	CAT number	Accession
50	409745	115237_1	AA077391 AI347618 AI361453 AI088754 AW207491 AW960912 AA921874 AA266833 AA150722 BE152353 AW188822 BE152450
	409867	1156530_1	AW502161 AW502587 AW502345
	422219	213547_1	AW978073 AW978072 AA807550 AA306567
	422689	215896_1	AW856665 AA315006 AW954733
	426384	266211_1	AI472078 AA377209 AA865807
55	426465	267664_1	AI758948 AA379527 AA379948 AA379262 AW963933
	428832	296144_1	AA578229 AA436432 AA481375 AA481353
	430704	322217_1	AW813091 AW206655 AA484440
	431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
	437938	44573_2	AI950087 N70208 R97040 N36809 AI308119 AW867677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598
60			AA251875 AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA884444 N92578 F13493
			AA927794 AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI741346 AI689062 AA282915
			AW102898 AI872193 AI763273 AW173586 AW150329 AI653832 AI762688 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975
			AW505512 AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669
			AA251874 AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628
65			N22388 H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AI373032 AI564269 F00531 H83488 W37181 W78802 R66056
			AI002839 R67840 AA300207 AW959581 T63226 F04005
	438993	467651_1	AA828995 AA834879 AI926361
	442438	542469_1	AA995998 AI916584 R61781 T77332 F07756 F08149 F07647
	443613	575391_1	AI079356 W23287
70	449034	794817_1	AI624049 AW117770 AI858360
	451105	859083_1	AI761324 AW880941 AW880937
	452771	930983_1	T05477 T07655 AI917711
	454392	115882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293
	454692	1229118_1	AW813350 AW816082 AW813476 AW813383
75	455666	1349545_1	BE065813 BE065788 BE065889 BE065832
	458154	491768_1	AW816379 AA888282 AA879046 AA879195
	458861	798085_1	AI630223 AI630470

TABLE 18C

80	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

5	Pkey	Ref	Strand	Nt_position
	401517	7677912	Plus	29278-29770
	402606	9909429	Minus	81747-82094
	403776	7770611	Minus	1414-1513,1624-1756
10	403899	7381715	Minus	9144-9350
	405174	7108030	Minus	102814-103063
	405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
	406030	8312328	Minus	96123-96547
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
15	406411	9256407	Plus	7400-7527

Table 19A: 225 Up-Regulated Genes Encoding Extracellular/Cell Surface Proteins, UTERINE Cancer Versus Normal Adult Tissues

Table 19A lists about 225 genes up-regulated in uterine cancer compared to normal adult tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 18A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. Ig, fn3, egf, 7tm domains, signal sequences, transmembrane domains). The predicted protein domains are noted.

25	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UnigeneID:	Unigene number				
	Unigene Title:	Unigene gene title				
	PSDomain:	Protein Structural Domain				
30	Rt:	Ratio of tumor vs. normal tissue				
	Pkey	ExAccn	UnigeneID	Unigene Title	PSDomain	Rt
35	452838	U65011	Hs.30743	Preferentially expressed antigen in melanoma	TM	27.3
	438993	AA828995	Hs.52620	integrin, beta 8	SS, TM, integrin_B	16.7
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stroma	SS, hemopexin	12.3
	446608	N75217	Hs.257846	ESTs	TM	8.9
	433426	H69125	Hs.133525	ESTs	TM	8.7
	440870	AJ687284	Hs.150539	Homo sapiens cDNA FLJ13793 fis, clo	TM, PAX	7.1
40	408562	AJ436323	Hs.31141	Roundabout homolog 2 transmembrane	SS, TM, Ig, fn3	7.0
	420610	AJ883183	Hs.99348	distal-less homeo box 5	TM, homeobox	6.2
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rab	TM, kinesin	6.0
	443715	AI583187	Hs.9700	cyclin E1	TM, cyclin	6.0
	432113	AA935065	Hs.152385	ESTs	TM	5.9
45	419503	AA243642	Hs.137422	ESTs	TM	5.5
	444342	NM_014398	Hs.10887	similar to lysosome-associated memb	TM, Lamp	5.4
	436076	AI193277	Hs.120954	ESTs	TM	5.4
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprot	TM, hemopexin	5.3
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	TM	5.2
50	459583	AI907673		gb:IL-BT152-080399-004 BT152 Homo s	TM	5.2
	400301	X03635	Hs.1657	Estrogen receptor 1	TM, hormone_rec, zf-C4	5.1
	405609			predicted exon	TM, Myosin_tail, myosin_head	5.0
	453922	AF053306	Hs.35708	budding uninhibited by benzimidazol	TM	5.0
	410102	AW248508	Hs.279727	ESTs	SS, TM,	5.0
55	433283	BE041135	Hs.175622	ESTs	TM	4.8
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gen	TM	4.8
	410247	AF181721	Hs.61345	RJ2S	TM	4.7
	422589	AA312735	Hs.179725	ESTs	TM	4.7
60	407275	AJ364186		gb:qw34h07.x1 NCL CGAP_UH Homo sap	TM	4.7
	420440	NM_002407	Hs.97644	mammaglobin 2	TM, Uteroglobulin	4.6
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate	TM, Ribosomal_S27e	4.6
	424115	AA335497	Hs.293965	ESTs	TM	4.6
	414245	BE148072	Hs.75850	WAS protein family, member 1	TM, WH2	4.6
	458861	AJ630223		PHD finger DNA binding protein iso	TM, PHD	4.4
65	449416	AJ651016	Hs.246311	ESTs	SS, TM,	4.3
	420149	AA255920	Hs.88095	ESTs	TM	4.3
	433479	AW511459	Hs.249972	ESTs	TM	4.3
	457551	AW821319	Hs.288928	Homo sapiens cDNA: FLJ23296 fis, cl	TM	4.3
	406411			predicted exon	TM, vwa, FG-GAP	4.2
70	416456	H57052	Hs.176626	hypothetical protein EDAG-1	TM	4.2
	454692	AW813350		gb:MR3-ST0192-100100-024-g07 ST0192	TM	4.1
	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	TM	4.1
	434988	AJ418055	Hs.161160	ESTs	TM	4.1
	444783	AK001468	Hs.62180	ESTs	TM, PH	4.0
75	440886	AW511032	Hs.190516	ESTs	TM, FG-GAP	4.0
	425176	AW015644	Hs.301430	ESTs, Moderately similar to TEF1_HU	TM, Glyco_transf_29, TEA	4.0
	445034	AW293376	Hs.160323	ESTs	TM	3.8
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box	TM, HMG_box	3.8
	400250			predicted exon	TM, Hist_deacetyl	3.8
80	428227	AA321649	Hs.2248	interferon-gamma induced protein	TM, IL8	3.8
	415138	C18356	Hs.78045	tissue factor pathway inhibitor 2 T	TM, Kunitz_BPTI, G-gamma	3.8
	458154	AW815379		gb:QV4-ST0234-181199-035-g01 ST0234	TM, WW	3.7
	421477	AJ904743	Hs.104650	hypothetical protein FLJ10292	TM	3.7

5	413472	BE242870	Hs.75379	solute carrier family 1 (glial high	TM,SDF	3.7
	447342	A1199258	Hs.19322	ESTs; Weakly similar to IIII ALU SU	TM	3.7
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopon	TM,Osteopontin	3.7
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length inser	TM	3.7
	441285	NM_002374	Hs.167	microtubule-associated protein 2	TM,tubulin-binding	3.6
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuro	TM,Thymosin	3.6
	441484	AA935481	Hs.58972	ESTs	TM,fn3,ig_Y_phosphatase	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrily	SS,Peptidase_M10	3.6
10	407905	AW103655	Hs.252905	ESTs	SS,TM,Ephrin	3.6
	436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellula	SS,TM,	3.6
	402606			predicted exon	TM	3.6
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1	TM	3.6
	437641	AA811452	Hs.291911	ESTs	TM	3.5
15	415211	R64730.comp	Hs.155986	ESTs; Highly similar to SPERM SURFA	TM,IQ,Rila	3.4
	443450	N66045	Hs.133529	ESTs	TM	3.4
	457438	NM_014053	Hs.270594	FLVCR protein	TM	3.4
	435031	A1632091	Hs.116877	ESTs	TM,RhoGEF,PH	3.3
	417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-1	TM	3.3
20	435174	AA687378	Hs.194624	ESTs	TM,SPRY	3.2
	444743	AA045648	Hs.11817	nudix (nucleoside diphosphate linke	TM,muT	3.2
	433420	A1674093	Hs.293961	ESTs	TM	3.2
	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E23	TM	3.1
	417728	AW138437	Hs.24790	KIAA1573 protein	TM	3.1
25	403776			predicted exon	SS,TM,IL8	3.1
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) supe	TM,TNF	3.1
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 tis, cl	TM,Ets	3.1
	405174			predicted exon	TM	3.1
30	431255	AA497043	Hs.115685	ESTs	TM	3.1
	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog	TM,homeobox	3.1
	416530	U62801	Hs.79361	kalikrein 6 (neurosin, zyme)	TM,trysin,pro_isomerase	3.1
	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapi	TM	3.1
	406400			kalikrein 8 (neuropsin/ovasin)	TM,trysin	3.0
	401517			predicted exon	TM,HMG14_17	3.0
35	417830	AW504786	Hs.132808	epithelial cell transforming sequen	TM	3.0
	435267	N23797	Hs.110114	ESTs	TM	3.0
	449722	BE280074	Hs.23960	cyclin B1	TM,cyclin	3.0
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2	TM,ank	3.0
40	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297	TM,SNF2_N	3.0
	441794	AW197794	Hs.253338	ESTs	TM,ank	2.9
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractura	TM,EGF,TB	2.9
	431130	NM_006103	Hs.2719	epitidylms-specific; whey-acidic pr	SS,wap	2.9
	418113	A1272141	Hs.83484	ESTs	TM,HMG_box	2.9
	402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome	TM,TEA	2.9
45	431989	AW972870	Hs.291059	ESTs	SS	2.9
	400284			Estrogen receptor 1	TM,hormone_rec,zf-C4	2.9
	438578	AA811244	Hs.164168	ESTs	TM,formyl_transf,AIRS,GARS	2.9
	423513	AF035960	Hs.129719	transglutaminase 5	TM,Transglutamin_N	2.8
	448966	AW372914	Hs.287462	Homo sapiens cDNA FLJ11875 tis, clo	TM	2.8
50	431870	AW449902	Hs.105500	ESTs	TM,MHC_Lig	2.8
	409457	AW818081		gb:CM4-ST0276-101299-059-b09 ST0276	TM	2.8
	438777	AA825487	Hs.142179	ESTs, Weakly similar to ORF2 [M.mus	TM	2.8
	451807	W52854	Hs.27099	DKFZP564J0863 protein	TM	2.8
	433326	A1379486	Hs.159430	ESTs	TM	2.8
55	448221	BE622615		gb:601440775T1 NIH_MGC_72 Homo sapi	TM	2.8
	448141	A1471598	Hs.197531	ESTs	TM,bZIP	2.8
	456311	AA225632	Hs.190016	ESTs	TM,Sec7	2.8
	405454			predicted exon	TM	2.8
60	459287	AL079369		gb:DKFZp564G2378_r1 564 (synonym: h	TM	2.8
	438935	H40665	Hs.31564	ESTs	TM	2.7
	421312	AA824627	Hs.291670	ESTs	TM,G-patch	2.7
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C	TM,ABC_membrane,ABC_tran	2.7
	424345	AK001380	Hs.145479	Homo sapiens cDNA FLJ10518 tis, clo	TM	2.7
65	417956	AA210704	Hs.190465	ESTs	SS,sushi	2.7
	445537	AJ245671	Hs.12844	EGF-like-domain; multiple 6	SS,EGF	2.7
	448089	A467945	Hs.173696	ESTs	SS,TM,	2.6
	446643	AA194417	Hs.282060	ESTs	TM,Cla1_adaptor_s	2.6
	456671	AB011142	Hs.114293	KIAA0570 gene product	TM	2.6
	457256	AA459443	Hs.231816	ESTs	SS	2.6
70	438986	AF085888	Hs.269307	ESTs	TM,Spin-Ssty	2.5
	435313	A1769400	Hs.189729	ESTs	TM,MBD	2.5
	417351	T90278	Hs.15049	ESTs	TM,CH	2.5
	412198	AA937111	Hs.69165	ESTs	TM	2.5
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 k	TM,ubiquitin	2.5
75	421502	AF111866	Hs.105039	solute carrier family 34 (sodium ph	TM,Na_P1_cotrans	2.5
	418092	R45154	Hs.106604	ESTs	TM,phkinase	2.5
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (TM,FG-GAP	2.5
	420362	U79734	Hs.97206	huntingtin interacting protein 1	TM,ENTH1_LWEQ	2.5
	431974	AW972689	Hs.200934	ESTs	TM,bZIP	2.5
80	438209	AL120659	Hs.6111	KIAA0307 gene product	TM,HUH,PAS	2.5
	447578	AA912347	Hs.136585	ESTs	TM	2.5
	414812	X72755	Hs.77367	monokine induced by gamma interfero	SS,IL8	2.5
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase	TM,Glyco_transf_29	2.4
	416402	NM_000715	Hs.1012	complement component 4-binding prot	TM,sushi	2.4

5	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HU	TM	2.4
	428242	H55709	Hs.2250	leukemia inhibitory factor (choline	SS,LIF_OSM	2.4
	417693	AW959741	Hs.40368	adaptor-related protein complex 1,	TM,Cla1_adaptor_s	2.4
	428679	AA431765		gbzw80c03.s1 Soares_testis_NHT Hom	TM,HECT	2.4
	436311	AA708958	Hs.168732	ESTs	TM	2.4
10	426920	AA393351	Hs.132121	ESTs	TM	2.4
	426698	AA394104	Hs.97489	ESTs	TM	2.4
	443426	AF098158	Hs.9329	Homo sapiens mRNA for fls353, compl	TM	2.4
	406815	AA833930	Hs.288036	IRNA isopentenylpyrophosphate trans	TM,IPPT	2.4
	434808	AF155108	Hs.256150	ESTs, Highly similar to NY-REN-41 a	TM	2.3
15	432441	AW292425	Hs.163484	EST	TM,Fork_head	2.3
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQ	TM	2.3
	402298			predicted exon	TM,zf-C2H2,KRAB	2.3
	435542	AA687376	Hs.269533	ESTs	TM	2.3
	442952	AI743261	Hs.131860	ESTs	TM	2.3
20	418203	X54942	Hs.83758	CDC28 protein kinase 2	TM,CKS	2.3
	429228	AI553633	Hs.104985	ESTs	TM	2.3
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	TM,SH3	2.3
	447570	AI658315	Hs.99669	ESTs	TM,PHD	2.3
	405032			predicted exon	TM,FMO-like	2.3
25	416566	NM_003914	Hs.79378	cyclin A1	TM,cyclin	2.3
	420900	AL045633	Hs.44269	ESTs	TM,FAD_binding_5	2.3
	430563	AA481269	Hs.178381	ESTs	TM,ABC_membrane,p450	2.3
	417372	T99755	Hs.290814	ESTs	TM	2.3
	449083	AI948808	Hs.191144	ESTs	TM	2.3
30	410361	BE391804	Hs.62661	guanylate binding protein 1, interl	TM,GBP	2.3
	434131	AI858275	Hs.143659	ESTs	TM	2.3
	431846	BE019924	Hs.271580	Uroplakin 1B	TM,transmembrane4	2.3
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific	TM	2.3
	440006	AK000517	Hs.6844	hypothetical protein FLJ20510	TM	2.3
35	445870	AW410053	Hs.13406	syntaxin 18	TM	2.3
	430639	AW025427	Hs.233552	ESTs	TM,pkinase	2.3
	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfam	SS,TM	2.3
	422095	AI658372	Hs.288966	ceruloplasmin (ferroxidase)	SS,TM,Cu-oxidase	2.2
	411558	AA102670	Hs.70725	*Human GABA-A receptor pl subunit m	TM,neur_chan	2.2
40	408380	AF123050	Hs.44532	diubiquitin	TM,7tm_3,ANF_receptor	2.2
	403721			predicted exon	TM	2.2
	440711	AA904389	Hs.143511	ESTs	TM,rm	2.2
	457285	AI038858	Hs.228780	ESTs, Highly similar to AF199597 1	TM,efhand	2.2
	422956	BE545072	Hs.122579	ESTs	TM	2.2
45	433482	AI953499	Hs.152617	ESTs	TM	2.2
	431980	AA523696	Hs.222695	Homo sapiens cDNA: FLJ20986 fis, cl	TM	2.2
	420777	AA280223	Hs.130865	ESTs	TM	2.2
	446859	AI333531	Hs.226376	ESTs	TM	2.2
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	TM	2.2
50	422282	AF019225	Hs.114309	apolipoprotein L	TM	2.2
	431701	AW935490	Hs.14658	ESTs	TM,Occludin	2.2
	426910	AA470023	Hs.190089	ESTs	TM,MMR_HSR1	2.2
	405636		Hs.153595	predicted exon	SS,TM,EGF,Jdl_recept_a	2.2
	401933			predicted exon	TM,Ion_trans	2.1
55	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed pro	TM	2.1
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 pr	TM	2.1
	410684	NM_006033	Hs.65370	lipase, endothelial	SS,TM,Ribosomal_L22,lipase	2.1
	449378	AW664026	Hs.59892	ESTs	TM	2.1
	433345	AI681545	Hs.152982	EST cluster (not in UniGene)	TM	2.1
60	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase	SS,TM,Branch	2.1
	431832	AW276866	Hs.192715	ESTs	TM,Ets,SAM_PNT	2.1
	448275	BE514434	Hs.20830	synaptic Ras GTPase activating prot	TM,kinesin_abhydrolase_2	2.1
	423049	X59373	Hs.188023	ESTs	TM,homeobox	2.1
	427510	Z47542	Hs.179312	small nuclear RNA activating comple	TM	2.1
65	418076	R61388	Hs.6724	ESTs	TM	2.1
	413570	AB000115	Hs.75470	hypothetical protein, expressed in	TM	2.1
	429183	AB014604	Hs.197955	KIAA0704 protein	TM	2.1
	439031	AF075079		gb:Homo saplens full length insert	TM	2.1
	431060	AF039307	Hs.249171	homeo box A11	TM,homeobox	2.1
70	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HU	TM	2.1
	419978	NM_001454	Hs.93974	forkhead box J1	TM,Fork_head	2.1
	404535	Z25884	Hs.121483	chloride channel 1, skeletal muscl	SS	2.1
	445181	AW338972	Hs.147471	ESTs	TM	2.1
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	TM,Hydrolase	2.1
75	443591	AI078281	Hs.179240	ESTs	TM	2.1
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2_HUMAN	TM,trypsin	2.1
	424310	AA338648	Hs.50334	ESTs	TM	2.0
	450193	AI916071	Hs.224623	ESTs	TM,pkinase	2.0
	436009	H57130	Hs.120925	ESTs	SS,TM,Ephrin	2.0
80	453313	BE005771	Hs.153746	Homo sapiens cDNA: FLJ22490 fis, cl	TM	2.0
	419833	AA251131	Hs.220697	ESTs	TM,WHEP-TRS	2.0
	437555	AA759263	Hs.14041	ESTs	TM,Nramp	2.0
	411828	AW161449	Hs.72290	wingless-type MMTV integration site	TM,wnt	2.0
	440052	AI633744	Hs.195648	ESTs	TM,PAC	2.0
	410718	AI920783	Hs.191435	ESTs	TM,SQS_PSY	2.0
	404767			predicted exon	TM	2.0
	447462	AW337214	Hs.158973	ESTs	TM	2.0

5	442255	AI701857	Hs.202368	ESTs	TM	2.0
	410292	AA843087	Hs.124194	ESTs	TM	2.0
	442748	AI016713	Hs.135787	ESTs	TM	2.0
	458760	AI498631	Hs.111334	ferritin, light polypeptide	TM,HCO3_cotransp	2.0
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	TM,Hydrofase	2.0
	401324			predicted exon	TM,myosin_head	2.0
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	SS	2.0
	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	TM,zf-CCHC	2.0
10	421379	Y15221	Hs.103982	small inducible cytokine subfamily	SS,TM,IL8	2.0

TABLE 19B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

	Pkey	CAT number	Accession
20	409457	1132521_1	AW818081 AW392887 AW514700 AW392881
	410008	116812_1	AA079552 BE142525 BE142527
	422689	219896_1	AW856665 AA315006 AW954733
	428679	294049_1	AA431765 AA432015
	438993	467651_1	AA828995 AA834879 AI926361
25	439031	46798_1	AF075079 H48601 H48795
	448221	75534_1	BE622615
	454392	115882_1	BE260893 AA078319 R85057 AW803024 H85811 AA078293
	454692	1229118_1	AW813350 AW816082 AW813476 AW813383
	458154	491768_1	AW816379 AA888262 AA879046 AA879195
30	458861	798085_1	AI630223 AI630470
	459287	977129_1	AL079369 D81804

TABLE 19C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NL_position
	401324	9863791	Plus	234057-234174
	401517	7677912	Plus	29278-29770
45	401933	3810668	Minus	48725-49057,51864-51955,52424-52589
	402298	6598824	Plus	36758-37953
	402606	9909429	Minus	81747-82094
	403721	7528046	Minus	156647-157366
	403776	7770611	Minus	1414-1513,1624-1756
50	404767	7882827	Minus	23244-23759
	405032	7107731	Minus	131945-132224
	405174	7108030	Minus	102814-103063
	405454	7656675	Plus	133807-134053
55	405609	5757553	Minus	42814-43010,43583-43783,44863-45033,45429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
	405636	5123990	Plus	56384-56587
	408400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
60	406411	9256407	Plus	7400-7527

Table 20A: 56 Up-Regulated Genes Encoding Extracellular/Cell Surface Proteins, Uterine Cancer Versus Normal Adult Tissues

Table 20A lists about 56 genes up-regulated in uterine cancer compared to normal adult tissues that are likely to encode either enzymes or proteins amenable to modulation by small molecules. These were selected as for Table 18A, except that the ratio was greater than or equal to 2.0, and the predicted protein contained a structural domain that is indicative of enzymatic function or of being modulated by small molecules (e.g. kinase, peptidase, isomerase, transporters). The predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 PSDomain: Protein Structural Domain
 R1: Ratio of tumor vs. normal tissue

75	Pkey	ExAccn	UnigenelD	Unigene Title	PSDomain	R1
	428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49)	7tm_1	24.2
	400289	X07820	Hs.2258	Matrix Metalloproteinase 10 (Stromelysin)	hemopexin	12.3
80	447350	AI375572	Hs.172634	HER4 (c-erb-B4)	kinase	9.8
	420610	AI683183	Hs.99348	distal-less homeo box 5	homeobox	6.2
	405609			predicted exon	Myosin_tail,myosin_head	5.0
	458861	NM_007358	Hs.31016	PHD finger DNA binding protein	PHD	4.4
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone	NA	4.3

5	436211	AK001581	Hs.80961	polymerase (DNA directed), gamma	NA	4.1
	444783	AK001468	Hs.62180	ESTs	PH	4.0
	418677	S83308	Hs.87224	SRY (sex determining region Y)-box 5	HMG_box	3.8
	413472	BE242870	Hs.75379	solute carrier family 1	SDF	3.7
	443613	AI079356	Hs.21807	gbroz39b09.s1 Soares_NhHMPu_S1 Homo s	zf-C2H2	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin)	Peptidase_M10	3.6
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780 1 re	NA	3.6
	435031	AI632091	Hs.116877	ESTs	RhoGEF,PH	3.3
10	417411	AW500008	Hs.6966	Human DNA sequence from clone RP1-187	NA	3.3
	435185	AA669490	Hs.289109	dimethylarginine dimethylaminohydrola	NA	3.1
	416530	U62801	Hs.79361	kalikrein 6 (neurosin, zyma)	trypsin_pro_isomerase	3.1
	406400	AA343629	Hs.104570	kalikrein 8 (neuropsin/ovaslin)	trypsin	3.0
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A	ank	3.0
	441794	AW197794	Hs.253338	ESTs	ank	2.9
15	402373	AL135225	Hs.301865	dopachrome tautomerase (dopachrome de	TEA	2.9
	423513	AF035960	Hs.129719	transglutaminase 5	Transglutamin_N	2.8
	448141	AI471598	Hs.197531	ESTs	bZIP	2.8
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	guanylate_cyc	2.7
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C	ABC_membrane,ABC_tran	2.7
20	448435	BE293439	Hs.182278	calmodulin 2	NA	2.6
	417351	T90278	Hs.15049	ESTs	CH	2.5
	430372	AI206173	Hs.211375	ESTs	SH3,efhand,C2,PH	2.5
	431974	AW972689	Hs.200934	ESTs	bZIP	2.5
25	428046	AW812795	Hs.155381	ESTs, Moderately similar to I38022 hy	ank	2.4
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I	Glyco_transf_29	2.4
	403095			predicted exon	homeobox,PAX	2.4
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transe	IPPT	2.4
	435815	Y15065	Hs.4975	potassium voltage-gated channel	ion_channel	2.3
	402298			predicted exon	zf-C2H2,KRAB	2.3
30	418203	X54942	Hs.83758	CDC28 protein kinase 2	CKS	2.3
	430563	AA481269	Hs.178381	ESTs	ABC_membrane,p450	2.3
	447570	AI868315	Hs.99669	ESTs	PHD	2.3
	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfam	NA	2.3
35	415539	AI733881	Hs.72472	BMPR-1b;	bone morphogenetic protein NA	2.2
	422095	AI868872	Hs.288966	ceruloplasmin (ferroxidase)	Cu-oxidase	2.2
	408380	AF123050	Hs.44532	diubiquitin	ANF_receptor,sushi,7tm_1	2.2
	440711	AA904389	Hs.143511	ESTs	rm	2.2
	457285	AI038858	Hs.228780	ESTs, Highly similar to AF199597 1 A-	efhand	2.2
40	418506	AA084248	Hs.85339	G protein-coupled receptor 39	NA	2.2
	410664	NM_006033	Hs.65370	lipase, endothelial	Ribosomal_L22,lipase,PLAT	2.1
	425851	NM_001490	Hs.159642	glucosaminyl (N-acetyl) transferase 1	Branch	2.1
	448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein	kinesin,PHD,abhydrolase_2	2.1
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-dom	rm,NTF2	2.1
45	404535	Z25884	Hs.121483	chloride channel 1, skeletal muscle	NA	2.1
	448105	AW591433	Hs.170675	ESTs, Weakly similar to TMS2	trypsin	2.1
	446342	BE298665	Hs.14846	Cationic amino acid transporter (ecto	NA	2.0
	458760	AA98631	Hs.111334	ferritin, light polypeptide	HCO3_cotransp,zf-C3HC4	2.0
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	Hydrolase	2.0
50	401324			predicted exon	myosin_head	2.0

TABLE 208

Pkey: Unique Eos probeset Identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accession
443613	575391_1	AI079356 W23287
458861	796085_1	AI630223 AI630470

TABLE 20C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401324	9863791	Plus	234057-234174
402298	6598824	Plus	36758-37953
403095	8954339	Plus	150025-150240,151564-151690
405609	5757553	Minus	42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

Table 21A: 270 Up-Regulated Genes, Uterine Cancer Versus Normal Uterus

Table 21A lists about 270 genes up-regulated in uterine cancer compared to normal uterus. These were selected as for Table 18A, except that the ratio was greater than or equal to 5.0, and the denominator was the median value for six non-malignant uterine specimens.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of tumor vs. normal tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1
449034	AI624049		gb:ts41a09.x1 NCL_CGAP_U11 Homo sapiens	55.7
435094	AI560129	Hs.277523	EST	45.2
438461	AW075485	Hs.286049	phosphoserine aminotransferase	19.5
434779	AF153815	Hs.50151	potassium inwardly-rectifying channel	15.6
441633	AW958544	Hs.112242	ESTs	15.2
429183	AB014604	Hs.197955	KIAA0704 protein	14.6
436775	AA731111	Hs.291891	ESTs	14.3
441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	14.0
446921	AB012113	Hs.16530	CC chemokine SCYA18 (MIP-4) (PARC)	13.0
413753	U17760	Hs.301103	Laminin, beta 3 (nicotin (125kD), kalinin	12.9
421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	12.2
414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	12.0
453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	11.7
425196	AL037915	Hs.155097	carbonic anhydrase II	11.4
444863	AW384082	Hs.301323	ESTs	11.3
449785	AI225235	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	11.1
446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	10.9
449801	AA477355	Hs.288300	Homo sapiens cDNA: FLJ23231 fis, clone C	10.3
411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	10.3
414812	X72755	Hs.77367	monokine induced by gamma interferon	10.2
410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	10.1
423645	AI215632	Hs.147487	ESTs	10.1
442438	AA959398		gb:os26b03.s1 NCL_CGAP_Kid5 Homo sapiens	10.0
415786	AW419196	Hs.257924	ESTs	10.0
458017	AA813426	Hs.192034	ESTs, Weakly similar to KIAA0705 protein	10.0
435525	AI831297	Hs.123310	ESTs	9.9
413335	AI613318	Hs.48442	ESTs	9.7
420297	AI628272	Hs.88323	ESTs	9.6
452799	AI948829	Hs.213766	ESTs	9.6
434311	BE543469	Hs.266263	Homo sapiens cDNA FLJ14115 fis, clone MA	9.4
408243	Y00787	Hs.524	interleukin 8	9.3
430713	AA351647	Hs.2642	eukaryotic translation elongation factor	9.3
452092	BE245374	Hs.27842	hypothetical protein FLJ11210	9.2
444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	9.2
443830	AI142095	Hs.143273	ESTs	9.1
442547	AA306997	Hs.268362	ESTs, Weakly similar to hypothetical pro	9.0
421633	AF121860	Hs.106260	sorting nexin 10	9.0
403381			0	8.9
426635	BE395109	Hs.129327	ESTs	8.8
440500	AA972165	Hs.150308	ESTs	8.7
436291	BE568452	Hs.5101	ESTs; Highly similar to protein regulati	8.7
431668	AW969610	Hs.151179	ESTs	8.7
439018	AW300867	Hs.26638	membrane-spanning 4-domains, subfamily A	8.7
424966	AU077312	Hs.153985	solute carrier family 7 (cationic amino	8.6
425495	AA358454	Hs.78026	ESTs, Weakly similar to similar to ankyr	8.6
428862	NM_000346	Hs.2316	SRF (sex-determining region Y)-box 9	8.5
438986	AF085888	Hs.269307	ESTs	8.4
422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3)	8.4
441081	AI584019	Hs.169006	ESTs, Moderately similar to plakophilin	8.3
415992	C05837	Hs.145807	Homo sapiens cDNA FLJ13593 fis, clone PL	8.2
431211	M86849	Hs.5566	Homo sapiens connexin 26 (GJB2) mRNA, co	8.2
409865	AW502208		gb:U1-HF-BR0p-gju-e-09-Q-U1.r1 NIH_MGC_5	8.0
448158	AI627292	Hs.190877	ESTs	8.0
401519			0	7.9
441730	AI243276	Hs.149017	ESTs	7.9
432441	AW292425	Hs.163484	EST	7.8
448275	BE514434	Hs.20830	synaptic Ras GTPase activating protein 1	7.8
438424	AI912498	Hs.25895	ESTs, Weakly similar to PI-3 kinase [Hs	7.8
447342	AI199268	Hs.19322	ESTs; Weakly similar to [Hs] ALU SUBFAM	7.7
408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	7.7
423081	AF262992	Hs.123159	sperm associated antigen 4	7.6
414484	BE314385		gb:601154649F1 NIH_MGC_19 Homo sapiens c	7.6
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	7.6
459142	AI903396		gb:RC-BT029-120199-219_1 BT029 Homo sapi	7.5
411094	BE066142		gb:CMA-BT0320-221199-047-g10 BT0320 Homo	7.5
436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	7.5
452607	AI160029	Hs.61438	ESTs	7.5
443171	BE281128	Hs.9030	TONDU	7.4
459081	W07808		gb:zb03a12.r1 Soares_fetal_lung_NbHL19W	7.4
431195	AA503083	Hs.79742	ESTs	7.4
444459	AI680624	Hs.148676	ESTs	7.4

	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	7.3
	414918	AI219207	Hs.72222	Hypothetical protein FLJ13459	7.3
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	7.3
5	448865	R35027		gb:yg60g02.r1 Soares infant brain 1N1B H	7.3
	409219	AA393383	Hs.133331	ESTs	7.3
	400491	H25530	Hs.50868	solute carrier family 22 (organic cation	7.2
	403485			0	7.2
	408350	AW183350	Hs.250127	ESTs	7.2
10	445873	AA250970	Hs.251946	Homo sapiens cDNA: FLJ23107 fis, clone L	7.1
	400995			0	7.1
	406086			0	7.1
	403378			0	7.0
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	7.0
15	422038	R39098	Hs.192028	ESTs	7.0
	431842	NM_005764	Hs.271473	epithelial protein up-regulated in carci	6.9
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.9
	427494	AI628365	Hs.130412	ESTs, Weakly similar to sre-2 [C.elegans	6.9
	429272	W25140	Hs.110667	ESTs	6.9
20	427258	AA400091	Hs.39421	ESTs	6.9
	449309	AW589823	Hs.224189	ESTs	6.9
	400104			0	6.9
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	6.8
	404767			0	6.8
25	406690	M29540	Hs.220529	CEA (carcinoembryonic antigen-related ce	6.8
	439750	AL359053	Hs.57664	ESTs	6.8
	403127	AI904493	Hs.99890	polymerase (DNA directed), delta 1, cata	6.8
	418203	X54942	Hs.83758	CDC28 protein kinase 2	6.8
	425858	AA364923		gb:EST75802 Pineal gland II Homo sapiens	6.8
30	421712	AK000140	Hs.107139	hypothetical protein	6.7
	456903	D49441	Hs.155981	mesothelin	6.7
	414564	AA164803	Hs.71994	ESTs	6.7
	457942	AW665665	Hs.153034	ESTs	6.7
	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	6.7
35	424596	AB020639	Hs.151017	estrogen-related receptor gamma	6.7
	445537	AJ245671	Hs.12844	EGF-like domain; multiple 6	6.7
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	6.6
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	6.6
	410664	NM_006033	Hs.65370	lipase, endothelial	6.6
40	428575	M19684	Hs.184929	serine (or cysteine) proteinase inhibito	6.6
	406400			kallikrein 8 (neurokinin-1)	6.6
	426317	AA312350	Hs.169294	transcription factor 7 (T-cell specific,	6.5
	441460	AI952478	Hs.226804	ESTs, Moderately similar to ALUC_HUMAN I	6.5
	412570	AA033517	Hs.74047	electron-transfer-flavoprotein, beta pol	6.5
45	424349	AF141289	Hs.145550	solute carrier family 7 (cationic amino	6.5
	448681	AL109781	Hs.21754	Homo sapiens mRNA full length insert cDN	6.4
	445258	AI635931	Hs.147613	ESTs	6.4
	456032	AW957446	Hs.301711	ESTs	6.4
	404727			0	6.4
50	422810	AA317400		gb:EST19374 Refina II Homo sapiens cDNA	6.4
	440044	AW665167	Hs.259563	EST	6.4
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	6.4
	426600	NM_003378	Hs.171014	VEGF nerve growth factor inducible	6.4
	422170	AI791949	Hs.112432	anti-Müllerian hormone	6.4
55	449611	AI970394	Hs.197075	ESTs	6.4
	402539	AW502761	Hs.30909	KIAA0430 gene product	6.3
	456983	AI081687	Hs.170225	thymopentin	6.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	6.3
	457887	AI240007	Hs.148812	ESTs	6.3
60	431765	AF124249	Hs.268541	novel SH2-containing protein 1	6.3
	420344	BE463721	Hs.97101	Putative G protein-coupled receptor GPCR	6.2
	443494	T99719	Hs.270404	Homo sapiens cDNA: FLJ22389 fis, clone H	6.2
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	6.2
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	6.2
65	413982	BE503035	Hs.279193	ESTs	6.2
	458091	AF150286		gb:AF150286 Human mRNA from cd34+ stem c	6.2
	402104			0	6.2
	428771	AB028992	Hs.193143	KIAA1069 protein	6.1
	435313	AI769400	Hs.189729	ESTs	6.1
70	441666	AI188346	Hs.301776	ESTs	6.1
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (6.1
	427308	D26067	Hs.174905	KIAA0033 protein	6.1
	423069	W15613	Hs.1613	adenosine A2a receptor	6.1
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	6.1
75	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	6.1
	449409	AI650935	Hs.301694	ESTs	6.1
	400855			0	6.1
	454692	AW813350		gb:MR3-ST0192-100100-024-g07 ST0192 Homo	6.0
80	414869	AA157291	Hs.72163	ESTs	6.0
	439662	H97552	Hs.269060	ESTs	6.0
	445181	AW338972	Hs.147471	ESTs	6.0
	437129	AL049327		gb:Homo sapiens mRNA; cDNA DKFZp564E016	6.0
	440128	AA962623	Hs.189144	ESTs, Weakly similar to NPT2_HUMAN RENAL	6.0
	443715	AI583187	Hs.9700	cyclin E1	6.0

	422355	AW403724	Hs.140	immunoglobulin heavy constant gamma 3	5.9
	405291			0	5.9
	432113	AA935065	Hs.152385	ESTs	5.9
5	441236	AA923489	Hs.130432	ESTs	5.9
	424418	BE503432	Hs.66170	HSKM-B protein	5.9
	453028	AB006532	Hs.31442	RecQ protein-like 4	5.8
	407137	T97307	Hs.199057	EST	5.8
	443462	AI064690	Hs.171176	ESTs	5.8
10	454392	BE260893		gb:601150677F1 NIH_MGC_19 Homo sapiens c	5.8
	456311	AA225632	Hs.190016	ESTs	5.8
	446501	AI302616	Hs.150819	ESTs	5.8
	433921	AA618174		gb:nq14f01.s1 NCI_CGAP_Thy1 Homo sapiens	5.8
	408615	AW444861		gb:U1-H-B13-ajz-a-04-0-UI.s1 NCI_CGAP_Su	5.8
15	459360	BE384526		gb:601277913F1 NIH_MGC_20 Homo sapiens c	5.8
	403824			0	5.8
	428187	AI687303	Hs.285529	G protein-coupled receptor 49 (GPR49)	5.8
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (raklines)	5.7
	410658	AW105231	Hs.192035	ESTs	5.7
20	426465	AI758948		gb:ty16f07.x1 NCI_CGAP_UI3 Homo sapiens	5.7
	443695	AW204099	Hs.112759	ESTs, Weakly similar to AF126780.1 retin	5.7
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	5.7
	405392			0	5.7
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	5.7
25	449796	AA004321	Hs.194397	ESTs	5.7
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	5.7
	428987	NM_004751	Hs.194710	glucosaminyl (N-acetyl) transferase 3	5.7
	404220			0	5.6
	420973	AA743415	Hs.291368	ESTs	5.6
30	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	5.6
	442549	AI751601	Hs.8375	TNF receptor-associated factor 4	5.6
	409867	AW502161		gb:U1-HF-BR0p-ajr-g-12-0-UI.r1 NIH_MGC_5	5.6
	451110	AI955040	Hs.301584	ESTs	5.6
	418216	AA662240	Hs.283099	AF15q14 protein	5.6
35	411897	AW875066		gb:RC6-PT0001-180100-021-F04 PT0001 Homo	5.6
	456181	BE264645	Hs.282093	Homo sapiens cDNA: FLJ21918 fis, clone H	5.6
	406536			0	5.6
	432540	AI821517	Hs.105866	ESTs	5.6
40	446315	NM_016293	Hs.14770	bridging Integrator 2	5.6
	443270	NM_004272	Hs.9192	Homer, neuronal immediate early gene, 1B	5.6
	451035	AU076785	Hs.430	plastin 1 (I isoform)	5.6
	406685	M18728		gb:Human nonspecific crossreacting antiq	5.5
	454590	AW809762	Hs.222056	Homo sapiens cDNA FLJ11572 fis, clone HE	5.5
	402430			0	5.5
45	446704	AI337228	Hs.197083	ESTs	5.5
	435282	AA677428	Hs.189731	ESTs	5.5
	426062	N57014	Hs.44013	ESTs	5.5
	415451	HI9415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	5.5
	456002	AI628729	Hs.191450	ESTs, Weakly similar to type II membrane	5.5
50	409613	AW444816	Hs.171537	Homo sapiens cDNA: FLJ21596 fis, clone C	5.5
	430259	BE550182	Hs.127826	RatGEF-like protein 3, mouse homolog	5.5
	434609	R76593		gb:yl60c11.r1 Soares placenta Nb2HP Homo	5.5
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	5.5
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	5.4
55	400379	NM_018432	Hs.283076	Homo sapiens ovarian cancer related prot	5.4
	436076	AI193277	Hs.120954	ESTs	5.4
	432119	T80289		gb:yd03h04.r1 Soares infant brain 1N1B H	5.4
	417175	R44558	Hs.94002	ESTs	5.4
	445774	AI254165	Hs.145504	ESTs	5.4
60	455604	BE011183		gb:PM3-BN0218-100500-003-d09 BN0218 Homo	5.4
	411426	BE141714		gb:QV0-HT0101-061059-032-c04 HT0101 Homo	5.4
	445262	AW205650	Hs.253503	ESTs	5.4
	412517	BE271584		gb:601141065F1 NIH_MGC_9 Homo sapiens cD	5.4
	434756	AA827650	Hs.259307	ESTs	5.3
65	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	5.3
	439949	AW979197	Hs.292073	ESTs	5.3
	414995	C18200		gb:C18200 Human placenta cDNA (TFujwara	5.3
	428071	AF212848	Hs.182339	transcription factor ESE-3B	5.3
	412323	AW937143		gb:PM1-DT0041-281299-001-f01 DT0041 Homo	5.3
70	434283	AW235341	Hs.59715	mouse thiamin pyrophosphokinase homolog	5.3
	447798	AI425049	Hs.119629	ESTs, Moderately similar to ALU1_HUMAN A	5.3
	401723			0	5.3
	406270			0	5.3
	452194	AI694413	Hs.298262	ESTs, Weakly similar to dJ88J8.1 [H.sapi	5.3
75	415757	AA830854	Hs.187810	ESTs	5.3
	430051	AA464611	Hs.52515	transducin (beta)-like 2	5.2
	435615	Y15065	Hs.4975	potassium voltage-gated channel, KQT-5k	5.2
	459583	AI907673		gb:L-BT152-080399-004 BT152 Homo sapien	5.2
	449009	BE044755	Hs.224812	ESTs	5.2
	424001	W67883	Hs.137476	KIAA1051 protein	5.2
80	409479	BE163800	Hs.136912	ESTs	5.2
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.s	5.2
	435928	HI64345	Hs.183961	ESTs	5.2
	447397	BE247676	Hs.18442	E-1 enzyme	5.2

5	449183	AW445022	Hs.195985	Homo sapiens cDNA: FLJ21135 fis, clone C	5.2
	410146	AW592655		gb:U45112x1 Soares_NFL_T_GBC_S1 Homo s	5.2
	458164	AJ208666	Hs.192081	ESTs	5.2
	410153	BE311926	Hs.15830	Homo sapiens cDNA FLJ12691 fis, clone NT	5.1
	439509	AF086332	Hs.58314	ESTs	5.1
	422569	BE552132	Hs.118442	cyclin C	5.1
	430664	AW969834		gb:EST381912 MAGE resequences, MAGK Homo	5.1
	411231	AW833501		gb:QV4-TT0008-091199-025-e09 TT0008 Homo	5.1
10	412194	AW900282	Hs.115412	Homo sapiens cDNA FLJ13881 fis, clone TH	5.1
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	5.1
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	5.1
	433279	AW971745		gb:EST383834 MAGE resequences, MAGL Homo	5.1
	454112	NM_000885	Hs.301806	ESTs	5.1
15	423261	Z43509		gb:HSC1EA031 normalized infant brain cDN	5.1
	434084	AJ061640	Hs.192788	hypothetical protein PRO1905	5.1
	446115	AJ733075	Hs.292682	ESTs, Weakly similar to S69913 hypertens	5.1
	416719	H79731		gb:yu81112.r1 Soares fetal liver spleen	5.1
	421462	AF016495	Hs.104624	aquaporin 9	5.1
20	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	5.1
	403383			0	5.1
	430832	AJ073913	Hs.100686	ESTs, Weakly similar to secreted cement	5.1
	436070	AK000073		gb:Homo sapiens cDNA FLJ20056 fis, clone	5.0
	416969	AI815443	Hs.283404	organic cation transporter	5.0
25	444929	AI685841	Hs.161354	ESTs	5.0
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	5.0
	439031	AF075079		gb:Homo sapiens full length insert cDNA	5.0
	414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	5.0
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	5.0
30	449986	AW864502		gb:PM4-SN0016-120400-004-b12 SN0016 Homo	5.0
	418717	AJ334430	Hs.86984	ESTs	5.0
	438769	AA830684	Hs.163426	ESTs	5.0
	441859	AW194364	Hs.128022	ESTs, Weakly similar to FIG1 MOUSE FIG-1	5.0
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase	5.0

35 TABLE 21B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accession
40		
	409615	1143425_1 AW444861 BE074994 BE074966 BE074992
45	409865	1156518_1 AW502208 AW502368 AW502148
	409867	1156530_1 AW502161 AW502587 AW502345
	410146	1178974_1 AW592655 R05927 R06916
	411094	1231982_1 BE066142 AW817074
	411231	1236356_1 AW833501 AW833506 AW833722 AW833332 AW833509 AW833511 AW833767 AW833339
	411426	1245515_1 BE141714 AW845993 AW845989
50	411897	1264907_1 AW875066 AW875079 AW875075 AW875062 AW875061 AW875074
	412323	1288770_1 AW937143 AW937150 AW937141 AW937151 AW937132 AW937160 AW937191 AW937174 AW937195 AW937173
		AW937159 AW937139 AW937171 AW937142 AW937145 AW937165 AW937163 AW937164 AW937137 AW937179
		AW937156 AW937140 AW937135 AW937170
55	412517	130281_1 BE271584 AA112511
	414484	1452830_1 BE314385
	414539	1460320_1 BE379046 BE395459
	414995	1511738_1 C18200 D76581 T82025
	416719	1611345_1 H79731 H79732
60	422731	220507_1 AL138411 AL138412 AA315860
	422810	221630_1 AA317400 AA434584
	423261	226553_1 Z43509 H09001 AA375202 AW954383
	425858	257265_1 AA364923 AW963483 BE182774 C21461
	426465	267664_1 AJ758948 AA379527 AA379948 AA379262 AW963933
	430664	321423_1 AW969834 AA528493 AA483165 AW969842
65	432119	34170_1 T80289 AF052168
	433279	361800_1 AW971745 AA581359 AA581358
	433921	377350_1 AA618174 AI114549 R36464 R36465
	434609	38950_1 R76593 AF147390 R76594
70	436070	41426_1 AK000073 AA380183 AA380181 AW963533
	437129	43343_1 AL049327 AA847105
	439031	46798_1 AF075079 H48601 H48795
	442438	542469_1 AA95998 AI916584 R61781 T77332 F07756 F08149 F07647
	448865	78535_1 R35027 R12034 BE407120
75	449034	794817_1 AJ624049 AW117770 AI858360
	449986	821463_1 AW864502 AW864369 AI678780
	454392	115882_1 BE260893 AA078319 R85057 AW803024 H85811 AA078293
	454692	1229118_1 AW813350 AW816082 AW813476 AW813383
	455604	1337197_1 BE011183 BE011170 BE011333 BE011188 BE011324 BE011161 BE011169
80	458091	472385_1 AF150286 AA835857
	459081	889426_1 W07808 AI822066
	459142	918906_1 AI903396 AI903361 AI903360

TABLE 21C

5	Pkey:	Unique number corresponding to an Eos probe set		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
10	400855	1931571	Minus	17801-18228
	400995	8099094	Plus	141186-141601
	401519	6649315	Plus	157315-157950
	401723	7656594	Plus	147273-147503
15	402104	8119072	Plus	122409-122600
	402430	9796372	Minus	62382-62552
	403378	9438244	Minus	44264-44443
	403381	9438267	Minus	26009-26178
20	403383	9438267	Minus	119837-121197
	403485	9966528	Plus	2888-3001,3198-3532,3655-4117
	403824	9798468	Plus	473-887
	404220	6706820	Plus	46107-46439
25	404727	8081050	Plus	115534-115747
	404767	7882827	Minus	23244-23759
	405291	3845420	Plus	19999-20473,20672-21036,21147-21285,21378-21667
	405392	6624069	Minus	116167-116289,118879-119030
30	406086	7107817	Plus	9418-9573
	406270	7534217	Plus	13136-13591
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
	406536	7711478	Plus	25655-25782

TABLE 22A: 430 SIGNIFICANTLY DOWN-REGULATED GENES, UTERINE CANCER VERSUS NORMAL UTERUS

Table 22A lists about 430 genes significantly down-regulated in uterine cancer compared to normal uterus. These were selected as for Table 21A, except that the numerator and denominator were switched, and the ratio was greater than or equal to 14 (i.e. 14-fold down-regulated in tumor vs. normal uterus).

40	Pkey:	Unique Eos probe set identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	Ratio of tumor vs. normal tissue			
45	Pkey	ExAccn	UnigeneID	Unigene Title	R1
	414063	H26904	Hs.75736	apolipoprotein D	93.0
	447990	BE048821	Hs.20144	small inducible cytokine subfamily A, member 14	75.7
	407815	AW373860	Hs.301716	ESTs	68.7
50	452547	AA335295	Hs.74120	adipose specific 2	61.1
	415165	AW887604	Hs.78065	complement component 7	55.1
	453655	AW960427	Hs.300878	ESTs, Moderately similar to TGR3_HUMAN TGF-BE	54.0
	429350	A1754634	Hs.131987	ESTs	52.6
55	407228	M25079	Hs.155376	hemoglobin, beta	52.0
	425869	AA524547	Hs.160318	FXFD domain-containing ion transport regulator	51.6
	416585	X54162	Hs.79386	leiomodin 1 (smooth muscle)	51.4
	408614	AL137698	Hs.46531	Homo sapiens mRNA; cDNA DKFZp434C1915 (from c	49.7
60	417542	J04129	Hs.82269	progesterone-associated endometrial protein (p	49.3
	412295	AW088826	Hs.22971	ESTs	48.0
	421998	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	47.0
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (from c	46.7
65	429707	W76631	Hs.211819	matrix metalloproteinase 23B	45.7
	416950	AL049798	Hs.80652	dermatopontin	45.6
	408221	AA912183	Hs.47447	ESTs	44.6
	406791	AJ220684	Hs.272572	hemoglobin, alpha 2	43.0
70	446500	U78093	Hs.15154	sushi-repeat-containing protein, X chromosome	42.6
	407938	AA905097	Hs.85050	phospholamban	41.1
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein)	41.0
	412524	AA417813	Hs.11177	ESTs	39.4
75	452426	AJ904823	Hs.31297	Homo sapiens cDNA: FLJ23001 fis, clone LNG002	38.6
	414290	AJ568801	Hs.71721	ESTs	38.2
	439627	BE621702	Hs.29076	Homo sapiens cDNA: FLJ21841 fis, clone HEP018	38.0
	400258		Hs.79064	deoxyhypusine synthase	37.0
80	414807	AJ738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(NAD)	36.1
	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	35.4
	407663	NM_016429	Hs.37482	COP22 for nonclathrin coat protein zeta-COP	34.3
	410286	AJ739159	Hs.61898	DKFZP586N2124 protein	33.8
85	418986	AJ123555	Hs.81796	ESTs	33.1
	409060	AJ815867	Hs.50130	necln (mouse) homolog	33.1
	436569	BE439539	Hs.278837	glutathione S-transferase M2 (muscle)	32.8
	420674	NM_000055	Hs.1327	butyrylcholinesterase	32.6
90	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, member	32.4
	450810	BE207588	Hs.25511	transforming growth factor beta 1 induced tra	31.7
	438150	AA037534	Hs.300878	ESTs, Moderately similar to TGR3_HUMAN TGF-BE	31.6

	430468	NM_004673	Hs.130699	ESTs	31.5
	453060	AW294092	Hs.21594	ESTs	31.3
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vascular	30.8
5	422126	AW973784	Hs.112028	Mississippi/NIK-related kinase	30.5
	406082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (isoform	30.3
	421639	NM_012082	Hs.297921	Homo sapiens mRNA full length insert cDNA cto	30.3
	402520				29.9
	418043	AW377752	Hs.83341	H.sapiens mRNA for tyrosine kinase receptor	29.7
10	443906	AA348031	Hs.7913	ESTs	29.7
	450958	AL137669	Hs.25700	Homo sapiens mRNA; cDNA DKFZp434M0435 (from c	29.4
	418828	AF020774	Hs.88844	Homo sapiens hair and skin epidermal-type 12-	29.4
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob dise	29.4
	429507	NM_003102	Hs.2420	superoxide dismutase 3, extracellular	29.2
	400545				29.1
15	425078	NM_002599	Hs.154437	phosphodiesterase 2A, cGMP-stimulated	29.1
	429942	AI338993	Hs.134535	ESTs	28.9
	436303	AB028998	Hs.6147	KIAA1075 protein	28.7
	419971	AA400027	Hs.296234	ESTs, highly similar to mitogen-activated pro	28.7
20	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	28.7
	452877	AI250789	Hs.32478	ESTs	28.6
	412442	AI983730	Hs.26530	serum deprivation response (phosphatidylinserin	28.6
	424378	W28020	Hs.184367	GTPase activating protein-like	28.6
	421823	N40850	Hs.28625	ESTs	27.9
25	447786	BE620810	Hs.39619	hypothetical protein LOC57333	27.6
	400023			AFFX control: 18S ribosomal RNA	27.5
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	27.2
	414134	X60188	Hs.861	mitogen-activated protein kinase 3	27.1
	428451	AW970451	Hs.98570	ESTs	26.9
30	435520	AA297990	Hs.9315	HNOEL-iso protein	26.6
	437179	AA393508	Hs.171409	serologically defined colon cancer antigen 8	26.4
	441481	AA935303	Hs.270553	ESTs	26.0
	450227	BE388192	Hs.78521	Homo sapiens cDNA: FLJ21193 fis, clone COL001	25.6
	403731				25.5
35	452814	AI092790	Hs.55016	hypothetical protein FLJ21935	25.5
	410036	R57171	Hs.57975	caldesmon 2, cardiac muscle	25.5
	416854	H40164	Hs.80296	Purkinje cell protein 4	25.4
	418421	R58620	Hs.85050	phospholamban	25.4
	407000	U12139		gb:Human alpha1(XI) collagen (COL11A1) gene,	25.3
40	421803	NM_012205	Hs.108441	3-hydroxyanthranilate 3,4-dioxygenase	25.3
	445613	BE550889	Hs.158491	ESTs	25.1
	432302	AA345857	Hs.274307	KIAA1442 protein	24.8
	420796	L34355	Hs.99931	sarcoglycan, alpha (50kD dystrophin-associate	24.8
	423720	AL044191	Hs.23388	Homo sapiens cDNA: FLJ21310 fis, clone COL021	24.7
	417302	BE245812	Hs.8941	ESTs	24.6
45	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mimecan)	24.6
	440130	AI083899	Hs.157527	ESTs	24.5
	431967	AI243653	Hs.283404	organic cation transporter	24.5
	424580	AA446539	Hs.35092	ESTs	24.4
50	406907	Z25427		gb:H.sapiens protein-serine/threonine kinase	24.2
	443745	AB039670	Hs.9728	ALEX1 protein	24.1
	429101	AW452174	Hs.173780	ESTs	23.5
	410691	AW239226	Hs.65450	reticulin 4	23.4
	408853	AW291484	Hs.254967	ESTs	23.3
55	407979	AA046306	Hs.62927	ESTs	23.1
	448619	AI867182	Hs.202255	ESTs	22.8
	424585	AA464840		gb:z43h11.1 Soares fetal_Nb2HF8_9w Ho	22.7
	407891	AA486620	Hs.41135	Endomucin 2	22.6
	407196	D11747	Hs.177415	Finkel-Biskis-Reilly murine sarcoma virus (FB	22.5
60	426990	AL044315	Hs.173094	Homo sapiens mRNA; cDNA DKFZp564H142 (from cl	22.5
	450493	M93718	Hs.166373	nitric oxide synthase 3 (endothelial cell)	22.1
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-like	22.0
	423690	AA329548	Hs.23804	ESTs	22.0
	402865				21.9
65	417387	AW021102	Hs.21509	ESTs	21.9
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	21.9
	458722			Homo sapiens cDNA: FLJ23449 fis, clone HSI058	21.8
	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	21.8
	402195				21.7
70	418213	AW978753	Hs.127327	ESTs	21.6
	440274	R24595	Hs.7122	scrapie responsive protein 1	21.6
	455818	AI733747		gb:zn86d04.y5 Stratagene lung carcinoma 93721	21.4
	420861	AI039044	Hs.88827	Homo sapiens mRNA for FLJ00033 protein, part	21.4
	405228				21.3
75	441292	AF131218	Hs.7765	chromosome 16 open reading frame 5	21.3
	432553	AA553334	Hs.211095	ESTs	21.3
	417098	AB017365	Hs.173859	frizzled (Drosophila) homolog 7	21.2
	453642	AI370936	Hs.34074	dipeptidylpeptidase VI	21.2
	405313				21.1
80	410243	D83402	Hs.289008	ESTs, weakly similar to alternatively spliced	21.1
	413186	AU077141	Hs.75231	solute carrier family 16 (monocarboxylic acid	21.1
	429954	AK000633	Hs.164476	hypothetical protein FLJ20526	21.0
	421770	AA374192	Hs.108124	ribosomal protein L41	21.0
	435265	AA779958	Hs.185932	ESTs	20.8

	430036	AL050284	Hs.227782	DKFZP586M1019 protein	20.7
	430233	AW357902	Hs.236443	Homo sapiens mRNA; cDNA DKFZp564N1063 (from c	20.7
	436130	AA341497	Hs.31408	ESTs	20.7
5	434843	R43707	Hs.133159	ESTs, Weakly similar to PIHUSD salivary proti	20.7
	429303	AW137635	Hs.44238	ESTs	20.6
	442422	AI344415	Hs.156082	ESTs	20.5
	410399	BE068889	Hs.63236	synuclein, gamma (breast cancer-specific prot	20.5
	435869	AF255910	Hs.54650	ESTs, Weakly similar to (define not availabl	20.5
10	447384	AI377221	Hs.40528	ESTs	20.5
	440510	AI733098	Hs.130800	ESTs	20.5
	445806	AL137516	Hs.13323	hypothetical protein FLJ22059	20.4
	433557	AI244368	Hs.8124	PH domain containing protein in retina 1	20.4
	435467	AW450278	Hs.91681	ESTs	20.3
15	440191	AI990417	Hs.116107	Homo sapiens genomic DNA, chromosome 21q, sec	20.2
	417511	AL049176	Hs.82223	chordin-like	20.2
	406976	M60299		gb:Human alpha-1 collagen type II gene, exons	20.1
	443547	AW271273	Hs.23767	ESTs	20.1
	417998	AW967420		gb:EST379495 MAGE resequences, MAGJ Homo sapi	20.1
20	419313	AA843387	Hs.87279	ESTs	20.1
	408322	AW181985	Hs.249986	ESTs	20.0
	448422	BE263813		gb:601194177F1 NIH_MGC_7 Homo sapiens cDNA cl	20.0
	403121				19.9
25	424198	AB029010	Hs.143026	KIAA1087 protein	19.9
	459060	H89244	Hs.79625	heterogeneous nuclear ribonucleoprotein D (AU	19.9
	457829	AI742291	Hs.210843	ESTs, Weakly similar to dJ1039K5.2 (H.sapiens	19.9
	445029	AF196481	Hs.12256	midline 2	19.9
	424362	AL137646	Hs.146001	Homo sapiens mRNA; cDNA DKFZp586F0824 (from c	19.8
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal monoa	19.7
30	413972	BE279548	Hs.162717	ESTs, Weakly similar to HPPD_HUMAN 4-HYDROXY	19.6
	435891	AW249394	Hs.5002	copper chaperone for superoxide dismutase	19.6
	447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac muscle,	19.6
	400637				19.5
	409882	AJ243191	Hs.56874	heat shock 27kD protein family, member 7 (car	19.4
35	430310	U60115	Hs.239069	four and a half LIM domains 1	19.4
	402741				19.4
	401703				19.3
	409229	H60333	Hs.251928	nuclear pore complex interacting protein	19.3
	453856	AA804789	Hs.19447	Homo sapiens mRNA for FLJ00106 protein, parti	19.3
40	430342	NM_005938	Hs.239663	myeloid/lymphoid or mixed-lineage leukemia (l	19.3
	404033				19.2
	411939	AI365585	Hs.146246	ESTs	19.2
	431227	X63755	Hs.2743	keratin, cuticle, ultrahigh sulphur 1	19.1
	452659	AA216363	Hs.262958	ESTs, Weakly similar to alternatively spliced	19.1
45	439698	AW779654	Hs.55876	ESTs	18.9
	416253	BE250659	Hs.15463	ESTs	18.9
	418556	T02850		gb:FB12A9 Fetal brain, Stratagene Homo sapien	18.9
	408877	AA479033	Hs.130315	ESTs	18.9
	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24kD	18.9
50	417054	AF017060	Hs.174151	aldehyde oxidase 1	18.8
	404654				18.8
	420174	AI824144	Hs.23912	ESTs	18.8
	400625				18.7
	406150				18.7
55	457835	BE256338	Hs.192375	ESTs, Highly similar to dJ127B20.3 (H.sapiens	18.6
	420105	AW015571	Hs.32244	ESTs	18.6
	404619	BE514535	Hs.77171	minichromosome maintenance deficient (S. cere	18.5
	423282	AL137563	Hs.126378	putative ABC transporter	18.5
	424097	M13981	Hs.1734	inhibin, alpha	18.5
60	448543	AW897741	Hs.21380	Homo sapiens mRNA; cDNA DKFZp586P1124 (from c	18.5
	427605	NM_000997	Hs.179779	ribosomal protein L37	18.4
	406535				18.4
	418947	W52990	Hs.22860	ESTs	18.4
	414323	NM_014759	Hs.239500	KIAA0273 gene product	18.3
65	457111	AA482027	Hs.142569	ESTs	18.3
	418373	AW750770	Hs.84344	CGI-135 protein	18.3
	424461	D83542	Hs.148090	cadherin 15, M-cadherin (myotubule)	18.2
	451565	NM_000897	Hs.456	leukotriene C4 synthase	18.2
	407751	BE276096	Hs.38205	from HaLa cyclin-dependent kinase 2 interacti	18.2
70	432031	AF039196	Hs.284126	hairless (mouse) homolog	18.1
	404608	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PLACE10	18.1
	451952	AW078832	Hs.226806	ESTs	18.1
	424100	AF793080	Hs.123525	ESTs, Weakly similar to NGAL RAT NEUTROPHIL G	18.1
	451509	AI969529	Hs.171637	Homo sapiens cDNA: FLJ21937 fis, clone HEP044	18.1
75	453512	AL040160	Hs.209542	ESTs, Weakly similar to B cell linker protein	18.0
	429924	W39693	Hs.226138	Homo sapiens mRNA; cDNA DKFZp566H2446 (from c	17.9
	423780	AA352013		gb:EST59935 Infant brain Homo sapiens cDNA 5'	17.9
	427030	AA397600	Hs.97531	ESTs	17.9
	439872	T81058		gb:yd26c08.r1 Soares fetal liver spleen 1NLS	17.9
80	407836	T79340	Hs.22575	Homo sapiens cDNA: FLJ21042 fis, clone CAE112	17.9
	451427	AI091441	Hs.26401	tumor necrosis factor (ligand) superfamily, m	17.9
	424462	AU076666	Hs.148101	serum constituent protein	17.9
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidylinositol	17.8
	422319	AW403342	Hs.115232	splicing factor 3a, subunit 2, 66kD	17.8

	400489			17.8
	454421	BE409759	Hs.59563	17.8
	449282	AL048056	Hs.23437	17.7
5	420495	AI338247	Hs.98314	17.7
	429790	AK001352	Hs.221737	17.7
	422795	AW897265		17.7
	427980	AA418305		17.6
	409543	AW410200		17.6
10	440206	AI762232	Hs.46794	17.6
	455904	BE156173		17.5
	427707	NM_005578	Hs.180398	17.5
	437140	AA312799	Hs.283689	17.5
	417637	AA204969	Hs.234863	17.5
15	419171	NM_002846	Hs.89655	17.4
	417808	AF177909	Hs.12828	17.4
	426232	Z70024	Hs.168157	17.4
	440747	AW297226	Hs.137840	17.4
	415307	F05232	Hs.27495	17.3
20	407049	X72632		17.3
	454054	AI336329	Hs.301519	17.3
	411085	AF022991	Hs.68398	17.3
	443104	AA088470	Hs.83135	17.2
	424106	AA412442	Hs.98132	17.2
25	446716	AA436575	Hs.16602	17.1
	448677	AI560769	Hs.227051	17.0
	434919	AI821740	Hs.116531	17.0
	401171	AA360954	Hs.27268	17.0
	456804	AA421645	Hs.139851	17.0
30	453621	AW749983		16.9
	413419	BE093686	Hs.48938	16.9
	426515	BE394222	Hs.231444	16.9
	428937	T82221	Hs.56729	16.9
	424562	AI420859	Hs.150557	16.9
35	444555	AF088886	Hs.11590	16.9
	447424	AI681105	Hs.181641	16.8
	425439	D38024	Hs.157425	16.8
	445707	AI591214	Hs.156336	16.8
	405324			16.8
40	434340	AI193043	Hs.128685	16.8
	422942	AF054839	Hs.122540	16.8
	421820	AW662990	Hs.108675	16.8
	420037	BE299598	Hs.135569	16.7
	428818	AI131291	Hs.98866	16.7
45	426485	NM_006207	Hs.170040	16.7
	404947			16.6
	412677	AW029608	Hs.17384	16.6
	401551			16.6
50	408053	AW139474	Hs.246882	16.6
	425016	AA376049	Hs.154162	16.6
	418179	X51630	Hs.1145	16.6
	418994	AA296520	Hs.89546	16.5
	457514	AA775208	Hs.136423	16.5
	426275	BE151551		16.5
55	457924	AL390142	Hs.288597	16.5
	430712	AW044647	Hs.196284	16.5
	455144	AW875942		16.4
	407524	X64985		16.4
	426712	AW173177	Hs.197755	16.4
60	429954	AI918130	Hs.21374	16.4
	446208	BE258323	Hs.225795	16.4
	442792	AI352340	Hs.131194	16.3
	420485	AF218586	Hs.288835	16.3
	426767	AA384398	Hs.192491	16.3
65	436950	L05779	Hs.113	16.3
	415195	AK000150	Hs.78185	16.3
	442197	AW837912		16.3
	433457	AA830194	Hs.199417	16.2
	402316			16.2
70	409736	AA078628		16.2
	407964	AW130334	Hs.281111	16.2
	433677	AI791912	Hs.190885	16.2
	425507	AI684745	Hs.165983	16.2
	413724	AA131466	Hs.23767	16.2
75	408922	R87388		16.1
	413055	AV655701	Hs.75183	16.1
	435977	AL138079	Hs.5012	16.1
	442208	AW296984	Hs.255595	16.1
	402426			16.0
80	412399	N53816	Hs.14394	16.0
	413200	AA127395	Hs.222414	16.0
	404597			15.9
	453143	AA382234	Hs.170121	15.9
	455984	BE177442		15.9

	416193	T25400		gb:PTH1059 HTCDL1 Homo sapiens cDNA 5'/3' sim	15.9
	407065	Y10141		gb:H.sapiens DAT1 gene, partial, VNTR	15.9
	441785	AW138139	Hs.244598	ESTs	15.9
5	413784	BE155819		gb:CM0-HT0486-220300-301-d12 HT0486 Homo sapi	15.9
	429092	AI190864	Hs.178226	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	15.8
	408499	AW205323	Hs.253475	ESTs	15.8
	453754	AW972580	Hs.172753	ESTs	15.8
	450826	U43030	Hs.25537	cardiotrophin 1	15.8
10	428486	AW583497	Hs.184604	pancreatic polypeptide	15.7
	405895				15.7
	409108	AA339443	Hs.48793	ESTs	15.7
	423334	AK000906	Hs.127273	hypothetical protein FLJ10044	15.6
	422948	AW810824	Hs.21351	ESTs	15.6
15	447852	AW504781		gb:UH-HF-BN0-atn-c-04-0-U1r1 NIH_MGC_50 Homo	15.6
	419084	AA496539	Hs.179902	transporter-like protein	15.6
	456771	AW016739	Hs.232201	ESTs	15.6
	438564	AA381553	Hs.198253	major histocompatibility complex, class II, D	15.6
	448705	H05072	Hs.124984	ESTs, Moderately similar to unnamed protein p	15.6
20	454460	X66945	Hs.748	fibroblast growth factor receptor 1 (fms-rela	15.5
	458893	BE161733	Hs.97283	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	15.5
	426759	AI590401	Hs.21213	ESTs	15.5
	453769	R35261	Hs.24947	ESTs	15.4
	434179	AI743448	Hs.116177	ESTs	15.4
25	404111				15.4
	402056				15.4
	458602	AI262208	Hs.276489	ESTs	15.3
	427530	AA405093	Hs.126519	ESTs	15.3
	414716	AF199598	Hs.97044	Kv channel-interacting protein 2	15.3
30	400632				15.3
	443918	AA305475	Hs.22660	Homo sapiens cDNA FLJ11658 fis, clone HEMBA10	15.3
	432037	AW450592	Hs.300459	ESTs	15.3
	412921	BE009345	Hs.128942	ESTs	15.3
	421905	AI680247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H.sapi	15.3
35	441704	AI458766	Hs.201988	ESTs	15.3
	414272	AI651603	Hs.46988	ESTs	15.3
	448224	R48700	Hs.20733	EH-domain containing 2	15.2
	404611	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PLACE10	15.2
	448381	D61580	Hs.21036	Homo sapiens mRNA; cDNA DKFZp434A1010 (from c	15.2
40	454719	BE006547		gb:RC2-BN0130-040400-011-b03 BN0130 Homo sapi	15.2
	446973	H95724	Hs.4283	ESTs	15.2
	457760	AA668123	Hs.134170	ESTs	15.2
	440144	AW082297	Hs.88523	ESTs	15.2
	407387	AB000895		gb:Homo sapiens mRNA for cadherin FIB1, parti	15.2
45	427850	AA416756	Hs.161051	ESTs, Moderately similar to ALU6_HUMAN ALU SU	15.2
	404244				15.1
	402859				15.1
	435487	W07343	Hs.182538	phospholipid scramblase 4	15.1
50	414213	BE297765		gb:601176246F1 NIH_MGC_17 Homo sapiens cDNA c	15.0
	455916	BE156710		gb:QV0-HT0368-310300-181-d01 HT0368 Homo sapi	15.0
	448943	AI608810	Hs.193288	ESTs	15.0
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	15.0
	454082	AF283508	Hs.63168	cell death regulator even	14.9
	453308	AW959731	Hs.32538	ESTs	14.9
55	458823	AW207574	Hs.179501	ESTs	14.9
	452532	AI905811	Hs.110757	DNA segment on chromosome 21 (unique) 2056 ex	14.9
	418464	R87580		gb:ym89h07.r1 Soares adult brain N2b4HB55Y Ho	14.9
	409473	AL137716	Hs.286567	Homo sapiens mRNA; cDNA DKFZp434D2030 (from c	14.8
	449779	AA004258	Hs.25218	ESTs, Weakly similar to ALUB_HUMAN !!! ALU C	14.8
60	457546	AA568484	Hs.153632	ESTs	14.8
	403368				14.8
	432163	AK000440	Hs.272799	hypothetical protein FLJ20433	14.8
	421531	AA713505	Hs.291769	ESTs	14.8
	428283	AI439096	Hs.25832	Homo sapiens mRNA; cDNA DKFZp564P116 (from cl	14.8
65	443528	AK001778	Hs.9547	hypothetical protein FLJ10916	14.8
	402399				14.8
	410545	U32324	Hs.54310	interleukin 11 receptor, alpha	14.8
	450300	AL041440	Hs.58210	ESTs	14.8
	403552				14.7
70	406929	U04680		gb:Human olfactory receptor (OR17-210) gene,	14.7
	436365	AW444548	Hs.163118	ESTs	14.7
	402550				14.7
	441782	AW140126	Hs.132357	ESTs	14.7
	415672	N53097	Hs.193579	ESTs	14.7
75	430582	AI215509	Hs.143954	ESTs	14.7
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (sacsin	14.7
	432683	AW995441	Hs.10475	ESTs	14.7
	441871	AI306150	Hs.153450	ESTs, Weakly similar to 1909123A Na glucose c	14.6
	447481	AF052151	Hs.18686	Mouse Mammary Tumor Virus Receptor homolog	14.6
80	405114				14.6
	401082				14.6
	454316	AW366144		gb:QV0-HT0101-061099-032-b12 HT0101 Homo sapi	14.6
	421572	AA531607	Hs.125143	ESTs, Weakly similar to POL2 MOUSE RETROVIRUS	14.6
	424591	R55704	Hs.150968	hypocretin (orexin) receptor 1	14.6

5	441503	AW172263	Hs.185202	ESTs	14.6
	416199	R83537		gb:yq12a08.r1 Soares fetal liver spleen 1NFLS	14.6
	420360	U83171	Hs.97203	small inducible cytokine subfamily A (Cys-Cys	14.6
	425126	N32759	Hs.172944	chorionic gonadotropin, beta polypeptide	14.5
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, member	14.5
10	405100				14.5
	454012	M76424	Hs.37014	carbonic anhydrase VII	14.5
	402457				14.5
	454613	AW810814		gb:MR2-ST0129-201099-004-e01 ST0129 Homo sapi	14.5
	429821	AL096749	Hs.225433	Homo sapiens mRNA; cDNA DKFZp434G153 (from cl	14.5
15	431073	BE254470	Hs.249186	cone-rod homeobox	14.5
	421143	AB024536	Hs.102171	immunoglobulin superfamily containing leucine	14.5
	401223				14.4
	438627	AJ087335	Hs.123473	ESTs	14.4
	407124	R08160	Hs.268857	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAM	14.4
20	437217	AW779241	Hs.155316	ESTs	14.4
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G protein	14.4
	410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-bisphosp	14.4
	413237	AI468574	Hs.171965	ESTs	14.4
	412975	T70956	Hs.75106	clusterin (complement lysis inhibitor, SP-40,	14.4
25	426488	X03350	Hs.4	alcohol dehydrogenase 2 (class I), beta polyp	14.4
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519	14.4
	405479				14.3
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedin C)	14.3
	426316	NM_002430	Hs.301852	Human DNA sequence from clone 437G10 on chrom	14.3
30	412171	AW897452		gb:CMD-NN0058-150400-337-b08 NN0058 Homo sapi	14.3
	447241	BE382838	Hs.19322	ESTs	14.3
	402100				14.2
	438286	AW139266	Hs.134807	Homo sapiens cDNA FLJ12057 fis, clone HEMBB10	14.2
	407947	AJ500332	Hs.102367	ESTs, Weakly similar to hTcf-4 [H.sapiens]	14.2
35	402275				14.2
	402358				14.2
	439624	AA838771	Hs.124407	ESTs	14.2
	444455	AI149879	Hs.175024	Homo sapiens cDNA: FLJ23447 fis, clone HSI033	14.2
	455314	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	14.2
40	427872	AA835058	Hs.21111	ESTs	14.2
	409826	AW501112	Hs.34487	hypothetical protein FLJ23412	14.2
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene homolo	14.2
	426882	AI014545	Hs.231027	EST	14.1
	457033	AF029674	Hs.173422	KIAA1605 protein	14.1
45	410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	14.1
	401007				14.1
	458274	AF149297	Hs.8087	NAG-5 protein	14.1
	454106	D19687	Hs.245146	ESTs	14.1
	432928	AA570454	Hs.186467	ESTs, Moderately similar to ALU1_HUMAN ALU SU	14.1
50	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin) bet	14.1
	433887	AW204232	Hs.279522	ESTs	14.1
	434927	H46612	Hs.293815	ESTs, Weakly similar to PLM_HUMAN PHOSPHOLEMM	14.1
	404282				14.1
	422581	NM_016339	Hs.118562	Link guanine nucleotide exchange factor II	14.0
55	424823	NM_006226	Hs.153322	phospholipase C, epsilon	14.0
	408107	AA806754	Hs.62835	ESTs	14.0
	401577				14.0
	433883	AI925688	Hs.222312	ESTs, Weakly similar to B24264 prolins-rich p	14.0
	408104	AW972927	Hs.293968	ESTs	14.0
60	404642				14.0
	400675				14.0
	406059				14.0
	448386	AB037750	Hs.21061	KIAA1329 protein	14.0
	407287	AI578812	Hs.201658	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAM	14.0

TABLE 22B

65	Key:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
70	Key	CAT number	Accession	
	408922	109017_1	R87388 R84328 AA058916	
	409543	1138723_1	AW410200 AW409705 AW411433 BE296786 BE270309	
75	409736	115189_1	AA078628 R09051 AA078197 AA077334 AW748808 AW748807	
	412171	1280759_1	AW897452 Z20302 D55805 D52877 D60432	
	413784	1389150_1	BE165819 BE165853 W01386	
80	414213	1426375_1	BE297765 BE262051 BE302686 T83915	
	416193	1577102_1	T25400 H26834 H44554 R73193	
	416199	1577561_1	R83537 W80940 H27368	
	417998	171375_1	AW967420 AA210915 AA236991 AA210916	
	418464	1759038_2	R87580	
	418556	1767866_1	T02850	
	422796	221500_1	AW897265 AW897274 AL119504 AW897275 AW897270 AW897312 AW897318 AW897317 AA317240 AW961361	
			T06241 AA326794 AL138130 AW407975 AW999277	
	423780	231952_1	AA352013 AA330878 AA339379 AW966303	

5	424585	241151_1	AA464840 AA343628
	426275	263712_1	BE151551 AA373783 BE182852 BE008826 BE008827 BE008781 BE008699
	427980	285225_1	AA418305 AI264351
	439872	47823_1	T81058 AL357200 T70270
	442197	535550_1	AW837912 AW837934 AA984475 AW997490
	447852	73973_1	AW504781 BE620394
	448422	762770_1	BE263813 BE253504 AJ500202 BE251145
	453621	974526_1	AW749983 AL045823
10	454316	1109350_1	AW366144 AW366154 AW366142 AW366151 AW366140 AW366155 BE141715 BE141718 BE141698
	454613	1226904_1	AW810814 AW810787 AW810854 AW810773 AW810735 AW810785 AW810660 AW810834 AW810874 AW810723
	454719	1230546_1	AW810881 AW810791 AW810844 AW810659 AW810676
	455144	1254914_1	BE006547 AW815578 AW815311 AW856304
	455818	137219_1	AW875942 AW858234 AW875938 AW875941 AW858235 AW875958
15	455904	1382290_1	AI733747 AA129802
	455916	1382748_1	BE156173 BE156305 BE156196
	455984	1397288_1	BE156710 BE156726 BE156712
			BE177442 BE177439 BE177445 BE177440 BE177448 BE177444 BE177433
20	TABLE 22C		
	Pkey:	Unique number corresponding to an Eos probeset	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.	
25	Strand:	Indicates DNA strand from which exons were predicted.	
	NI_position:	Indicates nucleotide positions of predicted exons.	
	Pkey	Ref	Strand NI_position
30	400489	8954013	Plus 131475-131652
	400545	9800107	Minus 124618-124881
	400625	7228177	Minus 117266-117441
	400632	3818355	Plus 72875-73447,75874-76425
	400637	8894326	Plus 68901-69507
35	400675	8118750	Plus 11223-11816
	401007	8117333	Minus 140821-141050
	401082	3242744	Plus 22937-23494,27677-27966
	401223	8099088	Plus 148940-150214
	401551	8096896	Minus 189824-190728
40	401577	9280797	Minus 139377-139674,141195-141281,142217-142340
	401703	4826475	Plus 135-1229
	402056	8084234	Plus 207002-207288
	402100	8117697	Plus 133649-133792
	402195	7689778	Minus 147901-148884
45	402275	2935596	Minus 31065-31233,33680-33771,34345-34411,38890-39125,39779-39943
	402316	7527774	Minus 10751-10919,18817-19052,22131-22328
	402358	8886976	Minus 131788-132729
	402399	1905915	Minus 24502-24666,24986-25102
	402426	9796361	Minus 73590-73824
50	402457	9796782	Minus 16513-16577,16838-16926
	402520	7596899	Minus 171761-171996
	402550	7652009	Minus 80413-80673
	402741	9212200	Minus 18603-18760,19179-19890
	402865	9716300	Plus 3197-3429,3722-3914,5795-5987,6802-6961,8653-8815,9292-9660
55	402959	9368493	Plus 36729-37084
	403121	9180223	Plus 4059-4258
	403368	4388738	Plus 70286-70429,75165-75258
	403552	6862638	Minus 117504-117662
	403731	7543752	Minus 144000-144618
60	404033	8122195	Plus 7976-8156
	404111	9408736	Plus 161506-161781
	404244	5672609	Minus 98173-98517
	404282	2276311	Plus 61503-62205
	404597	9958262	Minus 114369-114599
65	404642	9796810	Plus 102999-103145
	404654	9797010	Plus 6275-6527
	404947	7382205	Plus 29740-30105,30176-30412
	405100	8076846	Plus 144114-144234
	405114	8096938	Minus 97013-97560
70	405228	7248990	Plus 92234-95905
	405313	3638954	Plus 68924-69093
	405324	3342751	Minus 5475-5677
	405479	6453391	Plus 1668-1844
	405895	7677903	Minus 66990-67484
75	406059	9103984	Minus 13856-14004
	406150	9886026	Minus 59331-59701
	406535	7711477	Plus 83135-83362

80 TABLE 23A: 626 genes upregulated in uterine cancer relative to normal body tissues

Table 23A lists about 626 genes upregulated in uterine cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59580 probesets on the Eos/Affymatrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis

was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

5	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar accession number, GenBank accession number
	UniGeneID:	UniGene number
	Pred.Prod.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
10	UniGene Title:	UniGene gene title
	R1	95th percentile of uterine cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator
15	Pkey; ExAccn; UniGeneID; Unigene Title; Pred.Prod.Domains; R1	
		428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrilysin, ; Peptidase_M10; 35.11
		420440; NM_002407; Hs.97644; mammaglobin 2; Uteroglobulin; 22.80
20		439335; AA742697; Hs.62492; NM_052863; Homo sapiens secretoglobulin, fa; none; 21.66
		425723; NM_014420; Hs.159311; dickkopf (Xenopus laevis) homolog 4; none; 21.11
		421481; AW391972; Hs.104696; KIAA1324 protein; none; TM=M; SS=M; 20.20
		437938; AI950087; Hs.369628; gb:wg05c02.x1 NCI_CGAP_Kid12 Homo sapien; none, none; 19.83
		406687; M31126; Hs.352054; matrix metalloproteinase 11 (stromelysin; hemopexin; Peptidase_M10; 17.68
25		446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin, ; Osteopontin; 17.60
		418281; U09550; Hs.1154; oviductal glycoprotein 1, 120kD (mucin 9; Glyco_hydro_18; TM=M; SS=M; 17.48
		431130; NM_006103; Hs.2719; HE4; epididymis-specific, whey-acidic pr; wap; TM=M; SS=Y; 16.59
		400301; X03635; Hs.1657; estrogen receptor 1; F-box, hormone_rec, zf-C4, OestL_recep, adh_zinc, ketoacyl-synt, pp-binding, AcylL_transl, Thioesterase, ketoacyl-synt, C_AAA, E7, RFX_DNA_binding; TM=M; SS=N; 16.11
30		419356; AI656166; Hs.7331; hypothetical protein FLJ22316; Asparaginase_2, none; 15.90
		433222; AW514472; Hs.238415; dickkopf (Xenopus laevis) homolog 4; none, PHO4; 15.39
		417931; W95642; Hs.82961; trefoil factor 3 (intestinal); trefoil; 15.39
		400284; ; NM_000125; Homo sapiens estrogen receptor; hormone_rec, zf-C4, OestL_recep; TM=M; SS=M; 15.23
		456662; NM_002448; Hs.1494; msh (Drosophila) homeo box homolog 1 (fo; homeobox, none; 15.04
35		438817; AI023799; Hs.163242; ESTs; none, none; 13.72
		453857; AL080235; Hs.35881; Ras-induced senescence 1 (RIS1); none; TM=Y; SS=M; 13.67
		424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2, hemopexin, Peptidase_M10; 13.51
		458627; AW088642; Hs.97984; SRY (sex determining region Y)-box 17 (S; HMG_box; TM=M; SS=N; 13.44
		410001; AB041036; Hs.57771; kallikrein 11; trypsin; TM=M; SS=M; 13.41
40		421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans_K_tetra, asp; 13.27
		449048; Z45051; Hs.22920; similar to S68401 (cattle) glucose induc; Lamp; TM=M; SS=M; 12.76
		436972; AA284679; Hs.25640; claudin 3; PMP22_Claudin; TM=Y; SS=M; 12.59
		450693; AW450461; Hs.203965; ESTs; Sema, lg, none; 12.52
		415457; AW081710; Hs.7369; Homo sapiens testes specific A2 homolog ; MORN_sugar_tr; TM=Y; SS=M; 12.46
45		413719; BE439580; Hs.75498; small inducible cytokine subfamily A (C; IL8; 12.23
		431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clo; none; TM=M; SS=Y; 12.09
		417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK; TM=M; SS=Y; 12.08
		407786; AA687538; Hs.38972; tetraspan 1; transmembrane4; TM=Y; SS=M; 11.91
		444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 11.86
50		446608; N75217; Hs.175622; ESTs; Armadillo_seg, HEAT_PBS; TM=M; SS=M; 11.72
		447835; AW591623; Hs.164129; ESTs, Weakly similar to I38022 hypothetical; none, UO_con; 11.59
		420181; AI380089; Hs.158951; ESTs; none, lg, pkinase, LRR_LRRCT; 11.49
		451253; H48299; Hs.26126; claudin 10; PMP22_Claudin, Peptidase_M1_K_tetra; TM=Y; SS=M; 11.45
		453968; AA847843; Hs.62711; High mobility group (nonhistone chromoso; HMG_box, none; 11.42
55		448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec, MIP; TM=M; SS=M; 11.37
		421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz, NTR; 11.08
		452367; U71207; Hs.29279; eyes absent (Drosophila) homolog 2; Hydrolase; 11.01
		409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm_1, zf-C3HC4, tn3, SPRY, KRAB, zf-C2H2, rve, zf-B_box; TM=Y; SS=M; 10.95
		415138; C18356; Hs.295944; tissue factor pathway inhibitor 2; Kunitz_BPTI, none; 10.91
60		416658; U03272; Hs.79432; fibrillin 2 (congenital contractural ara; EGF, TB, granulin, PSI, E8, TIL; TM=M; SS=M; 10.81
		411556; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A receptor; Neur_chan_LBD, Neur_chan_membr; TM=Y; SS=M; 10.72
		438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec, zf-C4, none; 10.66
		425071; NM_013989; Hs.154424; deiodinase, iodothyronine, type II; T4_deiodinase; TM=M; SS=Y; 10.66
		430832; AI073913; Hs.100688; ESTs, Weakly similar to JE0350 Anterior; none, none; 10.52
65		451497; H83294; Hs.284122; Wnt inhibitory factor-1; EGF, WIF; 10.50
		421478; AI683243; Hs.97258; ESTs, Moderately similar to S29539 ribos; none, none; 10.50
		409231; AA446644; Hs.692; GA733-2 antigen; epithelial glycoprotein; thyroglobulin_1; TM=Y; SS=M; 10.35
		443785; AW449952; Hs.180125; basic-helix-loop-helix-PAS protein; HLH_PAS; TM=M; SS=N; 10.34
		409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran, M_SMC_N, SMC_C, DUF164, none; 10.34
70		431846; BE019924; Hs.271580; uropod 1B; transmembrane4; TM=Y; SS=M; 10.34
		415539; AI733881; Hs.72472; NAME OMITTED ... receptor kinase; pkinase, Activin_rec, PDZ_ZU5, death; 10.31
		411274; NM_002776; Hs.69423; kallikrein 10; trypsin; TM=M; SS=N; 10.24
		423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage ; hemopexin, Peptidase_M10; TM=M; SS=M; 10.24
		441377; BE218239; Hs.202656; ESTs; none, none; 10.17
75		400292; AA250737; Hs.72472; NAME OMITTED ... receptor kinase; pkinase, Activin_rec, PDZ_ZU5, death; 10.17
		452594; AU076408; Hs.29981; solute carrier family 26 (sulfate transp; xan_ur_permease, Sulfate_transp, STAS, HMG_box; 10.12
		429663; M68874; Hs.211587; phosphatase A2, group IVA (cytosolic ; C2_PLA2_B; TM=M; SS=N; 9.87
		413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kin; SAM_PNT, none; 9.87
		408562; AI436323; Hs.31141; roundabout (axon guidance receptor; Dros; lg, tn3; TM=M; SS=N; 9.86
80		428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7tm_3; TM=Y; SS=M; 9.72
		438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec, zf-C4, none; 9.68
		411089; AA456454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none, none; 9.53
		450451; AW591528; Hs.202072; ESTs; none, none; 9.53
		456052; AI866286; Hs.71962; ESTs, Weakly similar to B36298 protine-r; none, none; 9.50

- 418113; AI272141; Hs.83484; SRY (sex determining region Y)-box 4; HMG_box,homeobox;TM=M;SS=N; 9.38
 412791; AI131192; Hs.143199; ESTs, Weakly similar to S72481 probable; plkinase,PBD,none; 9.36
 432435; BE218886; Hs.282070; ESTs; none,none; 9.35
 5 416530; U62801; Hs.79361; kallikrein 6 (neurosin, zyme); trypsin;TM=M;SS=M; 9.32
 439018; AW300887; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.23
 445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; EGF_MAM; 9.19
 410407; X66839; Hs.63287; carbonic anhydrase IX; carb_anhydrase;TM=M;SS=M; 9.19
 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp,STAS,HMG_box; 9.17
 10 453459; BE047032; Hs.257789; ESTs; none,none; 9.14
 431674; AA098901; Hs.301642; G-protein coupled receptor; none,GCV_H; 9.05
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member; aldedh;TM=M;SS=M; 9.00
 413278; BE563085; Hs.833; Interferon-stimulated protein, 15 kDa; ublquitin; 8.93
 436954; AA740151; Hs.130425; ESTs; none,none; 8.91
 15 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 8.89
 425397; AI10488; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisomV,HATPase_c; 8.85
 407792; AI077715; Hs.39384; putative secreted ligand homologous to f; none;TM=M;SS=Y; 8.80
 451027; AW519204; Hs.40808; Homo sapiens, Similar to RIKEN cDNA 2810; none,none; 8.79
 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; IQ;TM=M;SS=N; 8.72
 20 413385; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxygenase; IDO;TM=M;SS=N; 8.70
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodi; Somatomedin_B,Endonuclease,Phosphodiast;TM=Y;SS=M; 8.69
 421502; AF111856; Hs.105039; solute carrier family 34 (sodium phosphat; Ribosomal_L20,Na_Pi_cotrans;TM=Y;SS=N; 8.67
 437935; AW939591; Hs.5940; mucin 13, epithelial transmembrane; EGF_SEA;TM=Y;SS=M; 8.56
 408692; AL040127; Hs.34074; dipeptidylpeptidase VI; DPPIV_N_term,Peptidase_S9,none; 8.55
 25 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 8.53
 428187; AJ687303; Hs.285529; G protein-coupled receptor 49; 7tm_1,none; 8.49
 448672; AI955511; Hs.374290; ESTs; lig_chan,ANF_receptor,SBP_bac_3;TM=Y;SS=M; 8.44
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm_2,HRM;TM=Y;SS=M; 8.40
 443428; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M;SS=N; 8.40
 30 452093; AA447453; Hs.27860; Homo sapiens mRNA; cDNA DKFZp586M0723 (l; 7tm_1,none; 8.33
 407894; J278313; Hs.41143; phosphoinositide-specific phospholipase; C2,PI-PLC-Y,PI-PLC-X;TM=M;SS=N; 8.23
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M;SS=N; 8.21
 419508; AW997939; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=M; 8.20
 424441; X14850; Hs.147097; H2A histone family, member X; histone,CBFD_NFYB_HMF; 8.20
 408243; Y00787; Hs.624; interleukin 8; IL8;TM=M;SS=N; 8.00
 35 415752; BE314524; Hs.78776; putative transmembrane protein; none;TM=Y;SS=N; 7.99
 422608; AW160644; Hs.118895; potassium voltage-gated channel, subfam; ion_trans,K_tetra;TM=Y;SS=N; 7.99
 433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; none; 7.95
 409649; AA159216; Hs.55505; hypothetical protein FLJ20442; Y_phosphatase,DSPT;TM=M;SS=N; 7.95
 424078; AB006625; Hs.139033; paternally expressed 3; zf-C2H2,KRAB,none; 7.86
 40 432179; X75208; Hs.2913; EphB3; EPH_lbd,fn3,plkinase,SAM;TM=Y;SS=M; 7.85
 424581; M62062; Hs.150917; catenin (cadherin-associated protein), alpha Vinculin,DNA_ligase_ZBD;TM=M;SS=N; 7.84
 420610; AI683183; Hs.99348; distal-less homeo box 5; homeobox;TM=M;SS=N; 7.81
 436856; AI469355; Hs.127310; ESTs; plkinase,rrm;TM=M;SS=N; 7.81
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 7.80
 45 407811; AW190902; Hs.40098; cysteine knot superfamily 1, BMP antagon; TGF-beta,DAN; 7.78
 424399; AJ905687; Hs.348419; AI905687:IL-BT095-190199-019 BT095 Homo; none;TM=M;SS=M; 7.65
 418836; AI655499; Hs.161712; ESTs; plkinase,Activin_rec,PDZ_ZUS,death; 7.64
 435793; AB037734; Hs.4993; KIAA1313 protein; none;TM=M;SS=N; 7.61
 426201; AW182614; Hs.128499; ESTs; SH3,none; 7.59
 50 447400; AK000322; Hs.18457; hypothetical protein FLJ20315; zf-C3HC4;TM=Y;SS=M; 7.55
 410850; AW362867; Hs.302736; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp,STAS,HMG_box; 7.55
 453464; AI884911; Hs.32989; receptor (calcitonin) activity modifying; none;TM=Y;SS=N; 7.54
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypept; Sm,plkinase; 7.52
 55 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC,none; 7.38
 443991; NM_002250; Hs.10082; potassium intermediate/small conductance; CaMBD,SK_channel,ion_trans;TM=Y;SS=M; 7.36
 414617; AI339520; Hs.288817; ESTs, Moderately similar to N Chain N, M; hexokinase,hexokinase2;TM=Y;SS=N; 7.35
 422017; NM_003877; Hs.110776; STAT induced STAT inhibitor-2; SH2; 7.33
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none,none; 7.30
 60 409041; AB033025; Hs.50081; Hypothetical protein, XP_051860 (KIAA119; none;TM=M;SS=M; 7.28
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; 7.28
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPT,Y_phosphatase,Ribosomal_S3_N;TM=M;SS=N; 7.28
 418506; AA084248; Hs.372651; Unknown protein for MGC:29643 (formerly; none,none; 7.27
 448913; AA194422; Hs.22564; myosin VI; rrm,zf-RanBP,plkinase,GST_C,Elts,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,FTLS,AT_hook,SAM;TM=M;SS=N; 7.26
 65 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBO,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 7.26
 424317; AI865032; Hs.26017; ESTs; none,plkinase; 7.21
 410361; BE391804; Hs.62661; guanylate binding protein 1, Interferon-; GBP,GBP_C;TM=Y;SS=M; 7.21
 70 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,plkinase;TM=M;SS=N; 7.14
 438707; L08239; Hs.5326; amino acid system N transporter 2; porcu; ACAT,MBOAT;TM=Y;SS=M; 7.05
 423011; NM_000683; Hs.123022; adrenergic, alpha-2C, receptor; 7tm_1;TM=Y;SS=M; 7.03
 435021; AA922192; Hs.73962; ESTs; EPH_lbd,plkinase,fn3,SAM,none; 7.02
 446163; AA026880; Hs.25252; prolactin receptor; none;NA,NA; 7.01
 75 447768; X86400; Hs.19520; FXYD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=M;SS=N; 7.00
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoaE;TM=M;SS=N; 6.99
 451035; AU076785; Hs.430; plasmin 1 (l isoform); ehand,CH,Adaplin_N; 6.99
 450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta,TGFb_propeptide; 6.95
 424054; AA334511; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 6.93
 80 432519; AI221311; Hs.130704; ESTs, Weakly similar to BCHUA S-100 pro; none,none; 6.93
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-con; UQ_con;TM=M;SS=N; 6.92
 419893; AA133749; Hs.301350; FXYD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 6.92
 437139; W73685; Hs.118513; ESTs, Weakly similar to RTA RAT PROBABLE; 7tm_1;TM=Y;SS=M; 6.87
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 6.87

- 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 6.86
 410467; AF102546; Hs.63931; dachshund (Drosophila) homolog; Ski_Sno; TM=M; SS=M; 6.86
 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin, hemopexin, Peptidase_M10); 6.85
 453064; R40334; Hs.89463; potassium large conductance calcium-act; none; none; 6.83
 452046; AB018345; Hs.27657; KIAA0802 protein; none; TM=M; SS=N; 6.79
 417771; AA804698; Hs.82547; retinoic acid receptor responder (lazarus); none; none; 6.79
 422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glut; aldedh, aakkinase; TM=M; SS=N; 6.77
 431470; AA832417; Hs.139650; ESTs; none; ig, pkinase, LRR, LRRCT; 6.76
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none; none; 6.75
 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory su; SH2; none; 6.74
 417886; AA214584; ; ESTs; SPRY, 7tm_3, ANF_receptor; none; 6.72
 412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C; MARCKS; 6.70
 437960; AI669586; Hs.369312; ESTs; none; none; 6.68
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily; 60s_ribosomal, Ribosomal_L10, TNFR_c6, DEAD; 6.66
 444006; BE395085; Hs.334762; type I transmembrane protein Fn14; kd_recept_a, PKD, MHC, I; TM=M; SS=Y; 6.65
 413040; AA183338; Hs.12321; sodium calcium exchanger; Na_Ca_Ex; TM=Y; SS=M; 6.64
 449656; AA002008; Hs.188633; ESTs; PIP5K; none; 6.64
 447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-induc; pyr_redox; TM=M; SS=N; 6.62
 446063; AI720140; Hs.151079; ESTs; ISK_Channel; none; 6.61
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor; none; none; 6.60
 421554; AW137676; Hs.97775; ESTs; none; none; 6.59
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank; 6.55
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; SS=N; 6.54
 448730; AB032983; Hs.21894; KIAA1157 protein; PP2C; TM=M; SS=N; 6.54
 433577; AW007080; Hs.284192; ESTs; none; none; 6.53
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fascidin, ABC_tran, ABC_membrane, GTP_EFTU; TM=M; SS=M; 6.53
 442133; AW874138; Hs.129017; ESTs; type Ia transmembrane protein; LRR, LRRNT, LRRCT; TM=Y; SS=M; 6.52
 430259; BE550182; Hs.375142; RafGEF-like protein 3, mouse homolog; fn3, RA, RasGEF; TM=M; SS=M; 6.52
 434263; N34895; Hs.79187; ESTs; ig; none; 6.49
 418322; AA284168; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase, DSPc; TM=M; SS=N; 6.48
 419942; U25138; Hs.93841; potassium large conductance calcium-act; CaKB; TM=Y; SS=M; 6.47
 421064; AI245432; Hs.101382; tumor necrosis factor, alpha-induced pro; none; TM=M; SS=N; 6.47
 432636; AA340884; Hs.278562; claudin 7; PMP22_Claudin; TM=Y; SS=M; 6.45
 431685; AW296135; Hs.267659; vav 3 oncogene; CH, DAG_PE-bind, PH, RhoGEF, SH2, SH3, DC1; TM=M; SS=N; 6.44
 428832; AA578229; Hs.324239; ESTs; Moderately similar to ZN91_HUMAN Z; Osteopontin; none; 6.39
 436775; AA731111; Hs.372225; ESTs; none; none; 6.39
 424343; AW956360; Hs.4748; adenylate cyclase activating polypeptid; 7tm_2, HRM; none; 6.37
 421071; AI311238; Hs.104476; ESTs; Weakly similar to CGHU1E collagen; none; TM=Y; SS=M; 6.37
 438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nuclear trans; HLH, PAS, IL8; TM=M; SS=N; 6.37
 438953; AA828995; ; gb:0077b08.s1 NCI_CGAP_Ov2 Homo sapiens; EGF, metalthio, integrin_B, PSI; none; 6.27
 406400; ; kallikrein 8 (neuropsin/ovasin) (KLK8); trypsin; TM=M; SS=M; 6.27
 429556; AW139399; Hs.314807; ESTs; none; TM=M; SS=N; 6.26
 409269; AA576953; Hs.22972; steroid 5 alpha-reductase 2-like; H5AR g; Steroid_dh; TM=Y; SS=M; 6.25
 435732; AF229178; Hs.123136; leucine rich repeat and death domain con; none; none; 6.24
 439568; AI091277; Hs.302634; frizzled (Drosophila) homolog 8; Frizzled, Fz, 7tm_2, toxin_2; TM=Y; SS=M; 6.24
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (; MIF, sugar_tr; none; 6.23
 436961; AW375974; Hs.156704; ESTs; none; none; 6.23
 434808; AF155108; Hs.256150; NY-REN-41 antigen; none; TM=M; SS=N; 6.22
 440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-I; AAA, NB-ARC, PAAD_DAPIN; NA; NA; 6.20
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; ehand; 6.20
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49, EGF, ig, Neureguin; TM=M; SS=N; 6.19
 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4; TM=Y; SS=M; 6.19
 452551; L27071; Hs.29877; TXK tyrosine kinase; Beach, WD40, SH2, SH3, pkinase; TM=M; SS=N; 6.14
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3; TM=M; SS=N; 6.12
 454562; AA378776; Hs.288649; hypothetical protein MGC3077; none; 6.11
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; UJM, PDZ, pkinase; 6.11
 449700; L02867; Hs.78358; paraneoplastic antigen; none; TM=M; SS=N; 6.10
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to; pkinase, ICE_p10, ICE_p20; TM=M; SS=M; 6.10
 416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient, yeast; h; HORMA; TM=M; SS=N; 6.09
 433159; AB035898; Hs.150587; kinesin-like protein 2; bZIP, kinesin; 6.08
 432432; AA541323; Hs.115831; ESTs; ig, Sema, PSI; none; 6.07
 409619; AK001015; Hs.55220; BCL2-associated athanogene 2; BAG; TM=M; SS=N; 6.04
 412723; AA648469; Hs.335951; hypothetical protein AF301222; none; TM=M; SS=N; 6.03
 424273; W40460; Hs.144442; phospholipase A2, group X; phoslip; TM=M; SS=Y; 6.03
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc, Rhodanese; none; 6.00
 421143; AB024538; Hs.102171; immunoglobulin superfamily containing le; ig, LRR, LRRNT, LRRCT; TM=M; SS=M; 6.00
 428677; AI657119; Hs.351582; troponin I, cardiac; none; TM=M; SS=N; 6.00
 450098; W27249; Hs.8109; hypothetical protein FLJ21080; SET, zf-MYND; TM=M; SS=N; 6.00
 410422; AL042014; Hs.63348; Homo sapiens, clone MGC:15203, mRNA, cont; C1q, Collagen; 5.99
 419972; AL041465; Hs.182982; golgin-67; none; none; 5.99
 421251; Z28913; Hs.102948; enigma (UIM domain protein); UIM, PDZ; 5.97
 403362; ; NM_001615; Homo sapiens actin, gamma 2; actin; 5.95
 451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg; TM=M; SS=N; 5.95
 420253; AI656055; Hs.96200; neighbor of A-kinase anchoring protein 9; none; NA; NA; 5.93
 421506; BE302798; Hs.105097; thymidine kinase 1, soluble; TK; TM=M; SS=N; 5.93
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2; TM=M; SS=N; 5.92
 450747; AI064821; Hs.129953; ESTs; Highly similar to 1818357A EWS gen, rm, zf-RanBP, GAS2; 5.92
 415211; R64730.comp; Hs.156986; DEAD/H (Asp-Glu-Ala-Asp/His) box polypep; DEAD, helicase_C, rm, Ndr, Cys_knot, TIL, vwa, vwc, wwd, IQ, Rila, abhydrolase, TGF-beta, DUF139, TPR, DSPc, lsp_1, Ribosomal_S21, rvp; TM=M; SS=N; 5.91
 429910; NM_000867; Hs.2507; 5-hydroxytryptamine (serotonin) receptor; 7tm_1; TM=Y; SS=N; 5.90
 447131; NM_004585; Hs.17468; retinoic acid receptor responder (lazarus); none; TM=Y; SS=N; 5.89
 437952; D63209; Hs.5944; solute carrier family 11 (proton-coupled; none; TM=Y; SS=M; 5.89
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT; TM=M; SS=Y; 5.89

- 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz, Frizzled, 7tm_2; TM=Y; SS=M; 5.87
 426761; AI015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing me; none; TM=Y; SS=M; 5.85
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none; TM=M; SS=Y; 5.85
 426108; AA622037; Hs.166468; programmed cell death 5; DUF122; TM=M; SS=N; 5.84
 5 450502; T08065; Hs.118262; ESTs; ion_trans, ion_trans; 5.84
 442652; AI005163; Hs.201378; Homo sapiens cDNA FLJ40427 f1s; none; TM=M; SS=N; 5.83
 424917; AI636208; Hs.96901; hypothetical protein FLJ23049; none; TM=M; SS=N; 5.83
 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2, STAT, STAT_bind, STAT_prot; TM=M; SS=N; 5.82
 10 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS, AIRS_C; TM=M; SS=N; 5.82
 445133; AW157646; Hs.198689; ESTs; ehfand, spectrin, GAS2, SH3, Plectin, RA_Xylose_isom, FfD, bZIP, Tropomyosin, Myc-LZ, Mldh_C, CHAIP3; TM=M; SS=N; 5.79
 426215; AW963419; Hs.155223; stanniocalcin 2; Stanniocalcin; 5.78
 414482; SS7498; Hs.76252; endothelin receptor type A; 7tm_1; TM=Y; SS=M; 5.75
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA; TM=Y; SS=N; 5.74
 15 452683; AI089575; Hs.374574; progesterone membrane binding protein; homeobox; none; 5.72
 422201; AI538613; Hs.298241; Transmembrane protease, serine 3; btl_recept_a, trypsin; TM=Y; SS=M; 5.72
 429345; R11141; Hs.199695; hypothetical protein; K_tetra, SAM; 5.72
 449458; AI805078; Hs.208261; ESTs; Frizzled, Fz; none; 5.72
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic); none; TM=Y; SS=M; 5.71
 10 418848; AI820961; Hs.193465; ESTs; PDZ, pkinase; none; 5.70
 428227; U57058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1; TM=Y; SS=M; 5.69
 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase, pkinase_C, HR1; TM=M; SS=N; 5.69
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associ; kinesin; TM=M; SS=N; 5.69
 445136; AI348014; Hs.143949; ESTs; Weakly similar to Achaete-Scute ho; ion_trans, ion_trans; 5.69
 409223; AA312572; Hs.362852; phosphoinositide-3-kinase, regulatory su; SH2, SH3, RhoGAP; none; 5.67
 25 430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX, EXS; TM=Y; SS=N; 5.66
 429638; AI916662; Hs.211577; kinesin 1 (kinesin receptor); bZIP, Tropomyosin, spectrin, LBP, BPL, CETP, B56, M; TM=Y; SS=M; 5.65
 450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2; TM=Y; SS=M; 5.64
 453950; AA156998; Hs.348037; eukaryotic translation initiation factor; none; 5.64
 425889; M57414; Hs.161305; tachykinin receptor 2; 7tm_1; TM=Y; SS=M; 5.64
 30 432527; AW975028; Hs.102754; ESTs; none; none; 5.64
 441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3; none; 5.63
 419080; AW150835; Hs.18878; hypothetical protein FLJ21620; 2OG-Fold_Oxy; TM=M; SS=N; 5.63
 447217; BE465754; Hs.17778; neuropilin 2; CUB, MAM, F5_F8_type_C; TM=M; SS=M; 5.61
 440422; AW452656; Hs.130760; myosin phosphatase, target subunit 2; BTB, Kelch, ank; none; 5.58
 35 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome; TM=M; SS=N; 5.58
 432805; X94630; Hs.3107; CD97 antigen; 7tm_2, EGF, GPS, FecCD; TM=Y; SS=M; 5.55
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; Ig, Isodh, Ribosomal_L6, F-box; TM=Y; SS=M; 5.55
 441607; NM_005010; Hs.7912; neuronal cell adhesion molecule; VWD40, fn3, ig; TM=M; SS=N; 5.54
 40 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none; none; 5.54
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C; none; 5.53
 404210; ; NM_005936; Homo sapiens myeloid/lymphoid ; FHA, PDZ, RA, DIL; TM=M; SS=N; 5.53
 408051; AI623351; Hs.172148; ESTs; PH, RhoGAP; none; 5.53
 436726; AA324975; Hs.198689; ESTs; Weakly similar to T00079 hypotheti; ehfand, spectrin, GAS2, SH3, Plectin, RA_Xylose_isom, FfD, bZIP, Tropomyosin, Myc-LZ, Mldh_C, CHAIP3; TM=M; SS=N; 5.53
 45 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none; none; 5.52
 428667; AI375550; Hs.348688; nucleolar protein p40; homolog of yeast; none; none; 5.51
 433907; AW296107; Hs.152686; ESTs; Armadillo_seg; none; 5.50
 442821; BE391929; Hs.8752; transmembrane protein 4; none; 5.50
 50 422282; AF019225; Hs.114309; apolipoprotein L; MolA, ExbB; TM=Y; SS=M; 5.49
 439820; AL360204; Hs.283853; Homo sapiens mRNA full length insert cDN; none; none; 5.49
 428771; AB028992; Hs.193143; KIAA1069 protein; C2, PI-PLC-Y, PI-PLC-X; TM=M; SS=N; 5.48
 452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 f1s, clone HE; GDI, 7tm_1; none; 5.48
 442013; AA506476; Hs.375009; Human DNA sequence from clone RP11-353C1; none; none; 5.48
 55 408056; AA312329; Hs.42331; ephrin-A4; Ephrin; TM=M; SS=M; 5.47
 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR; TM=M; SS=N; 5.47
 420297; AI628272; Hs.128757; ESTs; Weakly similar to ALU1_HUMAN ALU S; pkinase, TUDOR; none; 5.47
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2, SH3; 5.46
 424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 f1s, clone MA; SH2, STAT, STAT_bind, STAT_prot; none; 5.45
 441560; F13386; Hs.7888; v-erb-a avian erythroblastic leukemia v; pkinase, Recep_L_domain, Furin-like, YLP; none; 5.44
 60 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS; 5.43
 450402; BE218027; Hs.89969; ESTs; SH3; none; 5.42
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino ; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, PI3_P4_kinase, FAT, FATC, BclA, RUN; TM=M; SS=N; 5.42
 430696; AA531276; Hs.59509; ESTs; pkinase, PP2C; none; 5.42
 65 412350; AI659306; Hs.73826; protein tyrosine phosphatase, non-recept; Y_phosphatase, Band_41, PDZ; TM=M; SS=N; 5.42
 444783; AK001468; Hs.62180; anillin (Drosophila Scraps homolog), act; PH; none; 5.41
 448379; AI097463; Hs.21035; KIAA1130 protein; none; Zip; 5.41
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; rrm; TM=M; SS=N; 5.41
 70 411817; BE302900; Hs.72241; mitogen-activated protein kinase kinase ; pkinase; TM=M; SS=M; 5.40
 445413; AA151342; Hs.12677; CG1-147 protein; UPF0099; TM=M; SS=M; 5.39
 451863; AL120634; Hs.331803; ATPase, Ca transporting, plasma membrane; cpm60_TCP1, E1-E2, ATPase, Cation_ATPase_C, Cation_ATPase_N, Hydrolase; 5.38
 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequ; K_tetra, DUF51; none; 5.38
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase; PAF-AH, Ib, Lipase, GDSL; TM=M; SS=N; 5.36
 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ, Guanylate_kin; 5.34
 75 441031; AI110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen_C, G-alpha, af; TM=M; SS=M; 5.33
 408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+/-pep; PTR2; TM=Y; SS=N; 5.33
 435391; AA704588; Hs.58934; ESTs; PIP5K; none; 5.33
 411779; AA292811; Hs.72050; non-metastatic cells 6, protein expresse; NDK; 5.33
 80 422170; AI791949; Hs.112432; anti-Müllerian hormone; TGF-beta; 5.32
 447350; AI375572; Hs.172634; v-erb-a avian erythroblastic leukemia v; pkinase, Recep_L_domain, Furin-like, YLP; none; 5.32
 449964; AW001741; Hs.24243; hypothetical protein FLJ10706; pkinase; TM=M; SS=N; 5.31
 426427; M86699; Hs.169840; TTK protein kinase; pkinase; 5.30
 430407; H23551; Hs.30974; ESTs; pkinase, PBD; none; 5.29

- 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3; TM=M; SS=N; 5.27
- 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; ig,kringle,ptkinase,Fz; TM=Y; SS=M; 5.27
- 424596; AB020639; Hs.151017; estrogen-related receptor gamma; hormone_rec,zf-C4; TM=M; SS=N; 5.27
- 428013; AF151020; Hs.181444; hypothetical protein; none; TM=Y; SS=M; 5.26
- 447384; AJ377221; Hs.40528; ESTs; SH3,Sorb; none; 5.26
- 441824; AB007871; Hs.7977; KIAA0411 gene product; SH3,RhoGAP; TM=M; SS=N; 5.26
- 438493; AJ130740; Hs.6241; phosphoinositide-3-kinase, regulatory sur; SH2,SH3,RhoGAP; TM=M; SS=N; 5.26
- 428579; NM_005756; Hs.184942; G protein-coupled receptor 64; 7tm_2,GPS; TM=Y; SS=M; 5.25
- 414359; M82194; Hs.75929; cadherin 11, type 2, OB-cadherin (osteob; cadherin,Cadherin_C_term; TM=Y; SS=M; 5.25
- 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr; TM=Y; SS=M; 5.24
- 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG; TM=M; SS=N; 5.24
- 423685; BE350494; Hs.49753; uveal autoantigen with coiled coil domain; ank,bZIP,M,DUF164,AIP3; 5.23
- 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phos; MORN,sugar_tr; TM=Y; SS=M; 5.23
- 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase; TM=M; SS=N; 5.23
- 417821; BE245149; Hs.82643; protein tyrosine kinase 9; coflin_ADF; 5.23
- 412507; L36645; Hs.73964; EphA4; In3,ptkinase,SAME,EPH_1bd; TM=Y; SS=M; 5.23
- 426770; AJ948618; Hs.150178; ESTs; Sulfate_transp,STAS; TM=Y; SS=N; 5.23
- 422583; AA410506; Hs.27973; KIAA0874 protein; ank,G-alpha; TM=M; SS=N; 5.22
- 414368; W07171; Hs.75939; uridine monophosphate kinase; PRK,CoaE; 5.22
- 448093; AW977382; Hs.15898; 2,4-dienoyl CoA reductase 2, peroxisomal; adh_short; 5.21
- 443646; AJ085198; Hs.164226; Thrombospondin 1; EGF,isp_1,vwc,TSPN,isp_3; none; 5.18
- 457916; BE085271; Hs.8834; ring finger protein 3; pkinase; none; 5.18
- 433933; A754389; Hs.355397; Homo sapiens clone TCCCA00164 mRNA sequ; none; NA; NA; 5.18
- 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none; 5.17
- 433662; W07162; Hs.150826; RAB25, member RAS oncogene family; ras,ABC_tran,arf; TM=M; SS=M; 5.17
- 450511; R07423; Hs.85092; thyroid hormone receptor interactor 11; Myosin_1a,EGF; 5.16
- 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 no; none; TM=M; SS=N; 5.15
- 454438; AA224053; Hs.172405; cell division cycle 27; SPRY,7tm_3,ANF_receptor; 5.14
- 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none; TM=Y; SS=M; 5.14
- 422051; AW927546; Hs.111024; solute carrier family 25 (mitochondrial; mito_carr; TM=M; SS=N; 5.14
- 415474; NM_014252; Hs.78457; solute carrier family 25 (mitochondrial; mito_carr; TM=M; SS=N; 5.14
- 411704; AJ499220; Hs.71573; hypothetical protein FLJ10074; pkinase; TM=M; SS=N; 5.13
- 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2; TM=Y; SS=M; 5.13
- 454128; AL031259; Hs.367900; programmed cell death 2; zf-MYND; TM=M; SS=N; 5.13
- 431322; AW970622; Hs.376626; gbtEST382704 MAGE resequences, MAGK Homo; none; none; 5.13
- 444754; T83911; Hs.11881; transmembrane 4 superfamily member 4; none; TM=Y; SS=M; 5.12
- 422867; L32137; Hs.1584; cartilage oligomeric matrix protein (pse; tsp_3,EGF; 5.12
- 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans; TM=Y; SS=M; 5.11
- 436494; AA720997; Hs.128295; ESTs; none; CAP_GLY,HCO3_cotransp,Glyco_hydro_63,PH; 5.11
- 419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-tRNA synthetase; WHEP-TRS,tRNA-synt_1b; none; 5.10
- 453387; AJ990741; Hs.252809; ESTs; Na_Ca_Ex; none; 5.07
- 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase; TM=M; SS=N; 5.07
- 456906; AF117646; Hs.156637; Cas-Bir-M (murine) ectropic retroviral tr; zf-C3HC4,Cbl_N2,Cbl_N3; TM=M; SS=N; 5.07
- 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin,Guanlylate_kin,PDZ,SH3; 5.07
- 448520; AB002387; Hs.21355; doublecortin and CaM kinase-like 1; pkinase,DCX; TM=M; SS=N; 5.06
- 413745; AW247252; Hs.75514; nucleoside phosphorylase; Mtap_PNP; 5.06
- 407235; D20569; Hs.169407; SAC2 (suppressor of actin mutations 2, y; none; Ribosomal_S13,Galactosyl_T_Zip,adh_short,zf-C3HC4; 5.05
- 421369; NM_005089; Hs.171909; U2 small nuclear ribonucleoprotein auxd; rrm,zf-CCCH,lectin_c,integrin_B; TM=M; SS=N; 5.06
- 412170; D16532; Hs.73729; very low density lipoprotein receptor; ldl_recept_a,ldl_recept_b,EGF; TM=M; SS=N; 5.06
- 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank; TM=M; SS=N; 5.05
- 421109; L32832; Hs.101842; AT-binding transcription factor 1; HMG14_17,homeobox,zf-C2H2; TM=M; SS=M; 5.05
- 453880; AJ803166; Hs.135121; ESTs, Weakly similar to 138022 hypothetical; HSP70; none; 5.05
- 431512; BE270734; Hs.2795; lactate dehydrogenase A; ldh,ldh_C,SH3,ptkinase,UBA; TM=M; SS=N; 5.05
- 435411; AW444619; Hs.138211; ESTs; none; pkinase; 5.04
- 419088; AI538323; Hs.367688; Integrin, beta 8; Integrin_B; none; 5.04
- 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX; Troponin,Exo_endo_phos,IQ; TM=M; SS=N; 5.04
- 428376; AF119655; Hs.184011; pyrophosphatase (inorganic); Pyrophosphatase; TM=M; SS=N; 5.03
- 413073; AL038165; Hs.75187; translocase of outer mitochondrial membr; MAS20,zf-A20,VPS9; TM=M; SS=M; 5.03
- 436415; BE265254; Hs.343258; proliferation-associated 2G4, 38kD; Peptidase_M24,Furin-like,ptkinase,Recep_L_domain,efhand; 5.01
- 449674; AW444937; Hs.233482; ESTs; C2,PI-PLC-Y,PI-PLC-X; none; 5.01
- 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to; ras,arf,TK; 5.01
- 412133; U83460; Hs.104557; solute carrier family 31 (copper transp; none; TM=Y; SS=N; 5.01
- 446488; AB037782; Hs.15119; KIAA1361 protein; pkinase; 5.00
- 449474; AA019344; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T an; ThiF,UBACT,ptkinase,UCH-2,UCH-1,rrm,zf-C2H2,zf-RanBP,G-palch; 5.00
- 416365; U15131; Hs.79265; suppression of tumorigenicity 5; DENN,dDENN,uDENN; TM=M; SS=N; 5.00
- 421351; AU076667; Hs.103755; receptor-interacting serine-threonine kd; CARD,ptkinase; TM=M; SS=N; 4.99
- 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH,death,TNFR_c6,Acyl-CoA_hydro; 4.98
- 442007; AA301116; Hs.142838; nucleolar phosphoprotein Nopp34; rrm,IRK; 4.95
- 441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fis, clone NT; none; none; 4.95
- 426310; NM_000909; Hs.169266; neuropeptide Y receptor Y1; 7tm_1; TM=Y; SS=M; 4.95
- 457718; F18572; Hs.22978; ESTs, Weakly similar to ALU4_HUMAN ALU S; pkinase,ptkinase; 4.94
- 408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase; TM=M; SS=N; 4.94
- 427541; AJ789883; Hs.375835; solute carrier family 35 (CMP-sialic aci; none; none; 4.94
- 452792; AB037765; Hs.30652; KIAA1344 protein; thired; TM=M; SS=M; 4.93
- 430713; AA351647; Hs.2642; eukaryotic translation elongation factor; GTP_EFTU,GTP_EFTU_D3,GTP_EFTU_D2; 4.93
- 444838; AV651680; Hs.208558; ESTs; integrin_A,FG-GAP; none; 4.93
- 440516; S42303; Hs.161; cadherin 2, type 1, N-cadherin (neuronal; HNH,cadherin,Cadherin_C_term; TM=M; SS=N; 4.92
- 421302; T34462; Hs.103291; neuritin; none; TM=M; SS=Y; 4.91
- 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisi; pkinase; TM=M; SS=N; 4.91
- 408857; AA782601; Hs.378649; ESTs; B55; none; 4.91
- 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,Integrin_B,Ricin_B_lectin; 4.91
- 421462; AF016495; Hs.104624; aquaporin 9; MIP; TM=Y; SS=M; 4.90
- 424503; NM_002205; Hs.149609; Integrin, alpha 5 (fibronectin receptor; integrin_A,FG-GAP; TM=Y; SS=N; 4.89

- 438564; AA381553; Hs.198253; major histocompatibility complex, class I; ig.MHC_II_alpha; none; 4.89
- 427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8, SHMT, MIF, GST_C, EF1G_domain, GST_N, S1, Fz, Frizzled, catreticulon, 7tm_2, rrm, PAP_assoc; TM=Y; SS=M; 4.88
- 434521; NM_002267; Hs.3886; karyopherin alpha 3 (importin alpha 4); Armadillo_seg, IBB; TM=M; SS=N; 4.88
- 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig; TM=Y; SS=M; 4.88
- 424118; BE269041; Hs.140452; cargo selection protein (mannose 6 phosph; peritipin; 4.88
- 410639; BE269047; Hs.65234; hypothetical protein FLJ20596; DEAD, helicase_C, PRK, AIP3; TM=M; SS=N; 4.87
- 417089; H52280; Hs.18612; Homo sapiens cDNA: FLJ21909 fs, clone H; voltage_CLC, CBS; none; 4.86
- 429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C; Phosphodiesterase, Somatomedin_B, Endonuclease; none; 4.86
- 417666; AJ345001; Hs.82380; menage a trois 1 (CAK assembly factor); zf-C3HC4; TM=M; SS=N; 4.86
- 453864; AW021407; Hs.21068; hypothetical protein; none; none; 4.86
- 453082; H18835; Hs.31608; hypothetical protein FLJ20041; ion_trans; TM=Y; SS=M; 4.85
- 413407; A1356293; Hs.75339; inositol polyphosphate phosphatase-like; SH2, SAM, Exo_endo_phos; 4.85
- 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen, COLFI, TSPN, laminin_G, CorA; 4.85
- 435652; N32388; Hs.334370; uncharacterized hypothalamus protein HBE; none; TM=M; SS=N; 4.84
- 419355; AA428520; Hs.90061; progesterone binding protein; heme_1; TM=Y; SS=M; 4.83
- 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC; TM=Y; SS=N; 4.83
- 408983; NM_000492; Hs.663; cystic fibrosis transmembrane conductance; ABC_tran, ABC_membrane, PRK, Bac_export_3; TM=Y; SS=N; 4.83
- 425465; L18964; Hs.1904; protein kinase C, iota; pkinase, DAG_PE-bind, pkinase_C, OPR; TM=M; SS=N; 4.82
- 435232; NM_001262; Hs.4854; cyclin-dependent kinase inhibitor 2C (p1); ank; TM=M; SS=N; 4.81
- 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank, pkinase; TM=M; SS=N; 4.81
- 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2; TM=Y; SS=N; 4.81
- 453354; V55946; Hs.234863; Homo sapiens cDNA FLJ12082 fs, clone HE; transmembrane4; none; 4.81
- 450883; NM_001348; Hs.25619; death-associated protein kinase 3; pkinase; TM=M; SS=N; 4.79
- 429736; AF125304; Hs.212680; tumor necrosis factor receptor superfamily; TNFR_c6; TM=M; SS=M; 4.79
- 431183; NM_006855; Hs.250596; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept; TM=M; SS=M; 4.79
- 409960; BE261944; Hs.355264; hexokinase 1; none; none; 4.78
- 422795; AB033109; Hs.375610; KIAA1283 protein; 7tm_1, kazal, A2M, A2M_N; TM=Y; SS=M; 4.78
- 423619; L28691; Hs.249159; adrenergic, alpha-2A-, receptor; 7tm_1, 7tm_2; TM=Y; SS=M; 4.78
- 429305; AF095727; Hs.287832; myelin protein zero-like 1; ig, transmembrane4; TM=Y; SS=M; 4.78
- 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese, DSPc; TM=M; SS=N; 4.77
- 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none; none; 4.76
- 446572; Z95636; Hs.11669; laminin, alpha 5; laminin_EGF, laminin_G, EGF, TNFR_c6, laminin_B, laminin_Nterm, metalthio, Tropomyosin, DUF164, p450; TM=M; SS=N; 4.76
- 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; ptkB; TM=M; SS=N; 4.75
- 438330; AW450572; Hs.257316; ESTs; pkinase, zf-C4, ERM, CNH; none; 4.75
- 410587; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase; 4.75
- 411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiose; 4.75
- 425548; AA890023; Hs.1906; prolactin receptor; fn3; TM=Y; SS=M; 4.73
- 434158; T86534; Hs.14372; ESTs; adenylate kinase; none; 4.73
- 459035; AW291109; Hs.332563; ESTs, Weakly similar to T31611 hypothet; none, SH3, myosin_head, IQ; 4.73
- 409012; AL117435; Hs.49725; DKFZP434I216 protein; PH, RhoGEF; TM=M; SS=M; 4.73
- 434503; T96231; Hs.17762; ESTs; SH3, Sorb; none; 4.73
- 446342; BE298665; Hs.14846; solute carrier family 7 (cationic amino; none; TM=M; SS=N; 4.72
- 427418; AA402587; Hs.356667; LAT1-3TM protein; none; none; 4.71
- 449433; AJ672096; Hs.9012; ESTs, Weakly similar to S26550 DNA-bind; Frizzled, Fz, Frizzled, Fz; 4.71
- 418910; Z25821; Hs.89466; Homo sapiens, Similar to dodecenoyl-Coen; ECH; 4.70
- 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal_L37ae, pkinase, POLO_box, IRNA-synl_1b, dynamin, dynamin_2, GED, bZIP, M; 4.70
- 442199; BE277633; Hs.372542; eloposide-induced mRNA; none; TM=Y; SS=M; 4.69
- 418870; AF147204; Hs.89414; chemokine (C-X-C motif); receptor 4 (fus; 7tm_1, 7tm_2; TM=Y; SS=M; 4.69
- 453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1; none; 4.69
- 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domain; death, DED; 4.68
- 434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase; TM=M; SS=N; 4.68
- 443323; BE560621; Hs.9222; estrogen receptor binding site associate; none; TM=M; SS=M; 4.68
- 400288; X06256; Hs.149609; integrin, alpha 5 (fibronectin receptor); Integrin_A, FG-GAP; TM=Y; SS=N; 4.68
- 418838; AW385224; Hs.35198; ectonucleotide pyrophosphatase/phosphodiesterase; Phosphodiesterase; TM=Y; SS=M; 4.67
- 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF, laminin_Nterm, Integrin_B; 4.67
- 425976; C75094; Hs.334514; NG22 protein; voltage_CLC; TM=Y; SS=M; 4.66
- 407844; AW073716; Hs.8037; ESTs; transmembrane4; none; 4.66
- 450656; AA010539; Hs.18912; unnamed protein product; zf-C2H2; 4.66
- 420311; AW445044; Hs.38207; Human DNA sequence from clone RP4-53015; none; none; 4.65
- 404287; ; FGENESH predicted novel CUB-domain contig; none; none; 4.64
- 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; Ig, Rhabd_glycop; TM=Y; SS=M; 4.63
- 426680; AA320160; Hs.171811; adenylate kinase 2; adenylate kinase; TM=M; SS=N; 4.63
- 430397; AJ924533; Hs.105607; bicarbonate transporter related protein; HCO3_cotransp; TM=Y; SS=N; 4.63
- 447656; NM_003726; Hs.19126; src kinase-associated phosphoprotein of; SH3, PH; TM=M; SS=N; 4.63
- 414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain, PHD, PWWP, zf-MYND; TM=M; SS=N; 4.62
- 429126; AW172356; Hs.89083; ESTs; 7tm_1; none; 4.61
- 429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; COX8, SHMT, MIF, GST_C, EF1G_domain, GST_N, S1, Fz, Frizzled, catreticulon, 7tm_2, rrm, PAP_assoc; TM=Y; SS=M; 4.60
- 409220; BE243323; Hs.51233; tumor necrosis factor receptor superfamily; TNFR_c6, death, Lipoprotein_5, TIL; TM=Y; SS=M; 4.60
- 421921; H83363; Hs.355993; translocase of inner mitochondrial membr; zf-Tim10_DDP, efhand, CH, spectrin, serpin; TM=M; SS=N; 4.60
- 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2; TM=M; SS=N; 4.59
- 400290; H18836; Hs.31608; hypothetical protein FLJ20041; none, Cys_knot; 4.59
- 430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion_trans; TM=Y; SS=M; 4.59
- 409645; A1142265; Hs.55498; geranylgeranyl diphosphate synthase 1; polyprenyl_synt; TM=M; SS=N; 4.59
- 427373; AB007972; Hs.130760; myosin phosphatase, target subunit 2; ank; TM=M; SS=N; 4.58
- 437212; A1765021; Hs.210775; ESTs; UOPGT; none; 4.58
- 430398; D94742; Hs.241363; hyaluronan-binding protein 2; ank, death, ZU5, EGF, kringle, trypsin, Nebulin, LIM; 4.57
- 452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos; TM=M; SS=N; 4.56
- 416041; AA345547; Hs.53263; hypothetical protein FLJ13287; WD40; 4.55
- 434511; R28982; Hs.18106; ESTs; pkinase, Glyco_hydro_39; 4.55
- 410174; AA306007; Hs.59461; DKFZP434C245 protein; none, DSPc; 4.55
- 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase, RIO1; TM=M; SS=N; 4.55
- 451357; AA923729; Hs.26322; cell cycle related kinase; pkinase; TM=M; SS=N; 4.54

- 417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glycoprotein; LRR, LRRNT, LRRCT; TM=Y; SS=M; 4.54
- 411296; BE207307; Hs.10114; growth suppressor 1; 2OG-Fell_Oxy; TM=M; SS=M; 4.53
- 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triph; Ham1p_like; TM=M; SS=N; 4.53
- 431992; NM_002742; Hs.2891; protein kinase C, mu; pkinase, DAG, PE-bind, PH; TM=M; SS=M; 4.53
- 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase, ICE_p10, ICE_p20; TM=M; SS=M; 4.53
- 428005; AW302245; Hs.181390; casein kinase 1, gamma 2; pkinase; TM=M; SS=N; 4.52
- 407775; NM_004914; Hs.38772; RAB35, member RAS oncogene family; ras, arf; TM=M; SS=N; 4.52
- 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 4.51
- 447321; AW271217; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HE; none, none; 4.51
- 405484; ; C3002124::gij12737280[ref]XP_006682.2[k]; none; 4.50
- 443605; H06865; Hs.134131; ESTs; ethand, ion, trans, none; 4.50
- 431738; AW237726; Hs.288549; hypothetical protein FLJ14710; 7tm_1, zf-C3HC4, fn3, SPRY, KRAB, zf-C2H2, rve, zf-B_box; TM=Y; SS=M; 4.50
- 422112; BE540240; Hs.111783; Lsm1 protein; Sm, BAG; 4.49
- 418869; AW516565; ; gbxcq01d05.x1 Soares_NHCEC_cervical_tumo; none, RasGAP, WW, IQ; 4.48
- 447898; AW969638; Hs.112318; 6.2 kd protein; none, none; 4.48
- 450607; AL050373; Hs.25213; hypothetical protein; SH3; TM=M; SS=N; 4.48
- 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell; ig; TM=Y; SS=M; 4.48
- 424823; NM_006226; Hs.153322; phospholipase C, epsilon; C2, PH, PI-PLC-Y, PI-PLC-X; TM=M; SS=N; 4.48
- 426812; AF105355; Hs.172613; solute carrier family 12 (potassium/chloro; none; TM=Y; SS=N; 4.47
- 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase, Recep_L_domain, YLP; none; 4.47
- 435615; Y15065; Hs.4975; potassium voltage-gated channel, KQT-like; ion, trans, KCNQ1_channel; TM=Y; SS=M; 4.47
- 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR, LY6, ET, PLA2_inh; 4.47
- 428727; AF078847; Hs.78452; general transcription factor IIH, polype; PHO4, LUM; TM=M; SS=N; 4.46
- 412760; AW379030; Hs.41324; ESTs; Cbl_N, Cbl_N2, Cbl_N3, UBA, zf-C3HC4, none; 4.46
- 409093; BE243834; Hs.50441; CGI-04 protein; Ribosomal_L37ae, pkinase, POLO_box, tRNA-synt_1b, dynamin, dynamin_2, GED, bZIP; M; 4.46
- 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase, ATP-sulfurylase, PRK, Thymidylate_kin; 4.46
- 447434; R16890; Hs.137135; ESTs; pkinase, fn3, ig, pkinase, fn3; 4.45
- 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none, SDF, sugar_br; 4.45
- 414108; AD267592; Hs.75761; SFRS protein kinase 1; ank, PH, Oxysterol_BP, pkinase; TM=M; SS=N; 4.44
- 457001; J03258; Hs.2062; vitamin D (1,25-dihydroxyvitamin D3) re; hormone_rec, zf-C4, Metallothio_5; TM=M; SS=N; 4.44
- 409686; AK000002; Hs.55879; Homo sapiens mRNA; cDNA DKFZp434L0827 (f; ABC_tran, ABC_membrane; TM=M; SS=M; 4.44
- 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm_3, none; 4.44
- 436823; AW749865; Hs.110707; ESTs, Weakly similar to I38022 hypotheti; aa_permeases, zf-C2H2, KRAB, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, ODT, PI3_P14_kinase, FAT, FATC, BclA, RUN, TFIIS; TM=M; SS=N; 4.44
- 450505; NM_004572; Hs.25051; plakophilin 2; Armadillo_seg; TM=M; SS=N; 4.43
- 437915; AI537993; Hs.202312; Homo sapiens clone N11 Ntera2D1 teratoca; none, none; 4.43
- 417412; X16896; Hs.82112; Interleukin 1 receptor, type I; ig, TIR; TM=M; SS=M; 4.43
- 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 4.43
- 411027; AF072089; Hs.67846; leukocyte immunoglobulin-like receptor, ; inositol_P, ig; TM=M; SS=N; 4.43
- 452124; AA454220; Hs.61170; ESTs; pkinase, none; 4.43
- 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A); NDK, PH, Oxysterol_BP; 4.42
- 416202; AW964492; Hs.169624; ESTs; none; TM=M; SS=N; 4.42
- 441518; AW161697; Hs.294150; ESTs; Y_phosphatase, DSPc; none; 4.42
- 441680; AW444598; Hs.7940; RAP1, GTP-GDP dissociation stimulator 1; Armadillo_seg; TM=M; SS=N; 4.42
- 431429; AF072813; Hs.252831; reticulon 3; Reticulon_Fz, ig, kringle, pkinase; TM=Y; SS=N; 4.42
- 453870; AW385001; Hs.8042; Homo sapiens cDNA: FLJ23173 fis, clone L; FG-GAP, integrin_A, NIF; 4.41
- 421242; AW161386; Hs.13561; hypothetical protein MGC4692; none; NA; NA; 4.41
- 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none; TM=M; SS=N; 4.41
- 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death, ZU5; 4.41
- 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY_C; TM=M; SS=N; 4.41
- 413367; NM_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar_br; TM=Y; SS=N; 4.41
- 458097; AW341135; Hs.58104; ESTs; none, SH3, PID; 4.40
- 458248; BE407379; Hs.108082; ESTs, Weakly similar to T31636 hypotheti; C1q, Collagen; TM=M; SS=Y; 4.40
- 427681; AB018263; Hs.284232; tumor necrosis factor receptor superfam; death, TNFR_c6, PH, Xlnk, RhoGEF, Metallothio_5; TM=M; SS=M; 4.40
- 443693; A1344782; Hs.9683; DnaJ (Hsp40) homolog, subfamily C, member; rrm, DnaJ, TPR; TM=M; SS=N; 4.40
- 437162; AW005505; Hs.5464; thyroid hormone receptor coactivating pr; bromodomain; TM=M; SS=N; 4.39
- 453891; AB037751; Hs.301242; Homo sapiens mRNA full length insert cDN; none, none; 4.39
- 442572; AI001922; Hs.135121; hypothetical protein FLJ22415; none, HSP70; 4.39
- 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; ig; TM=Y; SS=M; 4.37
- 445817; NM_003642; Hs.13340; histone acetyltransferase 1; none; TM=M; SS=N; 4.37
- 444895; AI874383; Hs.22891; solute carrier family 7 (cationic amino; ASC, death, TNFR_c6; 4.37
- 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo_seg; TM=M; SS=M; 4.37
- 432108; N58323; Hs.269098; ESTs, Weakly similar to RETROVIRUS-RELAT; SH3, PDZ, Guanylate_kin, none; 4.37
- 418283; S79895; Hs.83942; cathepsin K (pycnodysostosis); Peptidase_C1; 4.37
- 445826; BE313754; Hs.13350; Homo sapiens mRNA; cDNA DKFZp586D0918 (f; ig, bsp_1, ZU5, Nucleoside_tran; 4.37
- 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase; TM=Y; SS=N; 4.36
- 400257; ; Hs.76365; ENSP0000000452:BAD protein (BCL-2 bindi; none; TM=M; SS=N; 4.36
- 431478; BE612705; Hs.256697; histidine triad nucleotide-binding prote; HIT; 4.36
- 416178; AI808527; Hs.192822; serologically defined breast cancer anti; none; TM=M; SS=N; 4.36
- 456629; AW891965; Hs.367942; histone deacetylase 3; HSP90, HATPase_c, zf-C2H2, PHD; none; 4.36
- 427716; L38951; Hs.180446; karyopherin (importin) beta 1; Armadillo_seg, HEAT; TM=M; SS=N; 4.35
- 425843; BE313280; Hs.159627; death associated protein 3; myb_DNA-binding, PAH, BAH, bromodomain, PHD, SET; TM=M; SS=N; 4.35
- 420261; AW206093; Hs.748; fibroblast growth factor receptor 1 (fms; pkinase, ig, pkinase, ig, p450, SET, PPWW; 4.35
- 445926; AF054284; Hs.334826; splicing factor 3b, subunit 1, 155kd; none; TM=M; SS=N; 4.35
- 410726; AI623859; Hs.15936; ESTs; pkinase, pro_isomerase, none; 4.35
- 433995; AW135357; Hs.192374; ESTs; HSP90, HATPase_c, UDG; 4.34
- 433592; NM_004642; Hs.3436; deleted in oral cancer (mouse, homolog); none; TM=M; SS=N; 4.34
- 437103; AW139408; Hs.152940; ESTs; Choline_kinase, none; 4.34
- 410068; AI633888; Hs.58435; FYN-binding protein (FYN-120V130); SH3; TM=M; SS=N; 4.34
- 427349; AA360154; Hs.177415; Finkel-Biskis-Reilly murine sarcoma viru; ubiquitin; TM=M; SS=N; 4.33
- 439807; AA376417; Hs.374608; hypothetical protein MGC5244; abhydrolase_2; TM=M; SS=M; 4.33
- 453308; AW959731; Hs.323099; ESTs; none, pkinase, Activin_rec; 4.33
- 424893; AW295112; Hs.153648; Homo sapiens cDNA FLJ13303 fis, clone OV; SAM; 4.33

- 444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-S; DSPC;TM=M;SS=N; 4.33
 429655; U48959; Hs.211582; myosin, light polypeptide kinase; pkinase,fn3,ig,none; 4.32
 409121; AA902256; Hs.78979; Golgi apparatus protein 1; cys_rich_FGFR,none; 4.32
 430280; AA361258; Hs.237868; Interleukin 7 receptor; fn3,none; 4.32
 423798; AF047033; Hs.132904; solute carrier family 4, sodium bicarbon; HCO3_cotransp;TM=Y;SS=M; 4.29
 425654; AB033022; Hs.158654; KIAA1196 protein; zf-C2H2;TM=M;SS=N; 4.29
 457500; NM_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm,pkinase;TM=M;SS=N; 4.29
 427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 4.29
 447191; NM_014521; Hs.17667; SH3-domain binding protein 4; SH3;TM=M;SS=N; 4.29
 408331; NM_007240; Hs.44229; dual specificity phosphatase 12; DSPC;TM=M;SS=N; 4.29
 441130; A160734; Hs.267604; Homo sapiens PNAS-129 mRNA, complete cds; BTB,Kelch,K_tetra,DSPC;TM=M;SS=N; 4.28
 430057; AW450303; Hs.2534; bone morphogenetic protein receptor, type 1; Activin_rec,pkinase;TM=Y;SS=M; 4.28
 430250; NM_016929; Hs.283021; chloride intracellular channel 5; none;TM=M;SS=N; 4.28
 406774; AW518383; Hs.177592; ribosomal protein, large, P1; 60s_ribosomat; 4.28
 413809; L25851; Hs.851; integrin, alpha E (antigen CD103, human; vwa,integrin_A,FG-GAP;TM=M;SS=Y; 4.27
 443950; A1093577; Hs.255416; hypothetical protein FLJ21986; TTL;TM=M;SS=N; 4.27
 427378; BE515037; Hs.177556; melanoma antigen, family D, 1; MAGE;TM=M;SS=N; 4.27
 412204; A125507; Hs.24937; ESTs; ig_rrm,none; 4.26
 439506; A1361238; Hs.41136; ESTs; MAM,pkinase,Nucleoplasmin,none; 4.26
 451295; A1557212; Hs.17132; ESTs; Moderately similar to I54374 gene; pkinase,DAG_PE-bind,pkinase_C,OPR,none; 4.26
 452488; N74921; Hs.184389; ESTs; none;TM=M;SS=N; 4.26
 450973; AF012072; Hs.25732; eukaryotic translation initiation factor; W2,MA3,MIF4G;TM=M;SS=N; 4.26
 452437; AA026237; Hs.181272; ESTs; ethand,ion_trans,none; 4.26
 438204; A1589645; Hs.128690; ESTs; none;7tm_1; 4.25
 424756; AW504657; Hs.152931; lamin B receptor; ERG4_ERG24,FKBP;TM=Y;SS=N; 4.25
 430570; A1417881; Hs.292464; ESTs; 7tm_2,Fz,Frtzied,none; 4.25
 445709; H02592; Hs.74280; ESTs; PDZ,none; 4.25
 428134; AA421773; Hs.161008; ESTs; Armadillo_seg,none; 4.24
 434149; Z43829; Hs.244624; hypothetical protein MGC5469; none;TM=M;SS=M; 4.24
 425118; AU076611; Hs.154572; methylene tetrahydrofolate dehydrogenase; myb_DNA-binding,THF_DHG_CYH,THF_DHG_CYH,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,M_xan_ur_permease,HCO3_cotransp;TM=M;SS=N; 4.24
 433376; A1249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD,ICE_p10,ICE_p20; 4.24
 447818; W79940; Hs.355279; Homo sapiens clone 24570 mRNA sequence; none,pkinase; 4.24
 450684; AA872605; Hs.25333; interleukin 1 receptor, type II; ig;TM=Y;SS=M; 4.23
 435542; AA687376; Hs.351226; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF,none; 4.23
 426224; BE085860; Hs.374468; karyopherin (importin) beta 2; Armadillo_seg,HEAT;TM=M;SS=N; 4.23
 413284; AU077055; Hs.289107; baculoviral IAP repeat-containing 2; zf-C3HC4,CARD,BIR,death,ig;TM=M;SS=N; 4.22
 421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3_P14_kinase,PI3Ka;TM=M;SS=N; 4.22
 431239; AL039971; Hs.251216; hypothetical protein DKFZp434A196; SH2,ank,WH2; 4.22
 419685; W76083; Hs.134185; ESTs; none;TM=M;SS=N; 4.22
 431630; NM_002204; Hs.265829; Integrin, alpha 3 (antigen CD49C, alpha; FG-GAP,Rhabd_glycop,integrin_A;TM=Y;SS=M; 4.22
 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none; 4.21
 422218; AW978073; Hs.1010; regulator of mitotic spindle assembly 1; pkinase,none; 4.21
 450748; D82673; Hs.278589; general transcription factor II, i; none,SH3,PX; 4.21
 428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone L; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 4.21
 416907; W69099; ; gb:zd29g10.s1 Soares_fetal_heart_NbHH19W; ion_trans,none; 4.21
 411768; NM_013371; Hs.171979; interleukin 19; IL10; 4.21
 425262; D87119; Hs.155418; GS3955 protein; pkinase; 4.21
 430035; NM_003463; Hs.227777; protein tyrosine phosphatase type IVA, m; Y_phosphatase,DSPC;TM=M;SS=N; 4.21
 411789; AF245505; Hs.72157; Adican; ig,LRR,LRRNT,LRRCT;TM=M;SS=M; 4.15
 416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none,none; 4.14
 419452; U33535; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pkinase;TM=Y;SS=M; 4.13
 431745; AW972448; Hs.163425; Novel FGENSESH predicted cadherin repeat; none,none; 4.10
 416955; N26223; Hs.160436; MDAC1; none;NA;NA; 3.94
 426890; AA393187; Hs.41294; ESTs; none,none; 3.88
 442438; AA995998; Hs.370007; gb:os26b03.s1 NCI_CGAP_Kid5 Homo sapiens; none,DNA_pol_B,DNA_pol_B_exo; 3.86
 412314; AA825247; Hs.356084; downstream of: G protein-coupled receptor; 7tm_1;TM=Y;SS=M; 3.84
 448243; AW369771; Hs.367688; Integrin, beta 8; integrin_B,none; 3.64
 439318; AW837046; Hs.6527; G protein-coupled receptor 56; 7tm_2,CytC_asm,GPS;TM=Y;SS=M; 3.61
 415999; AA172179; Hs.294029; ESTs; none,none; 3.60
 429466; M85835; Hs.12827; ESTs; none,none; 3.45
 407853; AA336797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none;TM=M;SS=Y; 3.34
 400517; ; ; lengsin; none;TM=M;SS=N; 3.17
 439180; A1393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.88
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.84
 414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigen; DAN;TM=M;SS=M; 2.81
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 90kD, poly; pkinase,pkinase_C; 2.70
 438167; R28363; Hs.24286; chemokine binding protein 2 (CCBP2), mRNA; none;TM=Y;SS=M; 2.68
 418888; AU076801; Hs.89436; cadherin 17, LI cadherin (liver-intestine; cadherin;TM=Y;SS=M; 2.17

TABLE 23B

75	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
80	Pkey	CAT Number Accession
	409745	MH1944_5 BI030997 AA921874 AW188822 BI027862 A1347618 A1361453 A1088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
	417886	1031334_1 AA210987 D57294 AA214584 AA207006 D56572
	438993	2580163_1 A1926361 AA834879 AA828995

418869 12789_14 AA229762 AA230035
416907 1112245_1 W60909 W61051 M78905 BG959483

TABLE 23C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
406400	9256298	Plus	1553-1712, 1878-2140, 4252-4385, 5922-6077
403362	8571772	Plus	64099-64260
404210	5006246	Plus	169926-170121
404287	2326514	Plus	53134-53281
405484	5922025	Plus	199214-199579, 199672-199920, 200262-20049
400517	9796686	Minus	49996-50346

TABLE 24A: 571 GENES UP-REGULATED IN HEAD AND NECK TUMORS COMPARED WITH NORMAL BODY TISSUES

Table 24A lists about 571 genes up-regulated in head and neck tumors compared with normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 70th percentile of AI for head and neck cancer samples vs. the 80th percentile of the AI for normal body tissues

Pkey	ExAccn	UnigeneID	Unigene Title	R1
421155	H87879	Hs.102267	lysyl oxidase	166.00
452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	156.00
434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	80.00
438274	AJ918906	Hs.55080	ESTs	28.00
401486				121.00
446999	AA151520	Hs.334822	hypothetical protein MGC4485	126.00
423887	AL080207	Hs.134585	DKFZP434G232 protein	13.00
419569	AJ971651	Hs.91143	jagged 1 (Alagille syndrome)	98.00
428505	AL035461	Hs.2281	chromogranin B (secretogranin-1)	1.00
420602	AF060877	Hs.99236	regulator of G-protein signalling 20	35.00
445019	AJ205540	Hs.281295	ESTs	93.00
452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	270.62
449722	BE280074	Hs.23960	cyclin B1	9.81
423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	373.00
424086	AJ351010	Hs.102267	lysyl oxidase	200.00
447078	AW885727	Hs.301570	ESTs	184.00
429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	177.00
409506	NM_006153	Hs.54589	NCK adaptor protein 1	170.00
426471	M22440	Hs.170009	transforming growth factor, alpha	158.00
413268	AL039079	Hs.75256	regulator of G-protein signalling 1	155.00
419948	AB041035	Hs.93847	NADPH oxidase 4	140.00
451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	139.00
442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	111.00
452795	AW392555	Hs.18878	hypothetical protein FLJ21620	109.00
420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	106.00
416283	NM_005429	Hs.79141	vascular endothelial growth factor C	95.00
450221	AA328102	Hs.24641	cytoskeleton associated protein 2	92.00
449101	AA205847	Hs.23016	G protein-coupled receptor	92.00
442611	BE077155	Hs.177537	hypothetical protein DKFZp761B1514	86.00
438533	AJ440266	Hs.170673	ESTs, Weakly similar to T24832 hypothesi	85.68
414132	AJ801235	Hs.48480	ESTs	85.00
447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	83.00
402047	AK001921	Hs.169575	hypothetical protein MGC2550	80.00
414972	BE263782	Hs.77695	KIAA0008 gene product	74.00
452943	BE247449	Hs.31082	hypothetical protein FLJ10525	74.00
416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	71.00
427099	AB032953	Hs.173560	odd Ozten-m homolog 2 (Drosophila, mous	70.19
449318	AW235021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	66.25
418345	AJ001696	Hs.241407	serine (or cysteine) proteinase inhibito	66.00
415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	64.00
414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	63.00
432865	AJ753709	Hs.152484	ESTs, Weakly similar to I38022 hypothesi	60.00
431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	58.00
411750	BE562298	Hs.71827	KIAA0112 protein; homolog of yeast ribos	57.00
418612	AB037788	Hs.224961	cleavage and polyadenylation specific fa	57.00
438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	54.00
452188	AJ097560	Hs.61210	ESTs, Weakly similar to I38022 hypothesi	54.00
423020	AA383092	Hs.1608	replication protein A3 (14kD)	49.00

	422426	W79117	Hs.58559	ESTs	49.00
	406747	AJ925153	Hs.217493	annexin A2	46.00
	445828	F05802	Hs.81907	ESTs	46.00
5	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfamily	44.00
	452909	NM_015368	Hs.30985	pannexin 1	43.95
	432226	AW182766	Hs.273558	phosphate cytidylyltransferase 1, cholin	43.00
	458027	L49054	Hs.85195	myeloid leukemia factor 1	43.00
	443354	AW970672	Hs.9247	protein kinase, AMP-activated, alpha 1 c	43.00
10	416049	AJ970536	Hs.16603	hypothetical protein FLJ13163	42.00
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	40.00
	433859	AW895758	Hs.273789	ESTs	38.00
	426753	T89832	Hs.170278	ESTs	37.00
	400792	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp434O0515 (f	36.00
15	402034				35.00
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	34.00
	458424	AJ084049	Hs.206761	ESTs	34.00
	435159	AA668879	Hs.116649	ESTs	33.00
	408269	AA576953	Hs.22972	hypothetical protein FLJ13352	32.00
20	444361	W76027	Hs.23920	hypothetical protein FLJ11105	31.00
	439128	AJ949371	Hs.153089	ESTs	29.20
	420795	AA323037	Hs.128645	sorting nexin 16	26.00
	422505	AL120862	Hs.124165	ESTs	25.00
	434828	D90070	Hs.96	phorbol-12-myristate-13-acetate-induced	24.00
25	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 f5, clone H	22.10
	422035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	19.00
	417655	AA780791	Hs.14014	hypothetical protein FLJ14813	19.00
	414869	AA157291	Hs.21479	ubiquitin 1	17.37
	453049	BE537217	Hs.30343	ESTs	16.00
30	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	14.00
	435243	AW292886	Hs.261373	hypothetical protein dJ434014.3	13.00
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	10.80
	407746	AK001962	Hs.38114	hypothetical protein FLJ11100	10.00
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	9.60
35	414231	AJ468004	Hs.278956	hypothetical protein FLJ12929	9.00
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	8.09
	439452	AA918317	Hs.57967	B-cell CLL/lymphoma 11B (zinc finger pro	8.07
	439999	AA115811	Hs.6838	ras homolog gene family, member E	8.07
	417791	AW965339	Hs.111471	ESTs	8.04
40	436486	AA742221	Hs.120633	ESTs	7.23
	432731	R31178	Hs.287820	fibronectin 1	7.00
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	5.18
	435039	AW043921	Hs.130526	ESTs	5.00
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	4.25
45	457001	J03258	Hs.2062	vitamin D (1,25-dihydroxyvitamin D3) re	4.24
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	3.74
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	3.19
	458531	AA367718	Hs.159083	ESTs	3.00
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	2.53
50	411388	X72925	Hs.69752	desmocollin 1	1.00
	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14235 f5, clone NT	1.00
	428370	C19097	Hs.89709	glutamate-cysteine ligase, modifier subu	1.00
	429921	AA526911	Hs.82772	collagen, type XI, alpha 1	1.00
	449467	AW205006	Hs.197042	ESTs	1.00
55	453102	NM_007197	Hs.31664	frizzled (Drosophila) homolog 10	1.00
	453637	NM_002589	Hs.34073	BH-protocadherin (brain-heart)	1.00
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	517.00
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	616.00
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	226.00
60	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	278.00
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	56.11
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	264.00
	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	124.00
	424735	U31875	Hs.272499	short-chain alcohol dehydrogenase family	1.00
65	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 f5, clone C	1.00
	415511	AT32617	Hs.182362	ESTs	1.00
	406467				141.00
	422330	D30783	Hs.115263	epiregulin	98.00
	452461	N78223	Hs.108106	transcription factor	159.00
70	415542	R13474	Hs.290263	ESTs, Weakly similar to I38022 hypotheti	1.00
	413324	V00571	Hs.75294	corticotropin releasing hormone	1.00
	431571	AW500486	Hs.180610	splicing factor proline/glutamine rich (7.60
	443211	AJ128388	Hs.143655	ESTs	99.00
	451844	T61430		gb:yc05a03.s1 Stratagene lung (937210) H	1.00
75	441877	AW273802	Hs.11340	hypothetical protein FLJ23047	3.00
	439926	AW014875	Hs.137007	ESTs	2.79
	432015	AL157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp585O0724 (f	94.00
	421103	AI625835	Hs.27104	Homo sapiens mRNA; cDNA DKFZp667D226 (fr	1.22
	448062	AW295923	Hs.255472	KIAA1843 protein	1.00
80	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	1.27
	421577	BE465451	Hs.105925	single-minded (Drosophila) homolog 1	1.00
	421187	NM_014721	Hs.102471	KIAA0680 gene product	5.00
	408908	BE296227	Hs.250822	serine/threonine kinase 15	89.00
	437214	BE092336		gb:IL2-BT0734-240400-072-A12 BT0734 Homo	1.00

	449773	R76294	Hs.302383	ESTs	1.00
	443054	A1745185	Hs.8939	yes-associated protein 65 kDa	90.00
	432097	X51730	Hs.2905	progesterone receptor	1.00
5	453216	AL137566	Hs.32405	Homo sapiens mRNA; cDNA DKFZp586G0321 (f	0.38
	430184	AB013802	Hs.234790	contactin 5	1.00
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.23
	415025	AW207091	Hs.72307	ESTs	1.00
	416575	W02414	Hs.38383	ESTs	1.00
10	443171	BE281128	Hs.9030	TONDU	0.92
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	20.30
	400844				0.60
	409402	AF208234	Hs.695	cystatin B (steffin B)	1.96
	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.38
15	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.60
	400751				1.34
	436361	AA825814	Hs.149065	ESTs	0.92
	455612	BE042896	Hs.274848	ESTs	0.81
	447437	U07225	Hs.339	purinergic receptor P2Y, G-protein coupl	1.55
	404148				0.77
20	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	1.00
	446619	AL076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.47
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	3.92
	442994	AL026718	Hs.16954	ESTs	0.40
25	415327	H22769		ghcym54c02.r1 Soares infant brain 1N1B H	0.47
	418624	AJ734080	Hs.104211	ESTs	1.90
	452850	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-in	0.54
	401747			Homo sapiens keratin 17 (KRT17),	7.22
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	5.10
30	418259	AA215404	Hs.137289	ESTs	1.28
	432374	V68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	8.13
	403381				21.00
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	0.00
	418216	AA662240	Hs.283099	AF15q14 protein	11.29
35	444649	AW207523	Hs.197628	ESTs	0.10
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	4.64
	402230				1.64
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	2.97
	447334	AA515032	Hs.91109	ESTs	0.62
40	432829	W60377	Hs.57772	ESTs	0.86
	418686	Z36830	Hs.87268	annexin A8	8.44
	421508	NM_004833	Hs.105115	absent in melanoma 2	2.68
	410553	AW016824	Hs.255527	hypothetical protein MGC14128	2.22
	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	78.00
45	425721	AC002115	Hs.159309	uroplakin 1A	0.86
	420370	Y13645	Hs.97234	uroplakin 2	0.87
	417720	AA205625	Hs.208067	ESTs	5.83
	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365O12.1 (h.sa	1.07
	431753	X76029	Hs.2841	neuromedin U	7.00
	402075				286.00
50	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	363.00
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	4.81
	405064				1.00
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	2.00
55	441233	AA972965	Hs.135568	ESTs	1.00
	456034	AW450979		gb:U1-H-B13-ata-a-12-0-UI.s1 NCL CGAP_Su	1.23
	414221	AW450979		gb:U1-H-B13-ata-a-12-0-UI.s1 NCL CGAP_Su	0.65
	412296	AW936233		gb:QV0-DT0020-090200-107-a06 DT0020 Homo	1.00
	405494				1.00
60	407189	AA598927		gb:ae37e03.s1 Gessler Wilms tumor Homo s	1.00
	403085				1.00
	408633	AW963372	Hs.46677	PRO2000 protein	2.46
	435257	AA677026	Hs.191217	ESTs	1.00
	410044	BE586742	Hs.58169	highly expressed in cancer, rich in leuc	1.00
65	445182	AW189787	Hs.147474	ESTs	0.50
	417275	X83578	Hs.295449	parvalbumin	1.00
	418406	X73501	Hs.84905	cytokeratin 20	1.00
	421110	AJ250717	Hs.1355	cathepsin E	1.00
	406081				2.13
70	449448	D60730	Hs.57471	ESTs	123.00
	451668	Z43948	Hs.326444	cartilage acidic protein 1	0.37
	408243	Y00787	Hs.624	interleukin 8	3.35
	436246	AW450963	Hs.119991	ESTs	51.00
	440304	BE159984	Hs.125395	ESTs	1.00
75	402778				1.00
	406117				1.00
	406360				71.00
	435347	AW014873	Hs.116963	ESTs	1.00
80	445550	AJ242754	Hs.137306	ESTs	1.00
	451359	H85334	Hs.336623	ESTs	1.00
	419559	Y07828	Hs.91096	ring finger protein	1.00
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	58.00
	425420	BE536911	Hs.234545	hypothetical protein NUF2R	1.00
	402901				0.85

5	414918	AI219207	Hs.72222	hypothetical protein FLJ13459	0.87
	417715	AW959587	Hs.86366	ESTs	5.12
	442577	AA292998	Hs.163900	ESTs	2.19
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	1.54
	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	1.11
10	412610	X90908	Hs.74126	fatty acid binding protein 6, fetal (gas)	1.27
	414683	S78296	Hs.76888	hypothetical protein MGC12702	0.67
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	0.03
	403903				0.87
	405033				0.13
15	422282	AF019225	Hs.114309	apolipoprotein L	2.13
	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	1.05
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.59
	430168	AW968343	Hs.24255	DKFZP434I1735 protein	1.69
	459702	AI204995			1.00
20	446082	AI274139	Hs.156452	ESTs	0.60
	400843				0.76
	417409	BE272508	Hs.82109	syndecan 1	1.78
	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	1.20
	437181	AI306615	Hs.125343	ESTs, Weakly similar to KIAA0758 protein	0.50
25	404875				0.80
	436293	AI601188	Hs.120910	ESTs	1.40
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.03
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	0.94
	404977			Insulin-like growth factor 2 (somatomedi	0.99
30	413347	AI133461	Hs.251664	insulin-like growth factor 2 (somatomedi	1.10
	413804	T64682		gb:yc48b02.r1 Stratagene liver (937224)	0.85
	432842	AW674093	Hs.334822	hypothetical protein MGC4485	1.20
	420876	AA918425	Hs.177744	ESTs	0.85
	422119	AI277829	Hs.111862	KIAA0590 gene product	0.71
35	400846			sortilin-related receptor, L(DLR class)	0.75
	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	4.01
	430152	AB001325	Hs.234642	aquaporin 3	1.74
	402777				0.70
	417151	AA194055	Hs.293858	ESTs	0.99
40	411248	AA551538	Hs.334605	Homo sapiens cDNA FLJ14408 fis, clone HE	1.48
	405034	AL035754	Hs.2474	tol-like receptor 1	1.00
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	18.68
	431070	AW408164	Hs.249184	transcription factor 19 (SC1)	1.94
	453134	AA032211	Hs.118493	ESTs	0.70
45	440006	AK000617	Hs.6844	hypothetical protein FLJ20510	2.19
	418058	AW971155	Hs.293902	ESTs, Weakly similar to ISHUS protein d	0.25
	424364	AW383226	Hs.201189	ESTs, Weakly similar to G01763 atrophin-	2.74
	439780	AL109688		gb:Homo sapiens mRNA full length insert	3.07
	438315	R56795	Hs.82419	ESTs	0.65
50	418937	T71508	Hs.13861	ESTs, Weakly similar to T4Z383 probable	1.18
	444163	AI126098		gb:qc54g07.x1 Soares_placenta_8to9weeks_	0.85
	444444	AI149332	Hs.14855	ESTs	0.59
	407581	R48402	Hs.173508	P3ECSL	0.82
	433078	AW015188	Hs.121575	Homo sapiens cDNA FLJ12231 fis, clone MA	0.92
55	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	0.62
	445024	AB040946	Hs.284227	KIAA1513 protein	0.92
	427747	AW411425	Hs.180655	serine/threonine kinase 12	1.42
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.68
	453883	AI638516	Hs.22630	cofactor required for Sp1 transcriptiona	1.57
60	426847	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor	0.08
	446009	AI989885	Hs.231926	ESTs	1.00
	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	0.98
	415949	H10562	Hs.21691	ESTs	0.61
	420281	AI623693	Hs.191533	ESTs	7.01
65	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	0.72
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	2.21
	414792	BE314949	Hs.87128	hypothetical protein FLJ23309	0.99
	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	0.54
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	0.08
70	426900	AW163564	Hs.142375	ESTs	0.48
	414595	AA641726	Hs.289015	hypothetical protein MGC4171	0.83
	402305				0.89
	453823	AL137967		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	0.04
	445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	0.49
75	436608	AA628980	Hs.192371	down syndrome critical region protein DS	0.65
	423916	AW993496	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	0.63
	406832				1.76
	401760				2.61
	452240	AI591147	Hs.61232	ESTs	453.00
80	421064	AI245432	Hs.101382	tumor necrosis factor, alpha-induced pro	1.04
	421373	AA808229	Hs.167771	ESTs	17.00
	427239	BE270447	Hs.174070	ubiquitin carrier protein	1.16
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	1.68
	422406	AF025441	Hs.116206	Opa-Interacting protein 5	3.19
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.73
	453389	BE273648	Hs.32963	cadherin 6, type 2, K-cadherin (fetal ki	1.00
	454789	BE156314		gb:QVD-HT0367-150200-114-d02 HT0367 Homo	1.00

	434487	AF143867	Hs.337588	ESTs, Moderately similar to S65657 alpha	0.06
	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	2.45
	418067	AI127958	Hs.83393	cystatin E/M	1.41
5	441801	AW242799	Hs.86366	ESTs	140.00
	423536	L22075	Hs.1666	guanine nucleotide binding protein (G pr	2.45
	410153	BE311926	Hs.15830	hypothetical protein FLJ12691	58.00
	400409	AF153341	Hs.283954	Homo sapiens winged helix/forkhead trans	1.17
	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	0.86
10	427587	BE348244	Hs.202628	ESTs, Weakly similar to I78885 serine/th	0.91
	451161	AA211329	Hs.26006	hypothetical protein FLJ10559	1.00
	453204	R10799	Hs.191990	ESTs	1.13
	437240	AA747537		gbmx85c05.s1 NCI_CGAP_GC81 Homo sapiens	1.00
	405531				0.92
15	440249	AI246590	Hs.337275	ESTs	1.32
	426783	Z19084	Hs.172210	MJF1 protein	1.17
	434192	AW387314	Hs.34371	ESTs	1.00
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	87.14
	402001				37.00
20	433967	AF113018	Hs.284302	PRO1621 protein	1.00
	451592	AI805416	Hs.213897	ESTs	10.00
	422170	AI791949	Hs.112432	anti-Mullerian hormone	0.67
	408947	AL080093	Hs.49117	Homo sapiens mRNA; cDNA DKFZp564N1662 (f	1.00
	452732	BE300078	Hs.80449	Homo sapiens, clone IMAGE:3535294, mRNA,	0.99
25	441940	AW298115	Hs.128152	ESTs	0.88
	425048	H05468	Hs.164502	ESTs	0.33
	444008	BE544855	Hs.220756	ESTs, Weakly similar to SFR4_HUMAN SPLIC	1.01
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	1.06
	423853	AB011537	Hs.133466	sfil (Drosophila) homolog 1	0.45
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	0.62
30	410348	AW182663	Hs.95469	ESTs	1.00
	419078	M93119	Hs.89584	insulinoma-associated 1	0.04
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	1.04
	441795	N58115	Hs.21137	AD024 protein	10.00
35	418583	AA604379	Hs.86211	hypothetical protein	1.22
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	106.67
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	2.30
	441495	AW294603	Hs.127039	ESTs	0.44
	417933	X02308	Hs.82962	thymidylate synthetase	2.48
40	412661	N32860	Hs.24611	ESTs, Weakly similar to I54374 gene NF2	1.00
	411880	AW872477		gbhm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	1.00
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	1.44
	430034	X60155	Hs.227767	zinc finger protein 41	1.00
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.87
45	454417	AI244459	Hs.110826	trinucleotide repeat containing 9	0.54
	429257	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase	2.27
	417599	AA204688	Hs.136201	ESTs	1.01
	438368	AA805760	Hs.303567	ESTs	1.00
	438746	AI885815	Hs.184727	ESTs	1.47
50	409691	T89983	Hs.246042	Homo sapiens, clone MGC:5437, mRNA, comp	1.00
	408827	AW275730	Hs.254825	ESTs	1.00
	414735	BE468016	Hs.281904	ESTs	1.00
	422278	AF072873	Hs.114218	fritzzled (Drosophila) homolog 6	5.21
	412719	AW016610	Hs.129911	ESTs	494.00
55	417034	NM_006183	Hs.80962	neurotensin	1.00
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	23.36
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	6.98
	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin	7.50
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	9.77
60	425550	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	445.00
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rakkin	13.93
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	12.77
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	45.00
	418663	AK001100	Hs.41690	desmocollin 3	10.89
65	409532	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.29
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	0.88
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	38.31
	421948	L42583	Hs.334309	keratin 6A	36.81
	431846	BE019924	Hs.271580	uroplakin 1B	1.37
70	424098	AF077374	Hs.139322	small proline-rich protein 3	8.85
	453964	AI961485	Hs.12744	ESTs	0.40
	446856	AI814373	Hs.164175	ESTs	1.16
	443648	AI085377	Hs.143610	ESTs	2.15
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK (human,	4.39
75	431384	BE158000		gb:MR2-HT0377-150200-202-e03 HT0377 Homo	1.18
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	4.22
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	164.00
	417366	BE185269	Hs.1076	small proline-rich protein 1B (comifin)	9.85
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	5.59
	441020	W79283	Hs.35962	ESTs	5.76
80	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.97
	448733	NM_005629	Hs.187958	solute carrier family 6 (neurotransmitte	1.09
	444371	BE540274	Hs.239	forkhead box M1	2.44
	422168	AA566894	Hs.112408	S100 calcium-binding protein A7 (psorias	8.39

5	429259	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	2.53
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	1.67
	437044	AL035864	Hs.69517	cDNA for differentially expressed CO16 g	2.30
	423662	AK001035	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.04
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.11
10	401781				11.07
	401780				9.54
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	1.62
	417389	BE260964	Hs.82045	midkine (neurile growth-promoting factor	1.12
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	947.00
15	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	2.79
	441362	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	3.16
	440704	M59241	Hs.162	insulin-like growth factor binding prote	1.08
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	5.20
	431221	AA449015	Hs.286145	SRB7 (suppressor of RNA polymerase B, ye	2.53
20	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	72.00
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	19.96
	409103	AF251237	Hs.112208	XAGE-1 protein	0.47
	417542	J04129	Hs.82269	progesterone-associated endometrial prote	0.66
	428471	X57348	Hs.184510	stratillin	3.39
25	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	1.61
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.31
	451541	BE279383	Hs.26557	plakophilin 3	1.82
	418203	X54942	Hs.83758	CDC28 protein kinase 2	5.60
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.78
30	437016	AU076916	Hs.5398	guanine monophosphate synthetase	2.01
	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	2.18
	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	2.58
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	4.63
	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	2.25
35	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	11.88
	430677	Z26317	Hs.94560	desmoglein 2	1.38
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.09
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.09
	422963	M79141	Hs.13234	ESTs	2.29
40	418462	BE001596	Hs.85266	Integrin, beta 4	1.40
	450832	AW970602	Hs.105421	ESTs	13.31
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	1.25
	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.89
	458933	AI639429	Hs.24763	RAN binding protein 1	1.54
45	439394	AA149250	Hs.56105	ESTs	3.89
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	1.77
	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	1.52
	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	3.11
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	2.10
50	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	1.84
	440325	NM_003812	Hs.7164	a disintegrin and metalloproteinase doma	0.61
	439606	W79123	Hs.58561	G protein-coupled receptor 87	303.00
	453884	AA355925	Hs.36232	KIAA0186 gene product	10.55
	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.38
55	451743	AW074266	Hs.23071	ESTs	2.90
	413129	AF292100	Hs.104613	RP42 homolog	2.38
	406974	M57293		gb:Human parathyroid hormone-related pep	1.00
	413281	AA861271	Hs.222024	transcription factor BMAL2	5.92
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	2.18
60	416819	U77735	Hs.80205	p1m-2 oncogene	1.01
	451320	AW118072	Hs.89981	diacylglycerol kinase, zeta (104kD)	0.67
	418543	NM_005329	Hs.85962	hyaluronan synthase 3	1.19
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	2.55
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	3.06
65	413004	T35901	Hs.75117	interleukin enhancer binding factor 2, 4	1.64
	407634	AW016569	Hs.135414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	7.04
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	203.00
	435013	H91923	Hs.110024	NADH:ubiquinone oxidoreductase MLRQ subu	1.33
	430337	M36707	Hs.239600	calmodulin-like 3	1.32
70	419121	AA374372	Hs.89526	parathyroid hormone-like hormone	81.00
	448993	AI471630	Hs.8127	KIAA0144 gene product	1.03
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	28.00
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	1.24
	425245	AI751768	Hs.155314	KIAA0095 gene product	1.40
75	430393	BE185030	Hs.241305	estrogen-responsive B box protein	1.55
	420462	AF050147	Hs.97932	chondromodulin I precursor	1.00
	418678	NM_001327	Hs.167379	cancer/testis antigen	0.82
	428182	BE386042	Hs.293317	ESTs, Weakly similar to GGC1_HUMAN G ANT	1.00
	427335	AA448542	Hs.251677	G antigen 7B	0.91
80	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	6.53
	438956	W00847	Hs.135056	Human DNA sequence from clone RP5-850E9	1.35
	421917	AB028943	Hs.109445	KIAA1020 protein	0.94
	404440				38.57
	409582	R27430	Hs.271565	ESTs	3.19
80	415669	NM_005025	Hs.78589	serine (or cysteine) proteinase inhibito	2.45
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	1.61
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	1.95

	408380	AF123050	Hs.44532	diubiquitin	7.23
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	1.35
	449976	H06350	Hs.135055	Human DNA sequence from clone RP5-850E9	0.81
5	446102	AW168067	Hs.252956	ESTs	1.03
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	137.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.91
	423761	NM_006194	Hs.132576	paired box gene 9	36.00
	436291	BE568452	Hs.5101	protein regulator of cytokinesis 1	5.35
10	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	207.00
	440659	AF134160	Hs.7327	claudin 1	3.06
	434360	AW015415	Hs.127780	ESTs	3.89
	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoma	1.28
	438898	AI819863	Hs.106243	ESTs	1.73
	441553	AA281219	Hs.121295	ESTs	1.47
15	418379	AA218940	Hs.137516	figetin-like 1	40.42
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	14.25
	429413	NM_014058	Hs.201877	DESC1 protein	5.17
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	1.95
	415380	F07953	Hs.16085	putative G-protein coupled receptor	0.18
20	423949	AI157425	Hs.133315	Homo sapiens mRNA; cDNA DKFZp761J1324 (f	1.00
	446292	AF081497	Hs.279682	Rh type C glycoprotein	2.09
	429538	BE182592	Hs.11261	small proline-rich protein 2A	6.14
	447289	AW247017	Hs.36978	melanoma antigen, family A, 3	1.00
25	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	44.00
	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	149.00
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	127.00
	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	20.00
	404996				147.00
30	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	1.00
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	54.00
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	139.00
	430563	AA481269	Hs.108660	ATP-binding cassette, sub-family C (CFTR	22.00
	438702	AB790664	Hs.54618	ESTs	1.00
	444378	RA1339	Hs.12569	ESTs	1.00
35	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	41.00
	407839	AA045144	Hs.161566	ESTs	7.50
	439223	AW238299	Hs.250618	UL16 binding protein 2	3.39
	409041	AB033025	Hs.50081	KIAA1199 protein	245.00
40	429228	AI553633	Hs.337139	ESTs	10.89
	409757	NM_001898	Hs.123114	cystatin SN	3.19
	411089	AA456454	Hs.183418	cell division cycle 2-like 1 (PITSLRE pr	0.78
	436511	AA721252	Hs.291502	ESTs	0.23
	449207	AL044222	Hs.23255	nucleoporin 155kD	1.68
45	453331	AI240665	Hs.8895	ESTs	5.21
	409935	AW511413	Hs.278025	ESTs	0.75
	428969	AF120274	Hs.194689	artemin	1.17
	445443	AV653838	Hs.322971	ESTs	1.00
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	11.42
50	401785				2.76
	412723	AA648459	Hs.335951	hypothetical protein AF301222	107.00
	450701	H39960	Hs.288467	Homo sapiens cDNA FLJ12280 fis, clone MA	2.17
	405770				2.42
55	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	4.24
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	4.50
	414774	X02419	Hs.77274	plasminogen activator, urokinase	1.95
	424629	M90656	Hs.151393	glutamate-cysteine ligase, catalytic sub	1.44
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	1.00
	454098	W27953	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.33
60	453968	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA	1.11
	427441	AA412605	Hs.178053	SPANX family, member C	5.00
	403478				0.78
	400842				0.16
	441525	AW241867	Hs.127728	ESTs	0.79
65	452865	AI924046	Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	1.50
	405646				1.05
	427260	AA663848		gb:ae70b06.s1 Stratagene schizo brain S1	0.79
	431413	AA504777	Hs.105293	ESTs	1.00
	401994				3.25
70	402420				0.05
	404298				0.64
	404927				88.00
	434105	AW952124	Hs.13094	presenilins associated rhomboid-like pro	0.96
	436961	AW375974	Hs.156704	ESTs	3.58
75	429563	BE619413	Hs.2437	eukaryotic translation initiation factor	0.92
	426067	AW664691	Hs.97053	ESTs	0.97
	428810	AF068236	Hs.193788	nitric oxide synthase 2A (inducible, hep	0.66
	426897	AW976570	Hs.97387	ESTs	1.29
	443892	AI889572	Hs.134791	ESTs	1.00
80	413223	AI732182	Hs.191866	ESTs	0.79
	413691	AB023173	Hs.75478	ATPase, Class VI, type 11B	1.51
	423934	U89995	Hs.159234	forkhead box E1 (thyroid transcription f	2.59
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	1.39
	420758	AW297536	Hs.33053	ESTs	0.89

5	423816	AL031985	Hs.133034	hypothetical protein	1.00
	447534	AW953935	Hs.30837	ESTs	1.88
	451919	W05086	Hs.114256	ESTs, Weakly similar to I78885 serine/th	0.11
	409228	R16811	Hs.22010	ESTs, Weakly similar to 2109260A B cell	0.92
	403715				0.89
	428645	AA431400	Hs.98729	ESTs, Weakly similar to 2017205A dihydro	1.00
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	37.00
	436839	AA767346	Hs.291614	ESTs	1.00
10	413582	AW295647	Hs.71331	hypothetical protein MGC5350	59.00
	413573	AI733859	Hs.149089	ESTs	78.00
	430686	NM_001942	Hs.2633	desmoglein 1	127.08
	438993	AA828995		gb:od77b08.s1 NC1_CGAP_Ov2 Homo sapiens	1.00
	448243	AW369771	Hs.52620	integrin, beta 8	133.00
15	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	232.00
	426427	M86699	Hs.169940	TTK protein kinase	65.00
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	148.00
	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	40.75
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	13.00
20	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	106.00
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	159.00
	415989	AI267700	Hs.317584	ESTs	196.00
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (Z30/240kD)	32.44
	453160	AI263307	Hs.239884	H2B histone family, member L	7.00
25	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	4.13
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	45.00

TABLE 24B

30	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accessions:	Genbank accession numbers	
35	Pkey	CAT number	Accessions
	411880	1263110_1	AW872477 BE088101 T05990
	412296	1288043_1	AW936233 AW936272
	413804	1390710_1	T64682 BE168190 BE168256
40	414221	142695_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363
	415327	1534137_1	H22769 R35182 Z43545 F05783 N92089 H71928
	427260	276598_1	AA653848 AA400100 AA401424
	431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
45	431384	33264_1	BE158000 BE157999 H75671 H70965 C18895 BE386512 BE385815 BE390298 AJ341995 BE074534 AA055592 AA132265 AI733757 AA134504 BE145037 AA055887 BE070191 R66492 AW858018 AW858058 AW817057 AW862031 AW861688 AW862029 AW858805 AW858792 AW862028 AW858017 AW819164 AW853698 AI522161 AW854789 AW817408 BE152005 AI732411 AA133084
	432222	343347_1	AI204995 AW827539 AW969908 AW440776 AA528756
	437214	434730_1	BE092336 BE092259 BE092497 BE092051 AA746882 AI336378
	437240	435139_1	AA747537 BE089068 BE089070
50	438993	467651_1	AA828995 AA834879 AI926361
	439780	47673_1	AL109688 R23665 R26578
	444163	593658_1	AI126098 AI184746 AI148521
	451844	888230_1	T61430 AI820546 AI821336
	453823	982526_1	AL137967 BE084160 BE084188
55	454789	1234742_1	BE156314 BE156316 AW820750
	456034	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363

TABLE 24C

65

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NT_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NT_position	
400751	7331445	Minus	35395-35533	
400842	1927148	Plus	90462-90673	
400843	9188605	Plus	5863-5970,7653-7764,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958	
400844	9188605	Plus	24746-24872,25035-25204	
400846	9188605	Plus	39310-39474	
75	401486	7341763	Plus	32585-32756,36281-36540,40791-40933,44018-44179
	401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
	401760	9929699	Plus	83126-83250,85320-85540,94719-95287
80	401780	7249190	Minus	28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573
	401781	7249190	Minus	83215-83435,83531-83656,83740-83901,84237-84393,84955-85037,86290-86814
	401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,45199-45281,46337-46732
	402001	9501818	Plus	68052-68223

402034	7684482	Minus	86227-86451
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402230	9966312	Minus	29782-29932
402305	7328724	Plus	40832-41362
402420	9796339	Plus	129750-129919
402777	9588235	Plus	126786-126948
402778	9588235	Plus	128560-128702
402901	8894222	Minus	175426-175667
403085	8954241	Plus	165035-165334,165420-165713
403381	9438267	Minus	26009-26178
403478	9958258	Plus	116458-116564
403715	7239669	Plus	85128-85292
403903	7710671	Minus	101165-102597
404148	9863703	Plus	78218-78418,79571-79709
404298	9944263	Minus	73591-73723
404440	7528051	Plus	80430-81581
404875	9801324	Plus	96588-96732,97722-97831
404927	7342002	Plus	68690-69563
404977	3738341	Minus	43081-43229
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,40557-40674,42351-42450
405033	7107731	Minus	142358-142546
405064	7658416	Plus	81207-81416
405494	8050952	Minus	70284-70518
405531	9665194	Plus	35602-35803
405646	4914350	Plus	741-969
405770	2735037	Plus	61057-62075
405932	7767812	Minus	123525-123713
406081	9123861	Minus	38115-38691
406117	9142932	Plus	54304-54584
406360	9256107	Minus	7513-7673
406467	9795551	Plus	182212-182958

TABLE 25A: 691 genes upregulated in head and neck cancer relative to normal body tissues

Table 25A lists about 691 genes upregulated in head and neck cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Altymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Key: Unique Eos probeset identifier number
 ExAccon: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Prod.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1 85th percentile of head and neck cancer AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Key: ExAccon; UniGeneID; UniGene Title; Pred.Prod.Domains; R1

422168; AA586894; Hs.112408; S100 calcium-binding protein A7 (psorias; ehand,S_100;TM=M;SS=N; 46.25
 408522; AJ541214; Hs.46320; Small proline-rich protein SPRK (human; none;Cornifin; 40.37
 417368; BE185289; Hs.1076; small proline-rich protein 1B (cornifin); Cornifin;TM=M;SS=N; 38.94
 401781; ; Target Exon; filament;TM=M;SS=N; 29.74
 422158; L10343; Hs.112341; protease inhibitor 3, skin-derived (SKAL; wap;TM=M;SS=Y; 29.54
 401780; ; NM_005557; Homo sapiens keratin 16 (foca; filament;filament; 28.58
 424098; AF077374; Hs.139322; small proline-rich protein 3; Cornifin;TM=M;SS=N; 28.55
 421948; L42583; Hs.334309; keratin 6A; filament;RhoGAP,DUF286,bZIP,Tropomyosin,tubulin,DUF164,TBCA,Collagen;TM=M;SS=N; 25.74
 428471; X57348; Hs.184510; stratifin; 14-3-3;TM=M;SS=N; 23.65
 417079; U65590; Hs.81134; Interleukin 1 receptor antagonist; IL1; 21.02
 421574; AJ000152; Hs.105924; defensin, beta 2; Defensin_beta2;TM=M;SS=N; 20.83
 409501; AF237621; Hs.80828; keratin 1 (epidermolytic hyperkeratosis); filament,bZIP,UvrD-helicase,TBCA;TM=M;SS=N; 20.72
 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR_LY6,toxin,Activin_recpt;TM=M;SS=Y; 19.63
 446292; AF081497; Hs.279682; Rh type C glycoprotein; Ammonium_transp,FecCD;TM=Y;SS=M; 19.53
 420783; AI659838; Hs.99923; lectin, galactoside-binding, soluble, 7; Gal-bind_lectin;TM=M;SS=N; 19.12
 407788; BE514982; Hs.38991; S100 calcium-binding protein A2; ehand,S_100,S_100,ehand; 17.93
 416091; AF295370; Hs.283082; defensin, beta 3; Defensin_beta3;TM=M;SS=M; 17.63
 431211; M86849; Hs.323733; gap junction protein, beta 2, 25kd (conn; connexin;TM=Y;SS=M; 16.94
 429259; AA420450; Hs.380088; Plakophilin; none;none; 14.92
 417515; L24203; Hs.82237; alzada-telangiectasia group D-associated; zf-B_box,zf-UBR1;TM=M;SS=N; 14.75
 423634; AW959908; Hs.16590; heparin-binding growth factor binding pr; none;TM=M;SS=M; 14.45
 418007; M13509; Hs.83169; matrix metalloproteinase 1 (interstitial; hemopexin,Peptidase_M10,Aslacin_PG_binding_1; 13.02
 409632; W74001; Hs.55279; serine (or cysteine) proteinase inhibitor; serpin; 12.82
 406621; X57809; Hs.181125; immunoglobulin lambda locus; ig_HSP70,Ppx-GppA;TM=M;SS=N; 12.81
 431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placenta; cadherin,Cadherin_C_term;TM=Y;SS=M; 12.45
 446921; AB012113; Hs.16530; small inducible cytokine subfamily A (Cr; IL8; 11.71
 401760; ; Target Exon; none;bromodomain; 11.68
 407839; AA045144; Hs.161566; ESTs; cadherin,cadherin; 11.65
 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member ; aldedh; 11.56
 444781; NM_014400; Hs.11950; GPI-anchored metastasis-associated prote; UPAR_LY6,lactamase_B; 11.31

- 453857; AL080235; Hs.35861; Ras-induced senescence 1 (RIS1); none; TM=Y; SS=M; 11.03
 424012; AW368377; Hs.137569; tumor protein 63 kDa with strong homolog; SAM, P53; TM=M; SS=N; 10.75
 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin; TM=M; SS=N; 10.58
 419693; AA133749; Hs.301350; FXD domain-containing ion transport reg; ATP1G1_PLM_MAT8; TM=Y; SS=M; 10.30
 411274; NM_002776; Hs.69423; kallikrein 10; trypsin; TM=M; SS=N; 10.25
 441633; AW958544; Hs.112242; normal mucosa of esophagus specific 1; none; TM=M; SS=M; 9.84
 446989; AK001898; Hs.16740; hypothetical protein FLJ11038; none; TM=Y; SS=N; 9.74
 402075; ; ENSP00000251056; Plasma membrane calcium; none; 9.50
 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 9.50
 431009; BE149762; Hs.48956; gap junction protein, beta 6 (connexin 3; connexin; TM=Y; SS=M; 9.48
 439310; AF086120; Hs.102793; ESTs; casein_kappa_kinase, ig, none; 9.43
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2; TM=M; SS=N; 9.33
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member; aldedh; TM=M; SS=M; 9.14
 408000; L11690; Hs.158689; bullous pemphigoid antigen 1 (230/240kD); ehband, spectrin, GAS2, SH3, Plectin, RA, Xylose_isom, Flid, bZIP, Tropomyosin, Myc-LZ, M, Jdh_C, CH, AIP3; TM=M; SS=N; 9.12
 451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg; TM=M; SS=N; 9.11
 425650; NM_001944; Hs.1925; desmoglein 3 (pemphigus vulgaris antigen; cadherin; TM=M; SS=M; 8.66
 452240; AI591147; Hs.61232; ESTs; none; none; 8.57
 429228; AI553633; Hs.356828; ESTs; none; none; 8.46
 400289; X07820; Hs.2258; matrix metalloproteinase 10 (stromelysin; hemopexin, Peptidase_M10, Astacin; 8.44
 425071; NM_013889; Hs.154424; diiodinase, diiodothyronine, type II; T4_deiodinase; TM=M; SS=Y; 8.15
 407242; M18728; ; gb:Human nonspecific crossreacting anti; ig; TM=M; SS=M; 8.05
 407944; R34008; Hs.239727; desmocollin 2; cadherin, Cadherin_C_term, Hanta_G2; TM=Y; SS=M; 7.90
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin; 7.82
 428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrilysin; ; Peptidase_M10; 7.82
 417308; H60720; Hs.81892; KIAA0101 gene product; none; TM=M; SS=N; 7.77
 413753; U17760; Hs.75517; laminin, beta 3 (nicotin (125kD), kalinin; laminin_EGF, laminin_Nterm; 7.76
 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolysin; Kunitz_BPT1, fn3, vwa, Collagen, beta-lactamase; TM=M; SS=M; 7.71
 430686; NM_001942; Hs.2633; desmoglein 1; cadherin, Cadherin_C_term; TM=Y; SS=M; 7.69
 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha, arf; TM=M; SS=N; 7.54
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, PI3_P14_kinase, FAT, FATC, BclA, RUN; TM=M; SS=N; 7.53
 418663; AK001100; Hs.41690; desmocollin 3; cadherin, Cadherin_C_term; none; 7.30
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGFb_propeptide, TGF-beta; none; 7.28
 429211; AF052693; Hs.198249; gap junction protein, beta 5 (connexin 3; connexin; TM=Y; SS=M; 7.26
 412719; AW016610; Hs.816; ESTs; none; none; 7.17
 446619; AU076543; Hs.313; secreted phosphoprotein 1 (osteopontin; ; Osteopontin; 7.10
 423961; D13666; Hs.136348; periostin (OSF-2os); Fasciclin; TM=M; SS=M; 7.09
 427666; AI791495; Hs.180142; calmodulin-like skin protein (CLSP); ehband; TM=M; SS=N; 7.08
 431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4; TM=Y; SS=M; 7.06
 423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage; hemopexin, Peptidase_M10; TM=M; SS=M; 7.03
 401747; ; Homo sapiens keratin 17 (KRT17); none, bromodomain; 7.01
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kinase; SAM_PNT; none; 6.98
 429002; AW248439; Hs.2340; junction plakoglobin; Armadillo_seg; TM=M; SS=N; 6.96
 432239; X81334; Hs.2936; matrix metalloproteinase 13 (collagenase; hemopexin, Peptidase_M10; 6.87
 417715; AW969587; Hs.86366; ESTs; none; none; 6.72
 422440; NM_004812; Hs.116724; aldo-keto reductase family 1, member B10; aldo_ket_red, ROK; TM=M; SS=N; 6.50
 429359; W00482; Hs.2399; matrix metalloproteinase 14 (membrane-in; hemopexin, Peptidase_M10; TM=M; SS=M; 6.39
 418844; M62982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase, PLAT; TM=M; SS=N; 6.38
 420039; NM_004605; Hs.376147; sulfotransferase family, cytosolic, 2B; ; Sulfotransfer; 6.38
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB, DNA_topoisolV, HATPase_c; 6.35
 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3, ank; TM=M; SS=N; 6.30
 409420; Z15008; Hs.54451; laminin, gamma 2 (nicotin (100kD), kalini; laminin_B, laminin_EGF; 6.28
 424364; AW383226; Hs.163834; ESTs, Weakly similar to G01763 atrophin; ras; TM=M; SS=N; 6.27
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8; TM=M; SS=Y; 6.23
 424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; fn2, hemopexin, Peptidase_M10; 6.22
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none; TM=M; SS=N; 6.21
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabq; 7tm_3; TM=Y; SS=M; 6.12
 423017; AW178761; Hs.227948; serine (or cysteine) proteinase inhibitor; serpin; 6.08
 424834; AK001432; Hs.153408; Homo sapiens cDNA FLJ10570 fis, clone NT; none, none; 6.08
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_br; TM=Y; SS=M; 6.04
 439335; AA742697; Hs.62492; NM_052863; Homo sapiens secretoglobulin, fa; none; 5.81
 439223; AW238299; Hs.250618; UL16 binding protein 2; ldl_recept_a, PKD, MHC; TM=M; SS=Y; 5.77
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR, Lysyl_oxidase; TM=M; SS=M; 5.72
 454098; W27953; Hs.217493; Plakophilin; none, none; 5.71
 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevi; WD40; TM=M; SS=N; 5.70
 435505; AF200492; Hs.211238; interleukin-1 homolog 1; IL1; TM=M; SS=N; 5.69
 406685; M18728; ; gb:Human nonspecific crossreacting anti; ig; TM=M; SS=M; 5.67
 430280; AA361258; Hs.237688; interleukin 7 receptor; fn3, none; 5.63
 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none; TM=Y; SS=M; 5.61
 449722; BE280074; Hs.23960; cyclin B1; cyclin, cyclin_C; TM=M; SS=N; 5.61
 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1; TM=Y; SS=M; 5.60
 452862; AW378065; Hs.8687; ADAMTS2 (a disintegrin-like and metallo; Pep_M12B_propep, isp_1, Reprolysin; none; 5.58
 433662; W07162; Hs.150826; RAB25 RAB25, member RAS oncogene family; ras, ABC_tran, arf; TM=M; SS=M; 5.57
 411296; BE207307; Hs.10114; growth suppressor 1; ZO-G-Fell_Oxy; TM=M; SS=M; 5.55
 433848; AF095719; Hs.93764; carboxypeptidase A4; Zn_carbOpeptLPropep_M14; 5.54
 416819; U77735; Hs.80205; pim-2 oncogene; kinase; 5.48
 428368; BE440042; Hs.83326; matrix metalloproteinase 3 (stromelysin; hemopexin, Peptidase_M10, Astacin; 5.47
 452747; BE153855; Hs.61460; Ig superfamily receptor LNR; Ig, Rhabd_glycop; TM=Y; SS=M; 5.46
 444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase, abhydrolase_2; TM=Y; SS=M; 5.42
 413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8; 5.35
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 5.28
 418462; BE001596; Hs.85266; integrin, beta 4; fn3, integrin_B, Cax-beta, EGF; TM=M; SS=M; 5.26

- 429554; NM_012275; Hs.207224; interleukin 1, delta; IL1; TM=M; SS=N; 5.14
- 421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN_HIN; TM=M; SS=N; 5.13
- 439979; AW600291; Hs.6823; hypothetical protein FLJ10430; none; TM=M; SS=N; 5.11
- 427099; AB032953; Hs.173560; odd Oz/ten-m homolog 2 (Drosophila, mous; NHL; TM=M; SS=N; 5.11
- 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cy; IL8; TM=M; SS=Y; 5.08
- 436396; AI683487; Hs.152213; wingless-type MMTV integration site fami; wnt; none; 5.07
- 406690; M29540; Hs.220529; carcinoembryonic antigen-related cell ad; ig; TM=M; SS=M; 5.05
- 453905; NM_002314; Hs.35566; LIM domain kinase 1; pkinase, LIM, PDZ, zif-PARP; TM=M; SS=N; 5.04
- 414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibitor; serpin; 5.00
- 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH, death, TNFR, c6, Acyl-CoA_hydro; 4.96
- 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK; TM=M; SS=N; 4.93
- 412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like (rablins; kinesin, Tropomyosin; TM=M; SS=N; 4.92
- 445537; AJ245671; Hs.12844; EGF-like domain, multiple 6; EGF, MAM; 4.91
- 428953; AA306510; Hs.348183; tumor necrosis factor receptor superfam; 60s_ribosomal, Ribosomal_L10, TNFR, c6, DEAD; 4.90
- 436553; AW407157; Hs.181125; immunoglobulin lambda locus; ig, HSP70, Ppx-GppA; TM=M; SS=N; 4.89
- 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none, none; 4.84
- 430024; AI808780; Hs.227730; integrin, alpha 6; integrin_A, FG-GAP; TM=Y; SS=M; 4.81
- 439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_HUMAN DEATH; none, none; 4.80
- 444371; BE540274; Hs.239; forkhead box M1; Fork_head; TM=M; SS=N; 4.75
- 428582; BE336699; Hs.185055; BENE protein; none; TM=Y; SS=M; 4.74
- 419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; DSPc; 4.69
- 431630; NM_002204; Hs.265829; integrin, alpha 3 (antigen CD49C, alpha; FG-GAP, Rhabd_glycop, integrin_A; TM=Y; SS=M; 4.69
- 422310; AA316522; Hs.98370; cytochrome P450, subfamily IIS, polypept; none, pkinase, fn3, ig; 4.68
- 418067; AI127958; Hs.83393; cystatin E/M; cystatin; 4.66
- 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringla, trypsin, plant_thionins; 4.64
- 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudo; LIM, PDZ, pkinase; 4.62
- 410418; D31382; Hs.63325; transmembrane protease, serine 4; ldi_recept_a, trypsin; TM=Y; SS=M; 4.60
- 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen, COLFI, TSPN, laminin_G, CorA; 4.60
- 438113; AJ457908; Hs.8882; ESTs; 7tm_1, none; 4.60
- 418140; BE613836; Hs.83551; microfibrillar-associated protein 2; none; TM=M; SS=M; 4.57
- 408380; AF123050; Hs.44532; diubiquitin; ubiquitin; TM=M; SS=N; 4.55
- 422627; BE336587; Hs.118787; transforming growth factor, beta-induced; Fasciclin, ABC_tran, ABC_membrane, GTP_EFTU; TM=M; SS=M; 4.50
- 425247; NM_005940; Hs.155324; matrix metalloproteinase 11 (stromelysin; hemopexin, Peptidase_M10; 4.50
- 418558; AW082266; Hs.86131; Fas (TNFRSF6)-associated via death domain; death, DED; 4.49
- 408482; NM_000676; Hs.45743; adenosine A2b receptor; 7tm_1; TM=Y; SS=M; 4.48
- 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD, helicase_C, rrm, Ndr, Cys_knot, TIL, vwa, vwc, vwd, IQ, RIIa, abhydrolase, TGF-beta, DUF139, TPR, DSPc, tsp_1, Ribosomal_S21, rvp; TM=M; SS=N; 4.47
- 416178; AI808527; Hs.192822; serologically defined breast cancer anti; none; TM=M; SS=N; 4.47
- 411789; AF245505; Hs.72157; Adican; ig, LRR, LRRNT, LRRCT; TM=M; SS=M; 4.47
- 414561; AJ064813; Hs.195155; Homo sapiens amino acid transport system; Aa_trans; TM=Y; SS=N; 4.47
- 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (sur; BIR; TM=M; SS=N; 4.45
- 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR, LY6, ET, PLA2_inh; 4.43
- 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase, DSPc; TM=M; SS=N; 4.42
- 409041; AB033025; Hs.50081; Hypothetical protein, XP_051860 (KIAA119; none; TM=M; SS=M; 4.41
- 406908; Z25437; gb:HLsaptens protein-tyrosine kinase gen; none, none; 4.40
- 450701; H39960; Hs.288467; hypothetical protein XP_098151 (leucine; none, LRRCT, LRR; 4.40
- 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2, SH3, pkinase; TM=M; SS=N; 4.38
- 429500; X78565; Hs.289114; hexabrachion (tenascin C, cytostatin); EGF, fn3, fibrinogen_C, toxin_2, Keratin_B2; TM=M; SS=Y; 4.38
- 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2, STAT, STAT_bind, STAT_prot; TM=M; SS=N; 4.32
- 423725; AJ403108; Hs.132127; hypothetical protein LOC57822; none; TM=M; SS=N; 4.32
- 411573; AB029000; Hs.70823; KIAA1077 protein; Sulfatase; TM=M; SS=N; 4.31
- 408243; Y00787; Hs.624; interleukin 8; HLH, PAS, IL8; TM=M; SS=N; 4.31
- 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none, none; 4.30
- 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC; none; 4.29
- 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, jg, FAD_Synth, kdh, kdh_C, pkinase; 4.29
- 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig; TM=Y; SS=M; 4.29
- 404996; ; Target Exon; Peptidase_C1; TM=M; SS=M; 4.29
- 416539; Y07909; Hs.79368; epithelial membrane protein 1; PMP22, Claudin, oxldored_q5_N; TM=Y; SS=M; 4.28
- 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran, M, SMC_N, SMC_C, DUF164, none; 4.25
- 421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo_seg, HEAT; TM=M; SS=N; 4.25
- 424503; NM_002205; Hs.149609; Integrin, alpha 5 (fibronectin receptor; integrin_A, FG-GAP; TM=Y; SS=N; 4.24
- 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); PA; TM=Y; SS=N; 4.24
- 439720; AI935202; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none, SDF, sugar_tr; 4.23
- 437044; AL035864; Hs.69517; differentially expressed in Fanconi's an; none; TM=M; SS=M; 4.23
- 409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB alpha; TGF-beta, TGFb_propeptide, Tub; 4.20
- 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA, ABC_tran, CoaE; TM=M; SS=N; 4.20
- 417389; BE260964; Hs.82045; midline (neurite growth-promoting factor; PTN_MK; TM=M; SS=Y; 4.19
- 407137; T97307; gb:ye53h05.s1 Soares fetal liver spleen; GDA1_CD39, none; 4.18
- 419235; AW470411; Hs.288433; neurotrophin; none, none; 4.18
- 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema, PSI, TIG, integrin_B; TM=Y; SS=M; 4.18
- 456906; AF117646; Hs.156637; Cas-B-M (murine) ectropic retroviral tr; zf-C3HC4, Cbl_N, Cbl_N2, Cbl_N3; TM=M; SS=N; 4.17
- 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moi; NUDIX; TM=M; SS=M; 4.17
- 400288; X08255; Hs.149609; Integrin, alpha 5 (fibronectin receptor; integrin_A, FG-GAP; TM=Y; SS=N; 4.14
- 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase; TM=M; SS=N; 4.13
- 445417; AK001058; Hs.12680; a disintegrin-like and metalloprotease w; tsp_1, Reprolysin, Pep_M12B_propep; none; 4.12
- 433895; AI287912; Hs.3628; mitogen-activated protein kinase kinase; pkinase, zf-C4, CNH, ERM; TM=M; SS=N; 4.12
- 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank, pkinase; TM=M; SS=N; 4.09
- 419121; AA374372; Hs.89626; parathyroid hormone-like hormone; none, none; 4.08
- 416602; NM_006159; Hs.357895; Protein kinase C-binding protein NELL2; EGF, vwc, TSPN; 4.07
- 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1; TM=Y; SS=M; 4.07
- 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase; TM=M; SS=N; 4.06
- 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase; TM=M; SS=N; 4.03
- 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema, PSI, Integrin_B; TM=Y; SS=N; 4.02

- 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS;; 4.02
 413186; AU077141; Hs.374548; solute carrier family 16 (monocarboxylic; sugar_tr; TM=Y; SS=M; 4.01
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 4.01
 406906; Z25424; ; gbt; Hsapiens; protein-serine/threonine kt; none, none; 3.98
 5 450375; AA009647; Hs.352537; a disintegrin and metalloproteinase domain; Reprolysin, Pep_M12B_propep, disintegrin, Reprolysin, Pep_M12B_propep, disintegrin; 3.98
 410697; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl oxidase;; 3.96
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, rec; ITAM; TM=Y; SS=M; 3.95
 425849; AJ000512; Hs.295323; serum/glucocorticoid regulated kinase; pkinase, pkinase_C; TM=M; SS=M; 3.95
 10 417433; BE270266; Hs.82128; 5T4 oncofetal trophoblast glycoprotein; LRR, LRRNT, LRRCT; TM=Y; SS=M; 3.95
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily; SRP14, TNFR_c6;; 3.93
 407792; AI077715; Hs.39384; putative secreted ligand homologous to f; none; TM=M; SS=Y; 3.91
 424441; X14850; Hs.147097; H2A histone family, member X; histone, CBFD_NFYB_HMF;; 3.91
 415989; AI267700; Hs.351201; ESTs; none, none; 3.90
 423189; M59371; Hs.171596; EphA2; fn3, pkinase, SAM, EPH_1bd; TM=Y; SS=M; 3.90
 15 443859; NM_013409; Hs.9914; folistatin; kazal;; 3.89
 429612; AF062649; Hs.252587; pituitary tumor-transforming 1; none;; 3.89
 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death, ZUS;; 3.88
 450684; AA872605; Hs.25333; interleukin 1 receptor, type II; ig; TM=Y; SS=M; 3.88
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1, pkinase; TM=M; SS=N; 3.86
 20 413441; AI929374; Hs.75367; Src-like adapter; SH2, SH3; TM=M; SS=N; 3.84
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1; TIMP, pkinase, DAG_PE-bind, RBD; 3.83
 436291; BE568452; Hs.344037; protein regulator of cytokinesis 1; none; TM=M; SS=N; 3.82
 417512; X76534; Hs.82226; glycoprotein (transmembrane) nmb; PKD; TM=Y; SS=M; 3.81
 25 427647; W19744; Hs.180069; Homo sapiens cDNA FLJ20653 fis, clone KA; none, pkinase; 3.80
 431629; AU077025; Hs.265827; Interferon, alpha-inducible protein (clo; none; TM=M; SS=Y; 3.80
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HE; Nucleoside_tra2, none; 3.80
 430378; Z29572; Hs.2556; tumor necrosis factor receptor superfamily; IL2;; 3.79
 428157; AI738719; Hs.198427; hexokinase 2; hexokinase, hexokinase2, none; 3.78
 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD, helicase_C, CARD; TM=M; SS=N; 3.78
 30 417720; AA205625; Hs.208067; ESTs; none, none; 3.77
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase, Recep_L_domain, YLP; none; 3.77
 449029; N28989; Hs.22891; solute carrier family 7 (cationic amino; aa_permeases; TM=Y; SS=M; 3.76
 413436; AF238083; Hs.68051; sphingosine kinase 1; DAGK; TM=M; SS=N; 3.75
 416714; AF283770; Hs.79530; CD79A antigen (immunoglobulin-associated); ig, ITAM, Zn_cus; TM=Y; SS=M; 3.74
 35 413281; AA861271; Hs.222024; transcription factor BMAL2; HLH, PAS;; 3.74
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-con; UQ_con; TM=M; SS=N; 3.74
 431890; X17033; Hs.271988; integrin, alpha 2 (CD49B, alpha 2 subunit; vwa, integrin_A, FG-GAP; TM=Y; SS=M; 3.74
 424118; BE269041; Hs.140452; cargo selection protein (mannose 6 phosp; peritipic; 3.73
 40 426471; M22440; Hs.170009; transforming growth factor, alpha; EGF; TM=M; SS=M; 3.72
 422487; AJ010901; Hs.198267; mucin 4, tracheobronchial; EGF, vwd, AMOP;; 3.72
 450125; AA005418; Hs.158186; ESTs; CIDE-N, 7tm_1, none; 3.71
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; ig; TM=Y; SS=M; 3.70
 444006; BE395085; Hs.334762; type I transmembrane protein Fn14; Icl_recept_a, PKD, MHC_1; TM=M; SS=Y; 3.70
 45 422010; AA302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fis, clone C; none, SDF, sugar_tr; 3.70
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3; TM=M; SS=N; 3.69
 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-L; fn3, Y_phosphatase, carb_anhydrase; TM=Y; SS=M; 3.68
 443759; BE390832; Hs.134729; FXYD domain-containing ion transport reg; ATP1G1_PLM_MAT8; TM=Y; SS=M; 3.68
 452344; AF086457; Hs.55405; hypothetical protein MGC16212; Sulfate_transp, STAS;; 3.68
 439625; AF086453; Hs.58611; ESTs; Fork_head, glycolytic_enzy, Na_sulph_symp; 3.68
 50 426227; U67058; Hs.154269; Human proteinase activated receptor-2 mR; 7tm_1; TM=Y; SS=M; 3.66
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement comp; C1q, Collagen; 3.65
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (SH3, PH, RhoGEF; TM=M; SS=N; 3.64
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos; TM=M; SS=M; 3.64
 438707; L08239; Hs.5326; amino acid system N transporter 2; porc; ACAT, MBOAT; TM=Y; SS=M; 3.64
 55 422596; AF063611; Hs.118633; 2'-5'-oligoadenylate synthetase-like; ubiquitin;; 3.63
 449318; AW236021; Hs.78531; Homo sapiens, Similar to RIKEN cDNA 5730; none; TM=M; SS=N; 3.62
 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin, Guanylate_kin, PDZ, SH3; 3.62
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT; TM=M; SS=Y; 3.62
 452696; AI826645; Hs.211534; ESTs; ArfGAP, PH, Ank, Guanylate_kin, PDZ, SH3; 3.60
 60 407634; AW016569; Hs.136414; UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc; Galactosyl_T; TM=M; SS=Y; 3.59
 423575; C18863; Hs.163443; intron of perlestin (OSF-2os); Fasciclin, none; 3.59
 421391; AW304350; Hs.191958; immunoglobulin superfamily receptor tran; ig, none; 3.58
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig, pkinase; TM=Y; SS=M; 3.58
 65 419912; AF249745; Hs.6066; Rho guanine nucleotide exchange factor (SH3, PH, RhoGEF; TM=M; SS=N; 3.58
 431457; NM_012211; Hs.256297; Integrin, alpha 11; FG-GAP, vwa; TM=Y; SS=M; 3.57
 430379; AF134149; Hs.240395; potassium channel, subfamily K, member 6; ion_trans; TM=Y; SS=M; 3.55
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none; TM=Y; SS=M; 3.55
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog (E coli Rg; none; 3.53
 70 426500; NM_014638; Hs.170156; KIAA0450 gene product; C2, PI-PLC-Y; TM=M; SS=N; 3.53
 429556; AW139399; Hs.314807; ESTs; none; TM=M; SS=N; 3.52
 449101; AA205847; Hs.23016; G protein-coupled receptor, 7tm_1; TM=Y; SS=M; 3.52
 432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin; TM=Y; SS=M; 3.51
 433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none; TM=Y; SS=M; 3.51
 75 452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, subf. ABC_tran, ABC_membrane, SRP54, Thymidylate_kin; TM=Y; SS=M; 3.49
 425566; AW162943; Hs.250618; UL16 binding protein 2; Icl_recept_a, PKD, MHC_1; TM=M; SS=Y; 3.48
 402447; ; C1000201.gij204416[gb]AA02627.1 (LD519; none; TM=Y; SS=M; 3.48
 431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept; TM=M; SS=M; 3.48
 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A receptor, Neur_chan_LBD, Neur_chan_membr; TM=Y; SS=M; 3.48
 80 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3, TPR; TM=M; SS=N; 3.48
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX); Troponin_Ext_endo_phos, IQ; TM=M; SS=N; 3.47
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese;; 3.44
 446051; BE048061; Hs.37054; ephrin-A3; Ephrin_A, deamin, dsrmz-alpha; 3.43
 418641; BE243136; Hs.86947; a disintegrin and metalloproteinase domain; disintegrin, Reprolysin, Pep_M12B_propep, EGF; TM=Y; SS=M; 3.42

- 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF,laminin_Nterm,Integrin_B; 3.42
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-assoc; kinesin; TM=M;SS=N; 3.42
 430044; AA464510; Hs.152812; ESTs; none:none; 3.42
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPN,HIN; 3.39
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1; TM=Y;SS=M; 3.39
 428293; BE250944; Hs.183556; solute carrier family 1 (neutral amino acid transporter); TM=M;SS=N; 3.39
 443648; AI085377; Hs.143610; ESTs; Fork_head:none; 3.39
 418869; AW516565; ; gbxxq01d05.x1 Soares_NHCEC_cervical_tumor; none,RasGAP,WW,IQ; 3.38
 432179; X75208; Hs.2913; EphB3; EPH_Lbd,fn3,kinase,SAM; TM=Y;SS=M; 3.38
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell; ig; TM=Y;SS=M; 3.38
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK_CoaE; 3.37
 408716; AI567839; Hs.151714; Homo sapiens mRNA for KIAA1769 protein; ; UvrD-helicase,RNB,Rum; TM=M;SS=N; 3.37
 457001; J03258; Hs.2062; vitamin D (1,25-dihydroxyvitamin D3) receptor; hormone_rec,zf-C4,Metallothio_5; TM=M;SS=N; 3.37
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevisiae); CDC45; TM=M;SS=N; 3.37
 421817; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU; TM=M;SS=M; 3.36
 400298; AA032279; Hs.61535; six transmembrane epithelial antigen of; none; TM=Y;SS=N; 3.35
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3; 3.33
 400261; ; Hs.1802; Eos Control; Ig,MHC_II_beta; TM=Y;SS=M; 3.33
 410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3; TM=M;SS=N; 3.32
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none,lectin_c; 3.32
 415065; BE267931; Hs.78996; proliferating cell nuclear antigen; PCNA,PCNA_C; TM=M;SS=N; 3.31
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg,UQ_con:none; 3.31
 426840; BE244217; Hs.172690; diacylglycerol kinase, alpha (80kD); ehand,DAG_PE-bind,DAGKa,DAGKc,DC1; TM=M;SS=N; 3.31
 434419; AL040606; Hs.296938; dual specificity phosphatase 7; DSPc; TM=M;SS=N; 3.31
 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; kinase,RIO1; TM=M;SS=N; 3.31
 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4; TM=Y;SS=M; 3.31
 423973; AF038481; Hs.136574; arachidonate 12-lipoxygenase, 12R type; lipoxygenase,PLAT; TM=M;SS=N; 3.30
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (act); ig,kinase; TM=Y;SS=M; 3.30
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,Ig,Neuregulin; TM=M;SS=N; 3.28
 423778; Y09267; Hs.132821; flavin containing monooxygenase 2; FMO-like,pyr_redox; TM=Y;SS=M; 3.28
 426457; AW894667; Hs.380138; chimerin (chimaerin) 1; DAG_PE-bind,RhoGAP,SH2; TM=M;SS=N; 3.28
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none; TM=Y;SS=M; 3.27
 431886; L77964; Hs.271980; mitogen-activated protein kinase 6; kinase; TM=M;SS=N; 3.27
 430397; AI924533; Hs.105607; bicarbonate transporter related protein; HCO3_cotransp; TM=Y;SS=N; 3.27
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic; PI3_P4_kinase,FAT,FATC; TM=M;SS=N; 3.26
 446006; NM_004403; Hs.13530; deafness, autosomal dominant 5; none; TM=M;SS=M; 3.26
 444783; AK001468; Hs.62180; anillin (Drosophila Scrap homolog), act; PH; none; 3.25
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2; TM=Y;SS=M; 3.25
 405932; ; C15000305; gij3806122[gijAAC69198.1] (AF0); ras; TM=M;SS=N; 3.25
 400205; ; Hs.81848; NM_006265; Homo sapiens RAD21 (S. pombe); DUF173; 3.25
 432874; W94322; Hs.279651; melanoma inhibitory activity; SH3; TM=M;SS=Y; 3.24
 412942; AL120344; Hs.75074; mitogen-activated protein kinase-activat; kinase; TM=M;SS=N; 3.23
 435472; AW972330; Hs.283022; triggering receptor expressed on myeloid; ig; TM=M;SS=M; 3.22
 439285; AL133916; Hs.47860; hypothetical protein FLJ20093; ig,kinase,LRR,LRRNT,LRRCT; none; 3.22
 410434; AF051152; Hs.63668; toll-like receptor 2; LRR,LRRCT,TIR; TM=M;SS=M; 3.22
 427318; AF186081; Hs.175783; zinc transporter; Zip; TM=Y;SS=M; 3.22
 436075; BE090176; Hs.179902; transporter-like protein; none; TM=Y;SS=M; 3.22
 428598; AA852773; Hs.334838; KIAA1866 protein; none; NA;NA; 3.22
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M;SS=N; 3.22
 415149; X12451; Hs.78056; calhepsin L; Peptidase_C1; 3.21
 423393; R37772; Hs.21420; p21-activated protein kinase 6; kinase,PBD; TM=M;SS=N; 3.21
 424616; L29472; Hs.1802; major histocompatibility complex, class I; ig,MHC_II_beta; TM=Y;SS=M; 3.20
 438564; AA381553; Hs.198253; major histocompatibility complex, class I; ig,MHC_II_alpha; none; 3.20
 456181; L36463; Hs.1030; ras inhibitor; RA,SH2,VPS9; TM=M;SS=N; 3.20
 418613; AA744529; Hs.85575; mitogen-activated protein kinase kinase; kinase,CNH; TM=M;SS=N; 3.19
 440582; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin,bZIP; TM=M;SS=N; 3.18
 415010; NM_004203; Hs.77783; membrane-associated tyrosine- and threonine; ank,kinase,UFP0073; 3.16
 419216; AU076718; Hs.164021; small inducible cytokine subfamily B (C; IL8; 3.16
 450737; AW007152; Hs.63325; transmembrane protease, serine 4; trypsin,ldl_recept_L; none; 3.16
 426395; BE151985; Hs.355669; hypothetical protein FLJ23316; kinase; none; 3.15
 412939; AW411491; Hs.75069; eukaryotic translation elongation factor; none; none; 3.15
 433376; AI249381; Hs.74122; caspase 4, apoptosis-related cysteine protease; CARD,ICE_p10,ICE_p20; 3.15
 410668; BE379794; Hs.159651; hypothetical protein; death,TNFR_c6; TM=Y;SS=M; 3.15
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC; TM=Y;SS=N; 3.15
 432251; AW972383; Hs.232165; polycythemia rubra vera 1; cell surface; none; TM=M;SS=M; 3.15
 407844; AW073716; Hs.8037; ESTs; transmembrane4; none; 3.14
 408634; AW407254; Hs.356216; calmodulin 2 (phosphorylase kinase, delta); none; none; 3.14
 423061; AI290473; Hs.44807; ESTs; integrin_B,Sema,PSI,TIG; none; 3.14
 438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ; 3.13
 431236; AV656840; Hs.285115; interleukin 13 receptor, alpha 1; fn3; TM=Y;SS=M; 3.13
 425394; AA356730; Hs.323949; kangal 1 (suppression of tumorigenicity); transmembrane4; none; 3.13
 429336; AB005038; Hs.199270; cytochrome P450, subfamily XXVIB (25-hy; p450; 3.13
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; ig,Isodh,Fibosomal_L6,F-box; TM=Y;SS=M; 3.13
 429305; AF095727; Hs.287832; myelin protein zero-like 1; ig,transmembrane4; TM=Y;SS=M; 3.12
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,kinase; TM=M;SS=N; 3.12
 417386; AL037228; Hs.301957; D123 gene product; NUDIX,secY,E1_dehydrog,transkel_pyr; TM=Y;SS=M; 3.11
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ion_trans,SPRY,RYDR,ITPR,RyR,MIR; TM=Y;SS=N; 3.11
 440005; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-like; AAA,NB-ARC,PAAD_DAPIN; NA;NA; 3.10
 406467; ; Target Exon; ehand,Acyltransferase; none; 3.10
 422956; BE545072; Hs.122579; ECT2 protein (Epithelial cell transformant; BRCT,RhoGEF; TM=M;SS=N; 3.10
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazara; none; none; 3.09
 437016; AU076916; Hs.5398; guanine monophosphate synthetase; PHD,SET,zf-
 CXXC,EGF,ank,notch,WW,FCH,GATase,GMP_synth_C,Ocludin,YEATS,metallothio,EB,heme_1,RCC1,ZZ,FeThRed_A,ENTH,Band_41,HECT; TM=M;SS=N; 3.09

- 441384; AA447849; Hs.288560; retinoic acid induced 3; 7tm_3:none; 3.09
 416636; N32536; Hs.42645; solute carrier family 18 (monocarboxylic; none:none; 3.09
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans;TM=Y;SS=M; 3.09
 426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M;SS=N; 3.08
 5 414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS;TM=Y;SS=M; 3.08
 402233; ; NM_030760; Homo sapiens endothelial diff; 7tm_1;TM=Y;SS=M; 3.07
 430066; A929659; Hs.237825; signal recognition particle 72kD; TPR,ARC,SAICAR_synt; 3.07
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 3.06
 434263; N34895; Hs.79187; ESTs; Ig:none; 3.06
 10 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none;TM=M;SS=Y; 3.05
 409378; U42387; Hs.54426; pancreatic polypeptide receptor 1; 7tm_1;TM=Y;SS=M; 3.05
 410165; BE560228; Hs.71869; apoptosis-associated speck-like protein; PAAD_DAPIN,CARD;TM=M;SS=N; 3.05
 440270; NM_015986; Hs.7120; cytokine receptor-like molecule 9; tn3; 3.05
 15 449003; X76342; Hs.389; alcohol dehydrogenase 7 (class IV), mu alpha; adh_zinc;TM=M;SS=N; 3.05
 420189; AW296380; Hs.95821; osteoclast stimulating factor 1; SH3;ank; 3.05
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 doma; SH2; 3.05
 421541; NM_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, polyp; pkinase, pkinase_C;TM=M;SS=N; 3.04
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4,UAM;TM=M;SS=N; 3.03
 20 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb_DNA-
 binding,THF_DHG_CYH,THF_DHG_CYH_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,M, xan_ur_permease, HCO3_cotransp;TM=M;SS=N; 3.03
 449048; Z45051; Hs.22920; similar to S68401 (cattle) glucose induc; Lamp;TM=M;SS=M; 3.03
 413869; NM_000878; Hs.75595; interleukin 2 receptor, beta; none;TM=Y;SS=M; 3.02
 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequ; K_tetra,DUF51;none; 3.02
 25 436576; AJ458213; Hs.77542; ESTs; 7tm_1,DnaJ; 3.02
 446269; AW263155; Hs.14559; hypothetical protein FLJ10540; none;TM=M;SS=N; 3.02
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1,7tm_2;TM=Y;SS=M; 3.01
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cyr; IL8;TM=M;SS=Y; 3.00
 421267; BE314724; Hs.103081; ribosomal protein S6 kinase, 70kD, polyp; pkinase, pkinase_C;TM=M;SS=N; 3.00
 409705; M37762; Hs.56023; brain-derived neurotrophic factor; NGF; 2.99
 30 429903; AL134197; Hs.93597; cyclin-dependant kinase 5, regulatory su; CDK5_activator;none; 2.99
 430696; AA531276; Hs.59509; ESTs; pkinase,PP2C;none; 2.98
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), ly; integrin_B,EGF,PSI;TM=Y;SS=M; 2.97
 410026; A1912051; Hs.55016; hypothetical protein FLJ21935; none:none; 2.97
 35 448733; NM_005629; Hs.187958; solute carrier family 6 (neurotransmitter; SNF;TM=Y;SS=N; 2.97
 432562; BE531048; Hs.278422; DKFZP586G1122 protein; zf-C2H2;TM=M;SS=N; 2.97
 453035; AW581943; Hs.334; Rho guanine nucleotide exchange factor (i; none:none; 2.97
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none,spectrin,SH3,PH,CH; 2.97
 431941; AK001016; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone CO; pkinase,Furin-like,Recep_L_domain;none; 2.96
 441389; AF134838; Hs.7835; endocytic receptor (macrophage mannose r; tn2,Ictln_c;TM=Y;SS=M; 2.95
 40 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (i; MIF,sugar_tr;none; 2.94
 427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone L; 7tm_1;none; 2.94
 402556; ; C1000201;gi2044416(gb)AAA02627.1 (L0519; none;TM=Y;SS=M; 2.94
 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member; death,TNFR_c6;TM=Y;SS=M; 2.94
 442080; AW444761; Hs.72801; ESTs; ank; 2.94
 45 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M;SS=N; 2.93
 444809; BE207568; Hs.208219; occludin; transmembrane4;TM=Y;SS=N; 2.93
 449843; R85337; Hs.24030; solute carrier family 31 (copper transpo; none;TM=Y;SS=M; 2.93
 416110; Z42262; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,integrin_B;TM=Y;SS=M; 2.93
 453768; BE382870; Hs.198511; Homo sapiens mRNA; cDNA DKFZp7611177 (tr; arf,G-alpha;none; 2.92
 50 414825; X06370; Hs.77432; epidermal growth factor receptor (avian ; Furin-like,pkinase,Recep_L_domain;TM=M;SS=M; 2.92
 421429; NM_014922; Hs.104305; death effector filament-forming Ced-4-li; LRR,PAAD_DAPIN,AAA,CARD,NB-ARC;NA;NA; 2.92
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C;none; 2.91
 451292; AB037716; Hs.26204; KIAA1295 protein; SH3;TM=M;SS=N; 2.91
 55 422127; AW504286; Hs.112049; SET binding factor 1; dDENN,DENN,GRAM,PH; 2.91
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=M; 2.90
 430451; AAB36472; Hs.297939; cathepsin B; Peptidase_C1,pro_isomerase; 2.90
 424046; AF027866; Hs.138202; serine (or cysteine) proteinase inhibitor; serpin;TM=M;SS=N; 2.89
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal_L37ae,pkinase,POLO_box,IRNA-synt_1b,dynamnin,dynamnin_2,GED,bZIP,M; 2.89
 429619; AL120751; Hs.211568; eukaryotic translation initiation factor; none:none; 2.89
 60 413879; AA132861; Hs.212533; Homo sapiens cDNA: FLJ22572 fis, clone H; none:none; 2.89
 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related ; SH2,SH3,pkinase;TM=M;SS=N; 2.89
 422610; AF153820; Hs.1547; potassium inwardly-rectifying channel, s; IRK;TM=Y;SS=N; 2.89
 405556; ; homeodomain-interacting protein kinase 3; trypsin;TM=M;SS=N; 2.89
 65 423804; AW403448; Hs.1706; interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M;SS=N; 2.89
 425262; D87119; Hs.155418; GS3955 protein; pkinase; 2.88
 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) ; NDK,PH,Oxysterol_BP; 2.88
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin,tn2;TM=Y;SS=M; 2.88
 414703; BE243877; Hs.380063; ATPase, Na? transporting, beta 3 polypep; Na_K-ATPase;TM=Y;SS=M; 2.87
 70 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2;none; 2.86
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affi; SDF;TM=Y;SS=M; 2.86
 458039; AAB35884; Hs.130685; leukotriene b4 receptor (chemokine recep; CIDE-N;none; 2.86
 434417; AL110157; Hs.3843; Homo sapiens mRNA; cDNA DKFZp586F2224 (t; DSPc;none; 2.86
 425802; Y14838; chemokine-like receptor 1; 7tm_1;none; 2.86
 75 403112; ; Target Exon; eifhand,C2,PH,PI-PLC-Y,PI-PLC-X; 2.86
 435563; AF210317; Hs.95497; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;SS=N; 2.85
 442117; AW664964; Hs.128899; ESTs; hypothetical protein for IMAGE;447; none:none; 2.84
 457819; AA057484; Hs.35406; FLJ20522 Hypothetical protein FLJ20522; none:none; 2.84
 456629; AW891965; Hs.367942; histone deacetylase 3; HSP90,HATPase_c,zf-C2H2,PHD;none; 2.83
 408873; AL046017; Hs.356216; calmodulin 2 (phosphorylase kinase, delt; none:none; 2.83
 80 446947; AF146747; Hs.232165; polycythemia rubra vera 1; cell surface ; none;TM=M;SS=M; 2.83
 448386; AB037750; Hs.21061; KIAA1329 protein; PKD,BNR;TM=Y;SS=M; 2.82
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; myosin_head,IQ,zf-MYND;TM=M;SS=M; 2.82
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta2; ASC;TM=Y;SS=M; 2.82

- 459707; AA631362; Hs.120866; gb:np86b01.s1 NCI_OGAP_Thy1 Homo sapiens; 7tm_1:none; 2.82
 422699; BE410590; Hs.119257; ems1 sequence (mammary tumor and squamous; SH3,HS1_rep;TM=M;SS=N; 2.82
 438108; AJ471795; Hs.287776; vanilloid receptor-related osmotically a; ank,ion_trans;TM=Y;SS=N; 2.82
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin,fn3,Y_phosphatase;TM=M;SS=N; 2.82
 448595; AB014544; Hs.21572; KIAA0644 gene product; LRR,LRRCT;TM=Y;SS=M; 2.81
 423598; BE247600; Hs.377968; ESTs; 7tm_1;TM=Y;SS=M; 2.81
 412970; AB026438; Hs.177534; dual specificity phosphatase 10; Rhodanese,DSPC; 2.81
 414198; AW505308; Hs.75812; phosphoenolpyruvate carboxykinase 2 (mit; PEPCK; 2.81
 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 2.81
 432314; AA533447; Hs.285173; ESTs; Xlink:none; 2.81
 416207; NM_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, comp; none;TM=Y;SS=M; 2.80
 446985; AL038704; Hs.156827; ESTs, Weakly similar to ALU1_HUMAN ALU S; SAM,SH3,HS1_rep; 2.80
 428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone L;
 aa_pemeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_PI4_kinase,FAT,FATC,BolA,RUN;TM=M;SS=N; 2.80
 432886; BE159028; Hs.279704; chromatin accessibility complex 1; none;TM=M;SS=N; 2.80
 426006; R49031; Hs.22627; ESTs; pkinase,TBC; 2.79
 414217; AI309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none;NA;NA; 2.79
 411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiase;; 2.79
 450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypothet; ABC_tran,ABC_membrane,Ig,MHC_JI_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 2.78
 424291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 2.78
 421448; AF033850; Hs.104519; phospholipase D2; PH,PLDC,PX;TM=M;SS=N; 2.78
 410226; AI831958; Hs.61053; hypothetical protein; SH3,TPR;TM=M;SS=N; 2.78
 433535; AF111108; Hs.3382; protein phosphatase 4, regulatory subunit; HEAT;TM=M;SS=N; 2.78
 442503; AF147078; Hs.375031; p53-responsive gene 5; K_tetra,ion_trans:none; 2.77
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/H; TPR,PDZ,VWV,Guanylate_kin;TM=M;SS=N; 2.77
 454294; AB000734; Hs.50640; JAK binding protein; SH2;TM=M;SS=N; 2.77
 440188; AK001812; Hs.7036; N-Acetylglucosamine kinase; ROK;TM=M;SS=N; 2.77
 449539; W80363; Hs.58446; ESTs; pkinase,Furin-like,Recep_L_domain:none; 2.76
 422667; H25642; Hs.132821; ESTs; FMO-like,FMO-like; 2.76
 415012; NM_004383; Hs.77793; c-src tyrosine kinase; SH2,SH3,pkinase;TM=M;SS=N; 2.76
 402316; ; NM_013447;Homo sapiens egf-like module c; 7tm_2,GPS;TM=M;SS=M; 2.75
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M;SS=N; 2.75
 447250; AI878909; Hs.17883; protein phosphatase 1G (formerly 2C), ma; PP2C;TM=M;SS=N; 2.75
 438629; AI187380; Hs.257170; ESTs, Weakly similar to T12515 hypothet; TNFR_c6:none; 2.75
 451144; AW956103; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme; HATPase_c:none; 2.74
 408543; N78098; Hs.44289; ESTs; none;TM=M;SS=N; 2.74
 429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 2.74
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; ptkB;TM=M;SS=N; 2.73
 420602; AF060877; Hs.99236; regulator of G-protein signalling 20; RGS;TM=M;SS=N; 2.73
 407217; AA477136; Hs.105584; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C;TM=M;SS=N; 2.73
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPC,Y_phosphatase;TM=M;SS=N; 2.73
 410590; BE615216; Hs.64746; chloride intracellular channel 3; none;TM=M;SS=N; 2.73
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 2.73
 438022; AW517524; Hs.135201; NOD2 protein; LRR,CARD,GTP_CDC,Viral_helicase1;TM=M;SS=N; 2.72
 420829; AI694143; Hs.326248; programmed cell death 4; MA3;TM=M;SS=N; 2.72
 421155; H87879; Hs.102267; lysyl oxidase; Lysyl_oxidase,Aldose_epim,Epimerase;; 2.72
 448564; AL044982; Hs.21453; inositol 1,4,5-trisphosphate 3-kinase C; IPK; 2.71
 449961; AW265634; Hs.133100; ESTs; pkinase,Furin-like,Recep_L_domain:none; 2.71
 444633; AF111713; Hs.12284; junctional adhesion molecule 1; ig;TM=Y;SS=M; 2.71
 412259; AI560292; Hs.279909; protein phosphatase 2 (formerly 2A), reg; WD40;TM=M;SS=N; 2.71
 419569; AI971651; Hs.91143; jagged 1 (Alagille syndrome); DSL,EGF,janinin_EGF,vwc,metallo;TM=M;SS=M; 2.71
 452401; NM_007115; Hs.29352; tumor necrosis factor, alpha-induced pro; Xlink,CUB; 2.71
 458190; BE561793; Hs.21446; KIAA1716 protein; ASC,Galactosyl_LT:none; 2.70
 432126; AA865239; Hs.37196; ESTs; 7tm_1;TM=Y;SS=M; 2.70
 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS_C;TM=M;SS=N; 2.70
 424717; H03754; Hs.152213; wingless-type MMTV integration site fam1; vml:none; 2.70
 414108; AI267592; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol_BP,pkinase;TM=M;SS=N; 2.70
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3,HS1_rep;TM=M;SS=N; 2.70
 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kin; none:none; 2.69
 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG;TM=M;SS=N; 2.69
 404891; ; Target Exon; none:none; 2.69
 432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C;TM=M;SS=N; 2.69
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2,SH3,pkinase;TM=M;SS=N; 2.68
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan rec; Ig,kringle,pkinase,Fz;TM=Y;SS=M; 2.68
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor.; Ig,pkinase;TM=Y;SS=N; 2.68
 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, for; Ig,pkinase;TM=Y;SS=M; 2.68
 436856; AI469355; Hs.127310; ESTs; pkinase,rm;TM=M;SS=N; 2.68
 437429; H79981; Hs.5613; Homo sapiens mRNA; cDNA DKFZp564E2222 (f; SH2,SH3,BTB; 2.67
 450690; AA295696; Hs.333418; FXID domain-containing ion transport reg; ATP1G1_PLM_MATR;TM=Y;SS=M; 2.67
 452069; AB028949; Hs.183994; KIAA1026 protein; Metallophos;TM=M;SS=N; 2.67
 445330; RS2656; Hs.21691; ESTs; 7tm_1:none; 2.67
 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1;TM=Y;SS=M; 2.67
 419754; H52299; Hs.308467; Homo sapiens mRNA; cDNA DKFZp586I0523 (f; none;TM=M;SS=N; 2.67
 434237; AF119908; Hs.235516; hypothetical protein PRO2955; none; 2.67
 445828; BE313754; Hs.13350; Homo sapiens mRNA; cDNA DKFZp586D0918 (f; Ig,tsp_1,ZU5,Nucleoside_tran; 2.66
 446696; AF279265; Hs.298476; solute carrier family 26, member 6; Sulfate_transp,STAS,xan_ur_permease;TM=Y;SS=N; 2.66
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,integrin_B,Ricin_B_tectin; 2.66
 413745; AW247252; Hs.75514; nucleoside phosphorylase; Mtap_PNP;; 2.66
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M;SS=N; 2.66
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 2.66
 449030; AI365582; Hs.57100; Homo sapiens mRNA for FLJ00016 protein; ; transmembrane4;TM=Y;SS=M; 2.66
 434979; AI953054; Hs.89643; transketolase (Wernicke-Korsakoff syndr; ASC,transketolase,transket_pyr,transketolase_C,pkinase; 2.66
 406137; ; NM_000179;Homo sapiens mutS (E. coli) h; MutS_C,PWWP,MutS_N;TM=M;SS=N; 2.66

- 412935; BE267045; Hs.75064; tubulin-specific chaperone c; none; 2.66
 408633; AW963372; Hs.222088; PRO2000 protein; bromodomain,AAA,Sigma54_activat; 2.66
 412817; AL037159; Hs.74619; proteasome (prosome, macropain) 26S subu; PC_rep;TM=M;SS=N; 2.65
 452682; AA456193; Hs.374574; progesterone membrane binding protein; homeobox;none; 2.65
 401752; ; RAN binding protein 3; SH2,STAT,STAT_bind,STAT_proLon_trans,PAC,PAS,Orexin; 2.65
 450747; AI064821; Hs.129953; ESTs, Highly similar to 1818357A EWS gen; rrm,zf-RanBP,GAS2; 2.65
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm_2,HRM;TM=Y;SS=M; 2.64
 452701; NM_005110; Hs.30332; glutamine-fructose-6-phosphate transamin; GATase_2,SIS;TM=M;SS=N; 2.64
 433933; AI754389; Hs.355397; Homo sapiens clone TCCCA00164 mRNA sequ; none;NA;NA; 2.64
 421677; H64092; Hs.38282; ESTs; A1pp,Armadillo_seg,IBB; 2.64
 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none; 2.64
 423198; M81933; Hs.1634; cell division cycle 25A; Rhodanesa;none; 2.64
 435905; AW997484; Hs.5003; KIAA0456 protein; SH3,RhoGAP,FCH;TM=M;SS=N; 2.64
 437712; X04588; Hs.85844; neurotrophic tyrosine kinase, receptor, ; Tropomyosin,phkinase,LRR,LRRCT,Hydantoinase_B,Hydantoinase_A;TM=M;SS=N; 2.63
 458946; AA009716; Hs.42311; ESTs; none,DSPc,Y_phosphatase; 2.63
 447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5_FB_type_C;TM=M;SS=M; 2.63
 445462; AA378776; Hs.288649; hypothetical protein MGC3077; none; 2.63
 425075; AA506324; Hs.1852; acid phosphatase, prostate; acid_phosphat;TM=Y;SS=M; 2.63
 405588; ; NM_000299;Homo sapiens plakophilin 1 (q; Armadillo_seg;TM=M;SS=N; 2.63
 438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH;none; 2.63
 448243; AW369771; Hs.367688; integrin, beta 8; integrin_B;none; 2.63
 452012; AA307703; Hs.279766; kinesin family member 4A; kinesin,DNA_topoisolV,K-box;TM=M;SS=N; 2.63
 412182; AA205588; Hs.73737; Splicing factor, arginine/serine-rich, 4; rrm,hormone_rec,zf-C4,sugar_tr; 2.63
 423887; AL080207; Hs.134585; DKFZP434G232 protein; ABC_tran;TM=Y;SS=N; 2.63
 417497; AW402482; Hs.82212; CD53 antigen; transmembrane4;TM=Y;SS=M; 2.62
 413407; AI356293; Hs.75339; inositol polyphosphate phosphatase-like ; SH2,SAM,Exo_endo_phos; 2.62
 414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c;TM=Y;SS=M; 2.62
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule; EGF,lectin_c,sushi;TM=M;SS=M; 2.62
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone;TM=M;SS=N; 2.62
 401812; ; sorting nexin 14; AAA,NB-ARC,APS_kinase,cdc48_N,cdc48_2,none; 2.61
 417886; AA214584; ; ESTs; SPRY,7tm_3,ANF_receptor;none; 2.61
 457670; AF119668; Hs.23449; insulin receptor tyrosine kinase substr; SH3;TM=M;SS=N; 2.61
 428512; AI018187; Hs.375624; Human DNA sequence from clone RP11-243J1; none; 2.61
 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotat; Prbicosylran,OMPdecase;TM=M;SS=N; 2.61
 454042; H22570; Hs.47860; hypothetical protein FLJ20093; lg,phkinase,LRR,LRRNT,LRRCT;none; 2.61
 421077; AK000061; Hs.101590; hypothetical protein; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dENN,DENN,uDENN;TM=M;SS=N; 2.60
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; pkinase;TM=M;SS=N; 2.60
 416661; AA634543; Hs.79440; IGF-II mRNA-binding protein 3; KH-domain,rrm;TM=M;SS=N; 2.60
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin_ADF; 2.60
 411133; AW819204; ; gb:CM1-ST0283-071299-061-h03 ST0283 Homo; ANF_receptor;none; 2.60
 405602; ; Target Exon; pkinase; 2.60
 400440; X83957; Hs.83870; nebulin; SH3,Nebulin; 2.60
 424848; AI263231; Hs.327090; EST; SH3,PDZ,Guanylate_kin,none; 2.59
 432268; BE311858; Hs.274230; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase,ATP-sulfurylase;TM=M;SS=N; 2.59
 452690; AI536070; Hs.15085; ESTs; pou/homeobox,lq_chan,ANF_receptor; 2.59
 422753; AI928995; Hs.1575; small nuclear ribonucleoprotein D3 poly; Sm; 2.59
 428028; U52112; Hs.182018; interleukin-1 receptor-associated kinase; death,pkinase;TM=M;SS=N; 2.58
 433573; AF234887; Hs.57652; cadherin, EGF LAG seven-pass G-type rece; 7tm_2,EGF,cadherin,laminin_EGF,laminin_G,Trypan_glycop,GPS,HRM;TM=Y;SS=M; 2.58
 422785; AI824114; Hs.289088; heat shock 90kD protein 1, alpha; zf-C2H2;none; 2.58
 418685; U76376; Hs.87247; harakiri, BCL2-interacting protein (cont; none;TM=M;SS=M; 2.58
 452329; N36626; Hs.29106; mitogen-activated protein kinase phosphat; DSPc;TM=M;SS=N; 2.58
 428405; Y00762; Hs.2266; cholinergic receptor, nicotinic, alpha p; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 2.58
 421251; Z28913; Hs.102948; enigma (LIM domain protein); LIM,PDZ; 2.57
 407245; X90568; Hs.172004; fliin; fn3,lg,SGXXSG,pkinase;TM=M;SS=N; 2.57
 422309; U79745; Hs.114924; solute carrier family 16 (monocarboxylic; sugar_tr;TM=Y;SS=M; 2.57
 401751; ; RAN binding protein 3; Orexin,SH2,STAT,STAT_bind,STAT_proLon_trans,PAC,PAS;none; 2.57
 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M;SS=N; 2.57
 422282; AF019225; Hs.114309; apolipoprotein L; MoLA_ExbB;TM=Y;SS=M; 2.57
 439863; BE547830; Hs.375208; paired immunoglobulin-like receptor beta; lipoygenase,PLAT,lipoygenase,PLAT; 2.57
 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 2.57
 401218; ; eukaryotic translation elongation factor; ion_trans;TM=Y;SS=N; 2.57
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L OR; PLDc;TM=M;SS=N; 2.57
 444743; AA045648; Hs.301957; nudix (nucleoside diphosphate linked moi; NUDIX,secY,E1_dehydrog,transke_l_pyr;TM=Y;SS=M; 2.56
 429782; NM_005754; Hs.220689; Ras-GTPase-activating protein SH3-domain; rrm,NTF2;TM=M;SS=N; 2.56
 442994; AI026718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal_S14; 2.56
 456602; AA411807; Hs.118964; ESTs, Weakly similar to KIAA1150 protein; none,pkinase; 2.56
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr; SH3,PX;TM=M;SS=N; 2.56
 441699; AW511126; Hs.127572; ESTs; none,Aa_trans; 2.56
 447912; AW576549; Hs.165728; ESTs, Weakly similar to I38022 hypotheti; none,GSPx,ABC_tran; 2.56
 442945; AI024849; Hs.131853; ESTs; pkinase;none; 2.56
 453199; AI336266; Hs.32353; mitogen-activated protein kinase kinase ; pkinase;TM=M;SS=N; 2.56
 451477; AI798425; Hs.42710; ESTs; SH3;none; 2.56
 415091; AL044872; Hs.77910; 3-hydroxy-3-methylglutaryl-Coenzyme A sy; HMG_CoA_synt; 2.55
 413529; U11874; Hs.846; interleukin 8 receptor, beta; 7tm_1;TM=Y;SS=N; 2.55
 425345; AU077297; Hs.155894; protein tyrosine phosphatase, non-recept; Y_phosphatase,DSPc;TM=M;SS=M; 2.55
 401321; ; receptor tyrosine kinase-like orphan rec; none;TM=M;SS=N; 2.55
 446999; AA151520; Hs.351416; hypothetical protein MGC4485; none;none; 2.55
 401057; ; eukaryotic translation elongation factor; ion_trans,IQ;TM=Y;SS=N; 2.55
 414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antigen); transmembrane4;TM=Y;SS=M; 2.55
 408204; AA454501; Hs.43666; protein tyrosine phosphatase type IVA, m; Y_phosphatase;TM=M;SS=N; 2.54
 424539; L02911; Hs.150402; Activin A receptor, type I (ACVR1) (ALK; pkinase,Activin_rec;TM=M;SS=M; 2.54
 459060; H89244; Hs.303527; heterogeneous nuclear ribonucleoprotein ; rrm,pkinase;TM=M;SS=N; 2.54
 450167; AA446404; Hs.24563; NTF2-related export protein 1; NTF2;TM=M;SS=N; 2.54

- 425966; NM_001761; Hs.1973; cyclin F; cyclin F-box; cyclin C; TM=M; SS=N; 2.54
 446566; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=M; 2.54
 412834; R71723; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone L; 7tm_1; none; 2.54
 457255; AL133011; Hs.253920; Homo sapiens mRNA; cDNA DKFZp434P201 (fr; none; none; 2.54
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome; TM=M; SS=N; 2.53
 417331; AW411297; Hs.81972; SHC (Src homology 2 domain-containing) t; SH2, PID, zc-C2H2, SCAN, AMP-binding, KRAB; TM=M; SS=N; 2.53
 414570; Y00285; Hs.76473; insulin-like growth factor 2 receptor; In2, CIMR; TM=M; SS=M; 2.53
 444838; AV651680; Hs.208558; ESTs; Integrin_A, FG-GAP; none; 2.53
 422609; Z46023; Hs.118721; sialidase 1 (lysosomal sialidase); BNR, SH2, SH3, pkinase; TM=Y; SS=M; 2.53
 450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyros; none; none; 2.53
 400702; ; Target Exon; lig_chan, SBP_bac_3, ANF_receptor; TM=Y; SS=M; 2.53
 432336; NM_002759; Hs.274382; protein kinase, interferon-inducible dou; dsrm, pkinase; TM=M; SS=N; 2.53
 442643; U82756; Hs.374973; PRP4/STK/WD splicing factor; WD40; 2.52
 452060; W26980; Hs.349089; ATP-binding cassette, sub-family F (GCN2; ABC_tran, IRK, SWIB; 2.52
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22, Claudin; none; 2.52
 428975; NM_004672; Hs.194694; mitogen-activated protein kinase kinase; pkinase; 2.52
 407608; A1928218; Hs.380063; ATPase, Na⁺ transporting, beta 3 polypep; none; none; 2.51
 414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1; TM=Y; SS=M; 2.51
 410293; AK000047; Hs.61960; hypothetical protein; K_tetra; TM=M; SS=N; 2.51
 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic; C2, PLA2_B; TM=M; SS=N; 2.51
 425424; NM_004954; Hs.157199; ELK1 motif kinase; pkinase, UBA, KA1; TM=M; SS=N; 2.51
 457013; AA037145; Hs.172865; cleavage stimulation factor, 3' pre-RNA; WD40; TM=M; SS=N; 2.51
 439221; AA737106; Hs.32250; ESTs, Moderately similar to I7885 serin; adh_short, Bcl-2, BH4; none; 2.51
 405429; ; Target Exon; Y_phosphatase; none; 2.51
 443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible Ik; pkinase, RIO1; TM=M; SS=N; 2.51
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank; 2.50
 408056; AA312329; Hs.42331; ephrin-A4; Ephrin; TM=M; SS=M; 2.50
 414419; F06829; Hs.76090; tumor necrosis factor, alpha-induced pro; K_tetra; TM=M; SS=N; 2.50
 405369; ; NM_005569; Homo sapiens LIM domain kinase; pkinase, LIM, PDZ; 2.50
 418216; AA662240; Hs.283099; AF15q14 protein; Hemagglutinin, squash; TM=Y; SS=N; 2.50
 404321; ; C7001741; [gi2499629]sp[Q63932]MPK2_MOUSE; none; none; 2.50
 430900; U91939; Hs.248123; G protein-coupled receptor 25; 7tm_1; TM=Y; SS=M; 2.49
 440861; BE244115; Hs.7482; KIAA0682 gene product; rrm, Guanylate_kin; TM=M; SS=N; 2.49
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity Iib, re; ig; TM=Y; SS=N; 2.49
 418741; H83265; Hs.8881; ESTs, Weakly similar to S41044 chromosom; pkinase, Activin_rec; pkinase, Activin_rec; 2.49
 417034; NM_006183; Hs.80962; neurotensin; none; 2.49
 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none; none; 2.49
 408805; H69912; Hs.48269; vaccinia related kinase 1; pkinase; TM=M; SS=N; 2.49
 418255; AW135405; Hs.37251; ESTs; pkinase; none; 2.49
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; SS=N; 2.44
 417791; AW965339; Hs.44269; ESTs; none, fer2, FAD_binding_5, Ald_Xan_dh_C, fer2_2, Ald_Xan_dh_C2, CO_deh_flav_C; 2.44
 453941; U39817; Hs.35820; Bloom syndrome; DEAD, helicase_C, HRDC; TM=M; SS=N; 2.41
 417849; AW291587; Hs.82733; nitroden 2; EGF, Idl_recept_b, thyroglobulin_1; TM=M; SS=M; 2.39
 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase; 2.32
 428513; BE220806; Hs.184697; plexin C1; PSI; none; 2.31
 426761; A1015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing me; none; TM=Y; SS=M; 2.31
 427585; D31152; Hs.179729; collagen, type X, alpha 1 (Schmid metaph; C1q, Collagen; 2.28
 412723; AA648459; Hs.335951; hypothetical protein AF301222; none; TM=M; SS=N; 2.28
 452461; N78223; Hs.108106; transcription factor; zc-C3HC4, ubiquitin, PHD, YDG_SRA; TM=M; SS=N; 2.26
 429547; AW009166; Hs.99376; FGENSEH predicted novel secreted protein; none; none; 2.15
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; SNF2_N, helicase_C; TM=M; SS=N; 2.15
 401486; ; C4000647; [gi4758508]refjNP_004253.1; al; none; TM=Y; SS=M; 2.15
 416209; AA236776; Hs.79078; MAD2 (mitotic arrest deficient, yeast, h; HORMA; TM=M; SS=N; 2.14
 424399; AI905687; Hs.348419; AI905687:IL-BT095-190199-019 BT095 Homo ; none; TM=M; SS=M; 2.14
 423761; NM_006194; Hs.132576; paired box gene 9; PAX; TM=M; SS=N; 2.13
 439670; AF088076; Hs.59507; ESTs, Weakly similar to AC004858 3 U1 sm; none; none; 2.13
 439318; AW837046; Hs.6527; G protein-coupled receptor 56; 7tm_2, CytC_asm, GPS; TM=Y; SS=M; 2.03
 445019; AI205540; Hs.281295; ESTs; none; none; 2.00
 443211; AI128388; Hs.143655; ESTs; none; none; 1.98
 449448; D60730; Hs.57471; ESTs; none; none; 1.92
 435243; AW292886; Hs.348932; hypothetical protein dJ434014.3; IRF; none; 1.85
 406360; ; Target Exon; WD40; TM=M; SS=N; 1.84
 411388; X72925; Hs.69752; desmocollin 1; cadherin; TM=Y; SS=N; 1.84
 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz, Frizzled, 7tm_2; TM=Y; SS=M; 1.79
 419183; U60669; Hs.89663; cytochrome P450, subfamily XXIV (vitamin; p450; 1.78
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5; TM=Y; SS=M; 1.77
 432842; AW674093; Hs.334822; hypothetical protein MGC4485; Ribosomal_L4; TM=M; SS=N; 1.76
 419743; AW408762; Hs.5957; Homo sapiens clone 24416 mRNA sequence; none; none; 1.73
 426427; M86699; Hs.169840; TTK protein kinase; pkinase; 1.62
 437915; AI637993; Hs.202312; Homo sapiens clone N11 Ntera2D1 teratoc; none; none; 1.58
 433336; AF017986; Hs.31386; secreted frizzled-related protein 2 (str; Fz, NTR; 1.50
 434377; AW137148; Hs.306593; Intron of perlestin (OSF-2os); Fascidin; none; 1.47
 451592; AI805416; Hs.213897; ESTs; none; none; 1.47
 404927; ; Target Exon; Galactosyl_T; TM=M; SS=Y; 1.28
 421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz, NTR; 1.27
 427335; AA448542; Hs.278444; G antigen 7B; none; 1.25
 431808; M30703; Hs.270833; amphiregulin (schwannoma-derived growth; EGF; TM=Y; SS=M; 1.24
 447993; AW139525; Hs.170362; ESTs; none; none; 1.21
 428182; BE386042; Hs.293317; ESTs, Weakly similar to GGC1_HUMAN G ANT; none; TM=M; SS=N; 1.18
 453637; NM_002589; Hs.34073; BH-protocadherin (brain-heart); cadherin; TM=Y; SS=M; 1.14
 438274; AI918906; Hs.55080; ESTs; PAX; none; 1.14
 453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin, Idl_recept_a; none; 1.10
 413268; AL039079; Hs.75256; regulator of G-protein signalling 1; RGS; TM=M; SS=N; 1.07

429921; AA526911; Hs.82772; collagen, type XI, alpha 1; Collagen, COL11, TSPN, laminin, G, CorA; 1.00
452795; AW392555; Hs.18878; hypothetical protein FLJ21620; 2OG-Fell_Oxy; TM=4; SS=N; 1.00

TABLE 25B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession

406685 0_0 M18728
418869 12789_14 AA229762 AA230035
425802 8884_3 AA122298 AA360788
417886 1031334_1 AA210987 D57294 AA214584 AA207006 D56572
411133 1070995_1 AW819203 AW819204 AW819197 AW819202 AW819211 BE158469 AW819221 BE158473 AW819235 AW819207 AW819220 AW819208 AW819238
AW819198 AW819234

TABLE 25C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423
401780	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
401760	9929699	Plus	83126-83250,85320-85540,94719-95287
402075	8117407	Plus	121907-122035,122804-122921,124019-12416
401747	9789672	Minus	118596-118816,119119-119244,119609-11976
404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
405932	7767812	Minus	123525-123713
406467	9795551	Plus	182212-182958
402233	7690102	Plus	90261-91477
402558	9863760	Plus	19047-19145,21133-21293,33968-34069
405556	1552511	Plus	163497-163623,164715-164968,165369-16550
403112	8980973	Minus	113051-113195
402316	7527774	Minus	10751-10919,18817-19052,22131-22328
404891	7329392	Plus	84974-85125
406137	9166422	Minus	30487-31058
401752	9828651	Plus	144600-144794
405588	5002511	Plus	46180-46366
401812	7407975	Minus	55084-55391
405602	4753260	Plus	44647-44778
401751	9828651	Plus	139165-139322
401218	9929301	Minus	40793-41031
401321	9863631	Minus	104278-104748
401057	8117645	Plus	158309-159238
400702	8118856	Minus	11457-11585,26311-26536,27902-28067,3204
405429	7321905	Minus	51577-51723
405369	2078469	Minus	34183-34357,35686-35751
404321	9665209	Minus	76594-77805
401486	7341763	Plus	32585-32756,36281-36540,40791-40933,4401
406360	9256107	Minus	7513-7673
404927	7342002	Plus	68690-69563

TABLE 26A: 834 GENES UP-REGULATED IN EWING'S SARCOMA COMPARED TO NORMAL ADULT TISSUES

Table 26A lists about 834 genes up-regulated in Ewing's sarcoma compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" kidney cancer to "average" normal adult tissues was greater than or equal to 1.5. The "average" kidney cancer level was set to the 75th percentile amongst Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 7.5th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UniGeneID: Unigene number
UniGene Title: Unigene gene title
R1: Ratio of Ewing sarcoma to normal tissue

Pkey	ExAccn	UniGeneID	UniGene Title	R1
101447	M21305		gb:Human alpha satellite and satellite 3	38.4
115881	NM_005756	Hs.184942	G protein-coupled receptor 64	34.2
110278	AF061573	Hs.19492	protocadherin 8	32.2
121362	AF050147	Hs.97932	chondromodulin I precursor	30.3
101104	AW862258	Hs.169266	neuropeptide Y receptor Y1	26.3

	121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	24.4
	121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidyseri	23.4
	104659	AW969769	Hs.105201	ESTs	20.2
5	106533	AL134708	Hs.145998	ESTs	16.9
	124006	AI147155	Hs.270016	ESTs	15.0
	110728	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	14.8
	105782	HD9748	Hs.57987	B-cell CLL/lymphoma 118 (zinc finger pro	14.6
	102836	U94320	Hs.158330	neuropeptide Y receptor Y5	14.5
10	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	13.7
	121231	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	12.3
	129526	S69681	Hs.177582	surfactant, pulmonary-associated protein	12.1
	119791	AA554907	Hs.58291	ESTs	11.7
	116301	AW969706	Hs.293332	ESTs	11.2
15	123308	C14187	Hs.103538	ESTs	10.9
	127742	AW293496	Hs.180138	ESTs	10.8
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	10.7
	127489	AA650250	Hs.272076	ESTs	10.6
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.6
20	101063	D54745	Hs.80247	cholecystokinin	10.6
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	10.5
	100299	D49493	Hs.2171	growth differentiation factor 10	10.1
	127987	AI022103	Hs.124511	ESTs	10.1
	131313	R96290	Hs.336629	ribosomal protein L44	9.2
25	126799	AW753865	Hs.74376	oligomycin related ER localized protei	8.5
	125847	AW161885	Hs.249034	ESTs	7.0
	100380	D82343	Hs.18551	neuroblastoma (nerve tissue) protein	6.9
	114837	BE244930	Hs.166895	ESTs	6.6
	123049	BE047680	Hs.211869	dickkopf (Xenopus laevis) homolog 2	6.6
30	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.5
	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous r	6.5
	125186	AA610620	Hs.181244	major histocompatibility complex, class	6.4
	118844	AA443241	Hs.336629	ribosomal protein L44	6.3
	119717	AA918317	Hs.57987	B-cell CLL/lymphoma 118 (zinc finger pro	6.3
35	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	6.1
	113003	AW292315	Hs.7215	ESTs	5.8
	126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.7
	101050	AU077324	Hs.1832	neuropeptide Y	5.7
	116790	AW161357	Hs.101174	microtubule-associated protein tau	5.5
40	119082	AF252297	Hs.91546	cytochrome P450 reductase	5.1
	132315	AF091086	Hs.44563	hypothetical protein	5.0
	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	4.9
	126077	M78772	Hs.210838	ESTs	4.7
	126426	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	4.6
45	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	4.5
	123619	AA602964		gb:nc097c02.s1 NCL_CGAP_Pr2 Homo sapiens	4.4
	128361	AW172570	Hs.130246	ESTs	4.3
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	4.3
	100020				4.2
50	125556	AB033064	Hs.334806	KIAA1238 protein	4.2
	105316	AI671245	Hs.24835	hypothetical protein FLJ14594	4.0
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	4.0
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (3.9
	128132	AA225632		gb:nc08a07.r1 NCL_CGAP_Pr1 Homo sapiens	3.9
55	129012	R81936	Hs.336629	ribosomal protein L44	3.9
	125447	AI582222	Hs.128686	ESTs	3.8
	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	3.6
	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	3.6
	128391	AW188326	Hs.170652	ESTs	3.5
60	123829	AF251237	Hs.112208	XAGE-1 protein	3.4
	123949	AA621665	Hs.208957	EST	3.4
	126872	AW450979		gb:U1-H-BI3-ata-a-12-0-UI.s1 NCL_CGAP_Su	3.4
	101266	L36645	Hs.73964	EphA4	3.3
	121309	AA293834	Hs.97312	ESTs	3.3
65	130637	AA356764	Hs.17109	integral membrane protein 2A	3.2
	125464	N71807		gb:yz29d09.r1 Soares_multiple_sclerosis_	3.2
	135175	M91463	Hs.95958	solute carrier family 2 (facilitated glu	3.2
	107599	AW664072	Hs.60136	ESTs	3.2
	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.2
70	131688	AI935413	Hs.30692	p21 (CDKN1A)-activated kinase 2	3.1
	120147	AI917116	Hs.155376	hemoglobin, beta	3.1
	110343	AW136703	Hs.17268	ESTs	3.1
	127664	AA806164	Hs.116502	ESTs	3.0
	103076	NM_001034	Hs.75319	ribonucleotide reductase M2 polypeptide	3.0
75	126127	N95428		gb:zb0d09.s1 Soares_senescent_fibroblas	3.0
	125558	R59305		gb:yh16c10.r1 Soares infant brain 1NIB H	3.0
	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	2.9
	133421	AF134160	Hs.7327	claudin 1	2.8
	102581	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	2.8
80	113577	AI300699	Hs.278937	PRO0470 protein	2.8
	118397	BE139479	Hs.161492	ESTs	2.8
	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	2.8
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	2.8
	127262	AA828125		gb:xd71a09.s1 NCL_CGAP_Ov2 Homo sapiens	2.8

	106472	AI207162	Hs.3815	stathmin-like-protein RB3	2.7
	125032	T74884		gb:yc58d02.s1 Stratagene liver (937224)	2.7
	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	2.7
5	126600	AA699949	Hs.191385	ESTs	2.7
	120325	AA195651	Hs.104106	ESTs	2.7
	127256	AI738610	Hs.267957	ESTs, Moderately similar to ALU8_HUMAN	2.7
	117357	N24829		gb:yc58h12.s1 Soares melanocyte 2NbHM Ho	2.7
	126735	M69113	Hs.226795	glutathione S-transferase pi	2.7
10	102745	AW753865	Hs.74376	olfactomedin related ER localized protei	2.7
	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (2.6
	129706	AA443241	Hs.336629	ribosomal protein L44	2.6
	107731	AA016086	Hs.272106	ESTs, Weakly similar to I38022 hypotheti	2.6
	128283	AI076570	Hs.134053	ESTs	2.6
15	125165	W45350		gb:zc81h08.s1 Pancreatic Islet Homo sapi	2.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	2.6
	105577	AW852257	Hs.171391	C-terminal binding protein 2	2.6
	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	2.6
	130262	D63216	Hs.153684	frizzled-related protein	2.6
20	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.6
	102479	NM_001991	Hs.194669	enhancer of zeste (Drosophila) homolog 1	2.6
	128531	H03721	Hs.2953	ribosomal protein S15a	2.6
	126165	AI741816	Hs.125897	ESTs	2.6
	126086	H75681		gb:yr77g01.r1 Soares fetal liver spleen	2.5
25	118957	AI668670	Hs.216756	ESTs	2.5
	120830	AI568170	Hs.96886	ESTs	2.5
	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	2.5
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	2.5
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	2.5
30	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	2.5
	133761	AF041430	Hs.75922	brain protein I3	2.5
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.5
	126693	C05723		gb:C05723 Human pancreatic islet Homo sa	2.5
	126021	AA775894	Hs.187516	ESTs	2.5
35	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	2.5
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	2.5
	125743	H17151		gb:ym37a05.r1 Soares infant brain 1NIB H	2.5
	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	2.5
	113119	T47910		gb:yb18b11.s1 Stratagene fetal spleen (9	2.4
40	123110	AA486256	Hs.193510	EST	2.4
	113283	T66813	Hs.12947	EST	2.4
	107711	W96141	Hs.220687	ESTs	2.4
	128992	H04150	Hs.107708	ESTs	2.4
	106111	AW875398	Hs.6451	PRO0659 protein	2.4
45	129948	AI537162	Hs.263968	ESTs	2.4
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	2.4
	116728	F13687	Hs.227976	EST	2.4
	103100	NM_005574	Hs.184585	UIM domain only 2 (rhombotin-like 1)	2.4
	124971	T23800	Hs.151001	hypothetical protein FLJ14728	2.4
50	131019	W28614	Hs.306155	chorionic somatomammotropin hormone 1 (p	2.4
	128671	AI885045	Hs.211585	phosphoinositide-3-kinase, regulatory s	2.4
	111795	AI435437	Hs.24567	ESTs, Weakly similar to KBF3_HUMAN NUCL	2.4
	119127	AA708035	Hs.12248	ESTs	2.4
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	2.4
55	111898	R38944	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.4
	131916	AA025976	Hs.34569	ESTs	2.4
	130850	AB040922	Hs.20237	DKFZP566C134 protein	2.4
	100571	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	2.4
	126722	N66148	Hs.11125	HSPC033 protein	2.4
60	123720	AA609734	Hs.112755	EST	2.4
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retrovir	2.4
	131136	AB033099	Hs.23413	KIAA1273 protein	2.4
	129001	AA443323	Hs.107812	BPOZ protein	2.4
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	2.4
65	107593	AI093688	Hs.60051	ESTs	2.4
	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	2.4
	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	2.4
	103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	2.4
	128367	AW611791	Hs.150742	ESTs	2.4
70	123729	AL039779	Hs.278672	membrane component, chromosome 11, surfa	2.4
	112342	AW410273	Hs.92614	longevity assurance (LAG1, S. cerevisiae	2.3
	114721	D61939	Hs.103822	ESTs	2.3
	127768	AW085002	Hs.156187	ESTs	2.3
	127706	AI174238	Hs.186982	ESTs	2.3
75	126029	AA704253	Hs.169359	ESTs	2.3
	124250	AA350256	Hs.323875	EST, Weakly similar to 2109260A B cell	2.3
	117265	AA451966	Hs.43005	RAB9-like protein	2.3
	112501	AA972447	Hs.288833	Homo sapiens mRNA: cDNA DKFZp434K087 (tr	2.3
	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	2.3
80	127252	AI049545	Hs.94	DnaJ (Hsp40) homolog, subfamily A, membe	2.3
	129228	U40714	Hs.239307	lysyl-tRNA synthetase	2.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.3
	109252	BE440157	Hs.85944	ESTs	2.3
	127889	AI147408	Hs.144941	ESTs	2.3

	121292	AA401807		gbzv65f11.s1 Soares_total_fetus_Nb2HF8_	2.3
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	2.3
	132985	AL045579	Hs.62113	KIAA0717 protein	2.3
	125174	W51835	Hs.231082	EST	2.3
5	125401	AI204637	Hs.337585	ESTs, Highly similar to KIAA0350 [H.sapi	2.3
	135278	AA399542	Hs.229671	EST, Moderately similar to PEPTIDYL-PROL	2.3
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN	2.3
	123423	AA598484		gb:ae38f04.s1 Gessler Wilms tumor Homo s	2.3
	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	2.3
10	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	2.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC	2.3
	101086	AA382524	Hs.250959	histatin 1	2.3
	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	2.3
	126879	D90391	Hs.1265	branched chain keto acid dehydrogenase E	2.3
15	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	2.3
	124691	R05835	Hs.110153	ESTs	2.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	2.3
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	2.2
20	129052	BE275031	Hs.158210	hypothetical protein MGC2555	2.2
	129248	W04605	Hs.171637	hypothetical protein MGC2628	2.2
	100780	BE561958	Hs.302053	immunoglobulin heavy constant mu	2.2
	135416	BE281018	Hs.99969	fusion, derived from t(12;16) malignant	2.2
	129928	AI338993	Hs.134535	ESTs	2.2
25	103319	X63492	Hs.82359	tumor necrosis factor receptor superfam	2.2
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	2.2
	120734	AA299948		gb:EST12544 Uterus tumor 1 Homo sapiens	2.2
	111777	AK001100	Hs.41690	desmocollin 3	2.2
	128953	J03890	Hs.1074	surfactant, pulmonary-associated protein	2.2
30	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	2.2
	134964	AI803516	Hs.272891	hippocampin-like protein 4	2.2
	127248	AA364195		gb:EST75015 Pineal gland II Homo sapiens	2.2
	125761	R68351		gb:rh99b03.r1 Soares placenta Nb2HP Homo	2.2
	101358	M10058	Hs.12056	asialoglycoprotein receptor 1	2.2
35	101613	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	2.2
	107121	AB015427	Hs.250493	zinc finger protein 219	2.2
	118751	N74210	Hs.50454	ESTs	2.2
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	2.2
	126581	W73306	Hs.306668	Homo sapiens cDNA FLJ14089 fis, clone MA	2.2
40	127634	AA633469	Hs.193283	ESTs, Weakly similar to unnamed protein	2.2
	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	2.2
	132867	AF226667	Hs.58553	CTP synthase II	2.2
	126323	N77584	Hs.68644	Homo sapiens microsomal signal peptidase	2.2
	111790	AW769683	Hs.6734	ESTs, Weakly similar to S26650 DNA-bind	2.2
45	125549	R20215		gb:yg18b09.r1 Soares infant brain 1N1B H	2.2
	128059	AA972446	Hs.145086	ESTs	2.2
	132342	AW162758	Hs.45232	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.2
	125722	H29796	Hs.269622	ESTs	2.2
	106383	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	2.2
50	127644	N88858	Hs.155101	ATP synthase, H+ transporting, mitochond	2.2
	128179	AW293689	Hs.127116	ESTs	2.2
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	2.2
	126962	R12014	Hs.20976	ESTs	2.2
	112369	AW966243	Hs.4243	hypothetical protein FLJ12650	2.2
55	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	2.2
	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypothet	2.2
	108743	AI580150	Hs.71074	ESTs	2.2
	133726	AI803188	Hs.252716	oxysterol-binding protein-related protei	2.2
	131263	ALU077002	Hs.24950	regulator of G-protein signalling 5	2.2
60	109929	AA773187	Hs.294027	ESTs	2.2
	129059	AW069534	Hs.279583	CGI-81 protein	2.2
	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	2.2
	116952	H79677		gb:yu76g10.s1 Soares fetal liver spleen	2.2
	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypotheti	2.2
65	106711	BE390125	Hs.143187	hypothetical protein	2.2
	135191	X16866	Hs.301086	cytochrome P450, subfamily IID (debrisoq	2.2
	125822	H03162	Hs.268768	ESTs	2.2
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	2.2
	133363	AI866286	Hs.71982	ESTs, Weakly similar to B36298 protine-r	2.2
70	126250	AL050391	Hs.321247	Homo sapiens mRNA; cDNA DKFZp586A181 (fr	2.2
	103392	X94563		gb:HLsapiens dbi/acbp gene exon 1 & 2.	2.2
	129794	AF161399	Hs.23259	hypothetical protein FLJ13433	2.2
	100253	D38024	Hs.157425	double homeobox, 2	2.2
	130743	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.2
75	125466	R08234	Hs.180461	ESTs	2.2
	122682	AA584531	Hs.159293	ESTs	2.2
	133347	BE257758	Hs.71475	acid cluster protein 33	2.2
	104455	AL110261	Hs.157211	DKFZP586B0621 protein	2.2
	116332	AA491208	Hs.62620	chromosome 6 open reading frame 1	2.2
80	131163	AA099524	Hs.23754	ESTs	2.2
	109592	AI198059	Hs.26370	ESTs	2.2
	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	2.1
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	2.1
	128434	AI190914	Hs.143880	ESTs	2.1

5	103163	AU077018	Hs.3235	keratin 4	2.1
	112379	AK001713	Hs.17860	hypothetical protein FLJ10851	2.1
	127507	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	2.1
	133097	W03512	Hs.6479	hypothetical protein MGC13272	2.1
	126153	H85692	Hs.40730	ESTs	2.1
10	122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	2.1
	100554	M95923		gb:Human 12-ipoxygenase mRNA, partial c	2.1
	104799	AA029703		gb:ze95h08.s1 Soares_fetal_heart_NbHH19W	2.1
	132664	AI740461	Hs.54542	ESTs	2.1
	114620	AA642974		gb:nr60h01.s1 NCL_CGAP_Lym3 Homo sapiens	2.1
15	115348	AA281562	Hs.292100	ESTs	2.1
	133231	AK000517	Hs.6844	hypothetical protein FLJ20510	2.1
	133160	N54968	Hs.66309	hypothetical protein MGC11061	2.1
	124656	AW297702	Hs.102915	ESTs	2.1
	133576	M19650	Hs.150741	2',3'-cyclic nucleotide 3' phosphodiester	2.1
20	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypothet	2.1
	126505	AA282881	Hs.190057	ESTs	2.1
	118865	AA736405	Hs.54530	ESTs	2.1
	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	2.1
	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	2.1
25	133493	AW998046	Hs.194369	arginine-glutamic acid dipeptide (RE) re	2.1
	112853	T02843		gb:FB11H5 Fetal brain, Stratagene Homo s	2.1
	117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU	2.1
	112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MA	2.1
	134869	AL157518	Hs.90421	PRO2463 protein	2.1
30	128869	AA768242	Hs.80618	hypothetical protein	2.1
	129179	AW969025	Hs.109154	ESTs	2.1
	104857	AI920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	2.1
	101651	AL037111	Hs.75641	galactose-1-phosphate uridylyltransferase	2.1
	129726	H15474	Hs.132898	fatty acid desaturase 1	2.1
35	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	126271	AI250773	Hs.270012	ESTs	2.1
	116925	H73110	Hs.260603	ESTs, Moderately similar to A47582 B-ce	2.1
	128468	T23625	Hs.150560	putative translation initiation factor	2.1
	116031	AA452239	Hs.103329	KIAA0970 protein	2.1
40	130724	AK001507	Hs.306084	Homo sapiens clone FLB6914 PRO1821 mRNA,	2.1
	121897	AA427419	Hs.229162	EST, Weakly similar to ZN91_HUMAN ZINC	2.1
	123808	AA620552		gb:ae58g11.s1 Stratagene lung carcinoma	2.1
	122333	AA625872	Hs.98977	ESTs, Moderately similar to T34561 hypot	2.1
	127841	AW136558	Hs.125246	ESTs	2.1
45	100023				2.1
	113002	BE243513	Hs.7212	hypothetical protein PP1044	2.1
	111567	F12628	Hs.334786	hypothetical protein MGC16040	2.1
	113697	T97183	Hs.17992	Homo sapiens mRNA; cDNA DKFZp434J1726 (f	2.1
	128033	AI248705	Hs.149321	ESTs	2.1
50	105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	2.1
	112370	AF052095	Hs.167344	Homo sapiens clone 23911 mRNA sequence	2.1
	132786	BE083422	Hs.56851	hypothetical protein MGC2658	2.1
	113226	AI821008	Hs.10697	ESTs	2.1
	117997	N52090	Hs.47420	EST	2.1
55	116996	H83935	Hs.40535	ESTs	2.1
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	2.1
	122591	AI188219	Hs.99311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	2.1
	107279	S57296	Hs.323910	v-erb-b2 avian erythroblastic leukemia	2.1
	103898	AA248884		gb:k3517.seq.F Human fetal heart, Lambda	2.1
60	110312	BE256986	Hs.11896	hypothetical protein FLJ12089	2.1
	127447	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	2.1
	128352	AW137413	Hs.169942	ESTs	2.1
	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	2.0
	128275	AI218235	Hs.131240	ESTs	2.0
65	125976	AA436760		gb:zv67d11.r1 Soares_fetal_liver_spleen	2.0
	120820	AA347417	Hs.95869	EST	2.0
	134937	AI251449	Hs.171939	ESTs	2.0
	129602	AI282193	Hs.198298	v-src avian sarcoma (Schmidt-Ruppin A-2)	2.0
	129535	AA397972	Hs.169965	chimerin (chimaerin) 1	2.0
70	106095	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.0
	128538	R44214	Hs.101189	ESTs	2.0
	105593	AA279341	Hs.174151	aldehyde oxidase 1	2.0
	105788	AB009698	Hs.23965	solute carrier family 22 (organic anion	2.0
	128148	AA918175	Hs.126637	ESTs	2.0
75	125982	R98091		gb:yr30e11.r1 Soares fetal liver spleen	2.0
	125746	AL137506	Hs.274256	hypothetical protein FLJ23563	2.0
	127835	AA748762	Hs.163113	ESTs, Weakly similar to I38022 hypotheti	2.0
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	2.0
	124282	AA018408	Hs.110287	ESTs	2.0
80	126926	AA179472	Hs.832	ESTs, Highly similar to A41029 integrin	2.0
	100221	D28383		gb:Human mRNA for ATP synthase B chain,	2.0
	126053	H54450		gb:yu62d01.r1 Weizmann Olfactory Epithel	2.0
	100944	L07518	Hs.159593	mucin 6, gastric	2.0
	125581	AI272848	Hs.75309	eukaryotic translation elongation factor	2.0
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	2.0
	114612	AI124557	Hs.95456	ESTs	2.0
	130453	U80735	Hs.173854	PAX transcription activation domain inte	2.0

	135060	AK001887	Hs.259842	protein kinase, AMP-activated, gamma 2 n	2.0
	114419	AI248013	Hs.106532	ESTs, Weakly similar to I38588 reverse l	2.0
	126283	N40359	Hs.271896	ESTs	2.0
5	112003	AW978731	Hs.301824	hypothetical protein PRO1331	2.0
	127391	AW380893	Hs.11039	hypothetical protein MGC2722	2.0
	127717	F12209	Hs.173380	CK2 interacting protein 1; HQ0024c prote	2.0
	126893	AJ252060	Hs.26320	TRABID protein	2.0
	106798	BE252749	Hs.20558	hypothetical protein FLJ20345	2.0
10	103760	AA642973	Hs.183842	ubiquitin 8	2.0
	118922	AW206193	Hs.91065	hypothetical protein DKFZp761B2423	2.0
	133195	AJ434760	Hs.279949	KIAA1007 protein	2.0
	133424	AA350994	Hs.20281	KIAA1700	2.0
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	2.0
	132347	BE271016	Hs.169850	ESTs, Weakly similar to T21554 hypotheti	2.0
15	125599	H13295	Hs.106135	ESTs	2.0
	114459	AW445217	Hs.103362	ESTs	2.0
	128478	AA708205	Hs.100343	ESTs	2.0
	127271	H96820		gbryv99b03.r1 Soares melanocyte 2NbHM Ho	2.0
20	111122	N63753	Hs.16492	DKFZP564G2022 protein	2.0
	130695	T97205	Hs.17998	ESTs, Weakly similar to 2109260A B cell	2.0
	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	2.0
	119244	AW407564	Hs.275865	ribosomal protein S18	2.0
	127603	AJ016798	Hs.9925	hypothetical protein FLJ20772	2.0
25	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	2.0
	128115	AJ435590	Hs.130168	ESTs	2.0
	117639	AA377165	Hs.44833	ESTs	2.0
	127033	AF169301	Hs.9098	sulfate transporter 1	2.0
	112411	R43090	Hs.271510	ESTs, Moderately similar to ALU1_HUMAN A	2.0
30	114601	AA075566		gbzcm88f06.s1 Stratagene ovarian cancer	2.0
	127573	AA594195	Hs.269464	ESTs, Weakly similar to S65657 alpha-1C-	2.0
	125500	AW952654	Hs.244624	ESTs	2.0
	119416	T97186		gbrye50h09.s1 Soares fetal liver spleen	2.0
	115467	AJ366784	Hs.48820	TATA box binding protein (TBP)-associate	2.0
35	128902	AA036637	Hs.107052	ESTs	2.0
	127684	AA668631	Hs.32556	KIAA0379 protein	2.0
	126288	AW449560	Hs.89576	inner mitochondrial membrane peptidase 2	2.0
	122059	AA431737	Hs.98749	EST, Moderately similar to T42671 hypoth	2.0
	125486	AJ023895	Hs.190587	ESTs	2.0
40	128895	AW467000	Hs.106985	ESTs	2.0
	105301	AW352357	Hs.7457	MAGE1 protein	2.0
	125536	F08266	Hs.77948	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
	121387	AA405854		gbzu66g08.s1 Soares_testis_NHT Homo sap	2.0
45	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankyrin-rela	2.0
	126860	BE242814	Hs.323494	ESTs, Weakly similar to T27544 zinc resi	2.0
	102907	BE409861	Hs.202833	heme oxygenase (decycling) 1	2.0
	127804	AA740634	Hs.292084	ESTs	2.0
	130566	R85474	Hs.16073	ESTs	1.9
	113782	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	1.9
50	124119	AA040123	Hs.248953	solute carrier family 27 (fatty acid tra	1.9
	132490	NM_001290	Hs.4980	LIM domain binding 2	1.9
	125494	AJ077029	Hs.177543	antigen identified by monoclonal antibod	1.9
	100237	D30715	Hs.306333	Human PAP (pancreatitis-associated prot	1.9
	127687	AW772383	Hs.300635	ESTs	1.9
55	103136	AF087917	Hs.247936	olfactory receptor, family 1, subfamily	1.9
	125704	R55094	Hs.26239	Human DNA sequence from clone RP11-438B2	1.9
	126208	N22588	Hs.288548	Homo sapiens cDNA FLJ12368 fis, clone MA	1.9
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	1.9
	128660	AA011597	Hs.177398	ESTs	1.9
60	118049	N53145		gbryv55f09.s1 Soares fetal liver spleen	1.9
	134624	AF035119	Hs.8700	deleted in liver cancer 1	1.9
	127432	AW067708	Hs.170311	heterogeneous nuclear ribonucleoprotein	1.9
	126414	AJ363157	Hs.24756	hepatocyte growth factor-regulated tyros	1.9
	120861	AA350394	Hs.96952	ESTs	1.9
65	124669	AJ571594	Hs.102943	hypothetical protein MGC12916	1.9
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-II	1.9
	103891	NM_007212	Hs.124186	ring finger protein 2	1.9
	128727	AJ223335	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	1.9
	126831	AJ929107	Hs.79933	cyclin I	1.9
70	125360	AW898892	Hs.189741	ESTs	1.9
	124276	H83465		gbrys91a11.s1 Soares retina N2b5HR Homo	1.9
	126524	Z45455	Hs.182447	heterogeneous nuclear ribonucleoprotein	1.9
	126647	AK000283	Hs.270502	hypothetical protein FLJ20276	1.9
	125957	H41694		gbryo06b06.r1 Soares adult brain N2b5HB5	1.9
75	121782	AW452957	Hs.334698	Homo sapiens, clone MGC:15203, mRNA, com	1.9
	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	1.9
	130945	U20582	Hs.2149	actin like protein	1.9
	126348	T16243	Hs.6473	Homo sapiens cDNA FLJ13392 fis, clone Y7	1.9
	103558	BE616547	Hs.2785	keratin 17	1.9
80	126982	AA211419		gbzcn55g05.s1 Stratagene muscle 937209 H	1.9
	125613	AA765957	Hs.21077	KIAA0532 protein	1.9
	129601	AB032964	Hs.115726	KIAA1138 protein	1.9
	126007	H51097	Hs.143261	ESTs	1.9
	123627	AA809619	Hs.112668	ESTs	1.9

5	111587	AI125867	Hs.20734	ESTs	1.9
	135231	BE613615	Hs.74280	hypothetical protein FLJ22237	1.9
	128897	AW979134	Hs.10700	hypothetical protein	1.9
	109891	H04757	Hs.323176	ESTs	1.9
	127704	AA679609		gb:ag72c02.s1 Cessler Wilms tumor Homo s	1.9
10	129340	H75334	Hs.11050	F-box only protein 9	1.9
	126502	T10077	Hs.13453	hypothetical protein FLJ14753	1.9
	129619	AA209534	Hs.284243	tetraspan NET-6 protein	1.9
	127136	R36277	Hs.7773	Homo sapiens ubiquitin conjugating enzyme	1.9
	110636	H72868	Hs.19110	ESTs	1.9
15	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	1.9
	104689	AA420450	Hs.292911	ESTs, Highly similar to S60712 band-6-pr	1.9
	130829	BE262530	Hs.2006	glutathione S-transferase M3 (brain)	1.9
	125768	AI557486	Hs.119122	ribosomal protein L13a	1.9
	123613	AA609158	Hs.291166	EST	1.9
20	127506	T61039	Hs.252574	ribosomal protein L10a	1.9
	123546	AA608817	Hs.112597	EST	1.9
	126516	R95872	Hs.117572	chemokine binding protein 2	1.9
	103973	AA305729	Hs.18272	amino acid transporter system A1	1.9
	127426	AA854756	Hs.124076	ESTs	1.9
25	112339	R56570	Hs.50547	ESTs	1.9
	129101	NM_013403	Hs.108665	zinedin	1.9
	109442	AW296134	Hs.85999	ESTs, Weakly similar to S65657 alpha-1C-	1.9
	118103	AA401733	Hs.184134	ESTs	1.9
	125752	AW136622	Hs.206673	ESTs	1.9
30	102926	W28363	Hs.239752	nuclear receptor subfamily 2, group F, m	1.9
	133975	C18356	Hs.295944	tissue factor pathway inhibitor 2	1.9
	134470	X54942	Hs.83758	CDC28 protein kinase 2	1.9
	127329	AW160551	Hs.124021	soggy-1 gene	1.8
	126659	T16245		gb:NIB1005R Normalized infant brain, Ben	1.8
35	127297	AW829485	Hs.140720	GSK-3 binding protein FRAT2	1.8
	127640	AI557486	Hs.119122	ribosomal protein L13a	1.8
	103409	NM_004454	Hs.43697	els variant gene 5 (els-related molecule	1.8
	127964	F06293		gb:HSC13F081 normalized infant brain cDN	1.8
	122365	AA813546	Hs.99034	GTP-binding protein Rho7	1.8
40	128193	AJ224442	Hs.155020	putative methyltransferase	1.8
	115173	BE612940	Hs.88252	ESTs	1.8
	125532	AJ734146	Hs.271800	ESTs, Weakly similar to alternatively sp	1.8
	126541	AJ271671	Hs.7854	zinc/iron regulated transporter-like	1.8
	127309	AI669765	Hs.133184	ESTs	1.8
45	129062	AA452970	Hs.155218	E1B-55kDa-associated protein 5	1.8
	125770	AI292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	1.8
	127775	AA128808	Hs.179902	transporter-like protein	1.8
	126994	AA455265	Hs.86686	ESTs, Moderately similar to I54374 gene	1.8
	130734	AW137091	Hs.18624	KIAA1052 protein	1.8
50	114461	AA531187	Hs.126705	ESTs	1.8
	100842	U05597		gb:Human anion exchanger 3 cardiac isofo	1.8
	127389	T65126	Hs.12743	camitine O-octanoyltransferase	1.8
	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine/th	1.8
	107736	AA016239	Hs.60715	ESTs	1.8
55	125669	R51308	Hs.333256	ESTs, Weakly similar to ALU8_HUMAN ALU	1.8
	100370	D79989	Hs.184884	KIAA0167 gene product	1.8
	113479	AI023133	Hs.10739	ESTs	1.8
	105165	BE280787	Hs.16079	hypothetical protein FLJ10233	1.8
	120602	AA808018	Hs.109302	ESTs	1.8
60	112399	R60920	Hs.296770	KIAA1719 protein	1.8
	123474	AA599209		gb:ag34b11.s1 Jia bone marrow stroma Hom	1.8
	134212	AA654353	Hs.17719	EBP50-PDZ interactor of 64 kD	1.8
	104204	AK001691	Hs.57655	hypothetical protein FLJ10829	1.8
	127464	AW971875	Hs.292071	ESTs	1.8
65	116715	AL117440	Hs.170263	tumor protein p53-binding protein, 1	1.8
	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	1.8
	132380	AW373665	Hs.46853	ESTs	1.8
	120087	AF186780	Hs.79219	RalGDS-like gene; KIAA0959 protein	1.8
	116356	AI371223	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HE	1.8
70	125499	H10543		gb:ym04c06.r1 Soares infant brain 1NIB H	1.8
	128846	AA730767	Hs.285753	SCG10-like-protein	1.8
	123869	AA620924	Hs.112923	EST	1.8
	108889	AA135722	Hs.61481	ESTs	1.8
	126528	Z24895		gb:HS867F122 STRATAGENE Human skeletal m	1.8
75	127629	AA293279	Hs.29173	hypothetical protein FLJ20515	1.8
	130004	AA703684	Hs.245474	ESTs, Moderately similar to ALU5_HUMAN A	1.8
	130847	AI672483	Hs.20220	lipase protein	1.8
	111620	R14853	Hs.307478	EST, Weakly similar to I39058 hypotheti	1.8
	131971	BE567100	Hs.154938	hypothetical protein MDS025	1.8
80	121360	AA405635	Hs.96854	ESTs, Weakly similar to OYLX_HUMAN CYTOP	1.8
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	1.8
	124687	AA833902	Hs.270745	ESTs	1.8
	126698	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypotheti	1.8
	126730	AA442429		gb:zv70g02.r1 Soares_total_fetus_Nb2HF8_	1.8
	127916	AI239950	Hs.294111	ESTs, Moderately similar to B34087 hypo	1.8
	128408	AI183407	Hs.143704	EST	1.8
	128440	AW090340	Hs.14337	Homo sapiens cDNA FLJ14407 fis, clone HE	1.8

	123783	AA610112		gb:af19g05.s1 Soares_total_fetus_Nb2HF8_	1.8
	109152	AW380723	Hs.73451	ESTs, Weakly similar to S55024 nebulin,	1.8
	107242	AB020672	Hs.175411	KIAA0865 protein	1.8
5	132804	AI805943	Hs.326067	hypothetical protein MGC5178	1.8
	125387	AJ243669	Hs.8127	KIAA0144 gene product	1.8
	121578	AA398791	Hs.178185	ESTs	1.8
	132944	T96641	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	1.8
	126295	AI281459	Hs.270114	ESTs	1.8
10	133335	BE251012	Hs.263812	nuclear distribution gene C (Anidulans)	1.8
	129879	AK001696	Hs.13109	Ran binding protein 11	1.7
	125175	W52355	Hs.303030	EST	1.7
	126919	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	1.7
	127773	AA725863	Hs.120508	ESTs	1.7
15	126495	AB028021	Hs.137732	KIAA1098 protein	1.7
	126948	AW968535	Hs.14328	hypothetical protein FLJ20071	1.7
	126571	C03105	Hs.285847	CGI-19 protein	1.7
	115428	AA284112	Hs.94680	ESTs, Weakly similar to I78885 serine/t	1.7
	128232	AI830319	Hs.334641	hypothetical protein DKFZp434i1916	1.7
20	126082	H81188	Hs.269571	ESTs	1.7
	120467	AW292562	Hs.187628	ESTs	1.7
	124041	AW590171	Hs.101413	ESTs	1.7
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	1.7
	123951	AB012922	Hs.173043	metastasis-associated 1-like 1	1.7
25	126449	AF223944	Hs.325443	breast cell glutaminase	1.7
	124554	N65961		gb:aa27d03.s1 Soares fetal liver spleen	1.7
	133651	AI301740	Hs.173381	dihydropyrimidinase-like 2	1.7
	126780	R12421	Hs.5811	chromosome 21 open reading frame 59	1.7
	125661	AA491830	Hs.25689	ESTs	1.7
30	125888	H18298		gb:yn48b09.r1 Soares adult brain N2b5HB5	1.7
	127245	AA323958		gb:EST26810 Cerebellum II Homo sapiens c	1.7
	111223	AA852773	Hs.334838	KIAA1866 protein	1.7
	115611	R44789	Hs.33191	Homo sapiens, Similar to transmembrane r	1.7
	124846	R59977	Hs.158196	transcriptional adaptor 3 (ADA3, yeast	1.7
35	100397	D84424	Hs.57697	hyaluronan synthase 1	1.7
	127180	T27097	Hs.22790	ESTs	1.7
	102598	BE250742	Hs.106673	eukaryotic translation initiation factor	1.7
	134076	AF086215		gb:Homo sapiens full length insert cDNA	1.7
	115659	W99382	Hs.283709	lipopolysaccharide specific response-7 p	1.7
40	125555	R19382	Hs.117869	ESTs	1.7
	128382	AI138886	Hs.143243	ESTs	1.7
	127710	AA682867	Hs.191901	ESTs	1.7
	125445	AI452722	Hs.7709	WW domain binding protein 1	1.7
	129951	AL110282	Hs.268024	Homo sapiens, clone IMAGE:3873720, mRNA	1.7
45	119898	R93325	Hs.58690	ESTs	1.7
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	1.7
	133531	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	1.7
	119726	AF086289	Hs.234766	skin-specific protein	1.7
	125198	W69474	Hs.323140	ESTs	1.7
50	121414	AW291477	Hs.188763	testis expressed sequence 13A	1.7
	112542	AI458867	Hs.24276	ESTs	1.7
	101368	M13058	Hs.73952	proline-rich protein HaeIII subfamily 2	1.7
	125820	AA730136	Hs.75561	teratocarcinoma-derived growth factor 1	1.7
	129091	AA056483	Hs.301463	Human Chromosome 16 BAC clone C17937SK-A	1.7
55	132609	U20165	Hs.53250	bone morphogenetic protein receptor, typ	1.7
	119447	W31714	Hs.122656	ESTs, Highly similar to formin 2-like pr	1.7
	113675	T81034	Hs.14841	ESTs	1.7
	113701	T97301	Hs.18026	ESTs	1.7
	116180	AA463902	Hs.13522	ESTs, Weakly similar to I38022 hypothet	1.7
60	127133	AA280740	Hs.292072	ESTs, Moderately similar to A46010 X-lin	1.7
	113316	T70318	Hs.268581	ESTs	1.7
	123316	AI290561	Hs.155361	ESTs	1.7
	122638	AL137476	Hs.123609	Homo sapiens mRNA; cDNA DKFZp434i0623 (f	1.7
	105053	AI884911	Hs.32989	receptor (calcitonin) activity modifying	1.7
65	103305	X82279		gb:HLsapiens Fas, Apo-1 gene (promoter a	1.7
	110384	H45282	Hs.268798	ESTs	1.7
	115626	AW630870	Hs.86674	ESTs, Weakly similar to hypothetical pro	1.7
	126905	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	1.7
	130820	AL353934	Hs.288798	hypothetical protein FLJ21012	1.7
70	112394	AK000373	Hs.8358	hypothetical protein FLJ20366	1.7
	129589	AW504292	Hs.11517	ESTs	1.7
	126446	NM_015670	Hs.118926	centrin/SUMO-specific protease 3	1.7
	126547	U47732	Hs.84072	transmembrane 4 superfamily member 3	1.7
	120287	AF219946	Hs.102237	tubby super-family protein	1.7
75	129991	R28386	Hs.179925	ESTs, Weakly similar to ALU8_HUMAN ALU	1.7
	123912	AA621283	Hs.332855	EST	1.7
	102071	AL120051	Hs.144700	ephrin-B1	1.7
	121046	AB033083	Hs.97377	KIAA1257 protein	1.7
	128403	AI908006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	1.7
80	104268	AL043864	Hs.70604	ATPase, Class II, type 9A	1.7
	111598	R11505	Hs.268912	ESTs	1.7
	128109	AW269421	Hs.128093	ESTs	1.7
	125435	R08480	Hs.272138	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.7
	133104	AI091195	Hs.65029	growth arrest-specific 1	1.7

	126826	AA099764		gbzn61f12.r1 Stratagene muscle 937209 H	1.7
	106483	NM_006548	Hs.30299	IGF-II mRNA-binding protein 2	1.7
	129765	M86933	Hs.1238	amelogenin (Y chromosome)	1.7
5	115904	AI167560	Hs.61297	ESTs	1.7
	125514	AB040912	Hs.191098	hypothetical protein FLJ11598	1.7
	125797	H03117	Hs.111497	similar to mouse neuronal protein 15.6	1.7
	133179	U81599	Hs.66731	homeo box B13	1.7
	115167	AA749209	Hs.43728	hypothetical protein	1.7
10	118036	AI471862	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	1.7
	124540	N63232		gbvz39a12.s1 Morton Fetal Cochlea Homo	1.7
	126183	BE018708	Hs.81972	SHC (Src homology 2 domain-containing) t	1.7
	127897	AA773681		gb:af77b12.r1 Soares_NhHMPu_S1 Homo sapi	1.7
	126680	F07097	Hs.133865	transmembrane 6 superfamily member 1	1.7
15	126972	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	1.7
	130605	BE514362	Hs.306024	FK506-binding protein 3 (25kD)	1.7
	127541	AA573449	Hs.171515	ESTs	1.7
	127392	AI816736	Hs.14896	DHHC1 protein	1.7
	106879	AI190785	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA,	1.7
20	128303	AI096444	Hs.7187	hypothetical protein FLJ10707	1.7
	126469	BE384361	Hs.182885	ESTs, Weakly similar to JC5024 UDP-galac	1.7
	125756	BE174587	Hs.289721	growth arrest specific transcript 5	1.7
	132332	AW978906	Hs.45005	hypothetical protein FLJ12960	1.6
	127142	AW452942	Hs.130393	ESTs	1.6
25	128416	F13165	Hs.12549	ESTs, Weakly similar to 2109260A B cell	1.6
	103790	AL122044	Hs.331633	hypothetical protein DKFZp566N034	1.6
	134578	AL110193	Hs.224137	hypothetical protein	1.6
	110023	AW294701	Hs.31040	ESTs	1.6
	125511	AJ271379	Hs.76194	ribosomal protein S5	1.6
30	111483	R06569	Hs.269534	ESTs	1.6
	127363	AF064104	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	1.6
	126231	AA991766	Hs.300793	ESTs	1.6
	106181	AI803651	Hs.191608	ESTs	1.6
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S	1.6
35	119929	W86464	Hs.304825	ESTs	1.6
	132542	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434I0812 (f	1.6
	127155	AA284993		gb:z123e10.r1 Soares ovary tumor NbHOT H	1.6
	125956	AK000214	Hs.129014	hypothetical protein FLJ20207	1.6
	126854	AJ275986	Hs.71414	transcription factor (SMIF gene)	1.6
40	131330	D13969	Hs.184669	zinc finger protein 144 (Maf-18)	1.6
	129445	W52452	Hs.29797	ribosomal protein L10	1.6
	113427	T85105	Hs.15471	ESTs	1.6
	106124	H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H	1.6
	128135	AA954381	Hs.269721	ESTs, Moderately similar to ALU1_HUMAN	1.6
45	111450	R02728	Hs.117331	ESTs	1.6
	125636	H12382	Hs.25119	ESTs, Weakly similar to YEX0_YEAST HYPOT	1.6
	134118	BE336680	Hs.182877	KIAA0116 protein	1.6
	111570	AF059203	Hs.20580	sterol O-acyltransferase 2	1.6
	113511	T89578	Hs.189740	ESTs	1.6
50	113296	AW449560	Hs.89576	inner mitochondrial membrane peptidase 2	1.6
	109875	H03260	Hs.30385	ESTs	1.6
	105930	AF016371	Hs.9880	peptidyl prolyl isomerase H (cyclophilin	1.6
	105564	BE616694	Hs.288042	hypothetical protein FLJ14299	1.6
	128063	AI377750	Hs.167177	ESTs	1.6
55	109779	AB029396	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur	1.6
	125334	T86569	Hs.182118	ESTs	1.6
	127206	AW816490	Hs.337508	ESTs	1.6
	108845	AW362901	Hs.68864	ESTs, Weakly similar to phosphatidylseri	1.6
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	1.6
60	114062	AI560984	Hs.27263	ESTs	1.6
	122550	AA451859	Hs.99253	ESTs	1.6
	113413	R08872	Hs.186512	ESTs	1.6
	127019	AI929355	Hs.286128	hypothetical protein FLJ23329	1.6
	106251	R12607	Hs.35101	proline-rich Glu (G-carboxyglutamic acid	1.6
65	112670	AL138012	Hs.183840	ESTs, Moderately similar to ALU7_HUMAN A	1.6
	114913	AI435189	Hs.58940	ESTs, Weakly similar to I38022 hypotheti	1.6
	126604	AI023299	Hs.269806	ESTs	1.6
	125324	R07785		gb:yl15c06.r1 Soares fetal liver spleen	1.6
	121438	AW445024	Hs.139389	ESTs	1.6
70	127289	AI041014	Hs.220752	ESTs, Weakly similar to unnamed protein	1.6
	126935	AI198535	Hs.89463	potassium large conductance calcium-acti	1.6
	132430	AW973652	Hs.283105	ESTs	1.6
	133541	H75334	Hs.11050	F-box only protein 9	1.6
	102612	U65402	Hs.248124	G protein-coupled receptor 31	1.6
75	120228	AI192528	Hs.164537	ESTs	1.6
	122652	AA454641		gb:zx99d05.s1 Soares_NhHMPu_S1 Homo sapi	1.6
	103456	AA496425	Hs.9629	papillary renal cell carcinoma (transloc	1.6
	105355	AL031447	Hs.26938	Homo sapiens, clone IMAGE:4053044, mRNA,	1.6
	108043	AA042873	Hs.160412	ESTs	1.6
80	128895	NM_003478	Hs.101299	cullin 5	1.6
	127984	AA846377	Hs.193706	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.6
	124405	AA228137	Hs.25005	hypothetical protein MGC3329	1.6
	103934	BE278111	Hs.134200	DKFZP564C186 protein	1.6
	124195	H83034		gb:yq48e07.r1 Soares fetal liver spleen	1.6

	110938	N48982	Hs.38034	Homo sapiens cDNA FLJ12924 fis, clone NT	1.6
	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	1.6
	121226	AA364109	Hs.177990	ESTs	1.6
5	120415	AA235810		gb:zs41a03.s1 Soares_NhHMPu_S1 Homo sapi	1.6
	123864	AA620882		gb:af95g01.s1 Soares_testis_NHT Homo sap	1.6
	125045	AI114630	Hs.208334	Homo sapiens cDNA: FLJ21874 fis, clone H	1.6
	133425	AA444390	Hs.155482	hydroxyacyl glutathione hydrolase	1.6
	126578	AF151861	Hs.107528	androgen induced protein	1.6
10	102406	U43177		(NONE)	1.6
	114126	BE566952	Hs.7063	Homo sapiens cDNA: FLJ20913 fis, clone A	1.6
	125233	W85713	Hs.110092	ESTs	1.6
	109635	F04296	Hs.169161	ESTs, Highly similar to MAON_HUMAN NADP-	1.6
	125675	BE294972	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL	1.6
15	129707	AW572317	Hs.12082	Homo sapiens mRNA: cDNA DKFZp566L203 (fr	1.6
	127569	AJ765107	Hs.274422	hypothetical protein FLJ20550	1.6
	113302	T66919	Hs.268575	ESTs	1.6
	119705	AJ984203	Hs.57874	ESTs	1.6
	127226	AL036559	Hs.3463	ribosomal protein S23	1.6
20	123489	AA599708		gb:ag11a10.s1 Gessler Wilms tumor Homo s	1.6
	107468	AA740979	Hs.91389	ESTs	1.6
	115916	AI052731	Hs.91910	ESTs	1.6
	127815	AA743490	Hs.255015	ESTs	1.6
	100364	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	1.6
25	125568	AW615395	Hs.105613	ESTs	1.6
	105260	N81201	Hs.31755	ESTs	1.6
	125659	T57693	Hs.87929	Homo sapiens cDNA FLJ13707 fis, clone PL	1.6
	111275	N70970	Hs.35006	ESTs	1.6
	106542	AA339541	Hs.24956	hypothetical protein FLJ22056	1.6
30	133423	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	1.6
	124770	AA984414	Hs.120429	ESTs	1.6
	117936	AI382904	Hs.47213	ESTs	1.6
	134385	M14660	Hs.169274	ESTs, Highly similar to IFT2_HUMAN INTER	1.6
	108367	AW410478	Hs.104019	transforming, acidic coiled-coil contain	1.6
35	131143	NM_000312	Hs.2351	protein C (inactivator of coagulation fa	1.6
	105441	N28522	Hs.8935	quinolinata phosphoribosyltransferase (n	1.6
	128215	AA973310		gb:zop91e06.s1 Soares_NFL_T_G8C_S1 Homo s	1.6
	127344	AI003929	Hs.80624	hypothetical protein MGC2560	1.6
	126478	BE541249	Hs.109697	ESTs	1.6
40	122053	AI637498	Hs.98745	ESTs	1.5
	111760	BE551929	Hs.268754	Homo sapiens cDNA FLJ11949 fis, clone HE	1.5
	112401	R61279	Hs.237536	ESTs, Weakly similar to AF151057 1 HSPC2	1.5
	130023	AW500470	Hs.117950	multifunctional polypeptide similar to S	1.5
	125575	H14983		gb:ym19h09.r1 Soares infant brain 1N1B H	1.5
45	128765	AF073310	Hs.143648	insulin receptor substrate 2	1.5
	108935	AA147848	Hs.67991	hypothetical protein DKFZp434G0522	1.5
	121221	AI140708	Hs.97461	ESTs	1.5
	120091	AW024672	Hs.59558	EST	1.5
	107375	BE011845	Hs.251064	high-mobility group (nonhistone chromoso	1.5
50	125803	AW876115	Hs.29852	ESTs	1.5
	115132	AA811762	Hs.71433	ESTs	1.5
	113346	AF143876	Hs.14318	Homo sapiens clone IMAGE:113399 mRNA seq	1.5
	107357	U63973	Hs.103501	rhodopsin kinase	1.5
	125443	BE251057	Hs.177592	ribosomal protein, large, P1	1.5
55	133803	M24461	Hs.76305	surfactant, pulmonary-associated protein	1.5
	113378	T80738	Hs.14757	ESTs	1.5
	105540	BE391690	Hs.9265	hypothetical protein FLJ20917	1.5
	127446	F13008		gb:HSC3HE011 normalized infant brain cDN	1.5
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	1.5
60	127585	AA604144	Hs.190632	ESTs	1.5
	125824	Z45258	Hs.286013	short coiled-coil protein	1.5
	127606	AA621135	Hs.136552	ESTs	1.5
	125585	AW298113	Hs.92909	SON DNA binding protein	1.5
	107757	BE621721	Hs.280792	hypothetical protein FLJ12387 similar to	1.5
65	109978	H09356	Hs.22528	ESTs	1.5
	132297	BE272446	Hs.265317	hypothetical protein MGC2562	1.5
	115784	AW402151	Hs.54673	tumor necrosis factor (ligand) superfamily	1.5
	127880	W39735	Hs.73818	ubiquinol-cytochrome c reductase hinge p	1.5
	102305	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	1.5
70	102868	X02419	Hs.77274	plasminogen activator, urokinase	1.5
	133457	J04948	Hs.333509	alkaline phosphatase, placental-like 2	1.5
	130339	AA435746		gb:z179e03.s1 Soares_testis_NHT Homo sap	1.5
	125444	N28476	Hs.159161	Rho GDP dissociation inhibitor (GDI) alp	1.5
	123470	AW303285	Hs.303632	Human DNA sequence from clone RP11-110H4	1.5
	100025				1.5
75	127063	AI276526	Hs.331564	Homo sapiens mRNA: cDNA DKFZp434H1215 (f	1.5
	127945	AA815031	Hs.123598	ESTs	1.5
	111557	R09510	Hs.20373	EST	1.5
	116009	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	1.5
80	119858	W01370	Hs.46824	ESTs	1.5
	106509	AB042309	Hs.64552	hypothetical protein MGC15563	1.5
	124124	AW294404	Hs.144515	Homo sapiens cDNA FLJ11672 fis, clone HE	1.5
	126713	AW249181	Hs.19954	ESTs, Weakly similar to T19873 hypotheti	1.5
	126475	AW959075	Hs.238797	ESTs, Moderately similar to I38022 hypot	1.5

5	126851	R40611	Hs.137565	ESTs	1.5
	104820	AW162768	Hs.22620	ESTs	1.5
	127235	AJ817309	Hs.225583	ESTs, Weakly similar to 2004399A chromos	1.5
	126552	AF168711	Hs.159397	x 010 protein	1.5
	127523	AA617637		gbnp34h12.s1 NCI_CGAP_Lu1 Homo sapiens	1.5
10	131692	BE559581	Hs.30736	KIAA0124 protein	1.5
	112974	AL353955	Hs.101174	microtubule-associated protein tau	1.5
	118921	N91914	Hs.54751	ESTs	1.5
	100676	X02761	Hs.287820	fibronectin 1	1.5
	127721	T59578	Hs.188440	ESTs, Weakly similar to ALUF_HUMAN !!!	1.5
15	115254	AA279024	Hs.269316	ESTs, Weakly similar to S65657 alpha-1C	1.5
	128173	AA457242	Hs.127024	ESTs	1.5
	126846	AA663527	Hs.116910	ESTs	1.5
	125294	R40025	Hs.106551	ESTs	1.5
	127494	AW978730	Hs.291956	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.5
20	134191	W26632	Hs.7979	KIAA0736 gene product	1.5
	107394	AA864798	Hs.186180	Homo sapiens cDNA: FLJ23038 fs, clone L	1.5
	131562	NM_003512	Hs.28777	H2A histone family, member L	1.5
	127310	AW450871	Hs.189284	ESTs	1.5
	122359	AA523486		gbni67111.s1 NCI_CGAP_Pr12 Homo sapiens	1.5
25	100524	M80902	Hs.183704	ubiquitin C	1.5
	128422	T77794		gb:yd20d09.r1 Soares fetal liver spleen	1.5
	129902	AA076278	Hs.13277	hypothetical protein FLJ22054	1.5
	126784	T81887	Hs.108854	HSPC163 protein	1.5
	123343	AJ761902	Hs.99597	ESTs	1.5
30	105458	AW954377	Hs.26412	ring finger protein 26	1.5
	112266	AI652534	Hs.25934	ESTs, Weakly similar to HSHU11 histone H	1.5
	127622	AA628222	Hs.97883	ESTs	1.5
	113659	R06545	Hs.189781	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.5
	116892	AJ573283	Hs.38458	ESTs	1.5
35	126995	NM_014351	Hs.189810	sulfotransferase family 4A, member 1	1.5
	111657	R07364	Hs.268667	ESTs, Weakly similar to ALU1_HUMAN ALU	1.5
	100243	AB028125	Hs.77854	regucalcin (senescence marker protein-30)	1.5
	116153	AF107203	Hs.57937	ataxin 2-binding protein 1	1.5
	108892	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp434L0827 (f	1.5
40	113294	AI037922	Hs.11000	leptin receptor overlapping transcript-l	1.5
	126691	W03046	Hs.283664	aspartate beta-hydroxylase	1.5
	106979	AW015227	Hs.289053	hypothetical protein FLJ14733	1.5
	125546	H09950		gb:ym01d12.r1 Soares infant brain 1NIB H	1.5
	113990	AI497945	Hs.83097	hypothetical protein FLJ22955	1.5
45	129295	U63127	Hs.110121	SEC7 homolog	1.5
	125431	AW851639	Hs.75584	polymyositis/scleroderma autoantigen 2 (1.5
	112558	AK001621	Hs.15921	hypothetical protein FLJ10759	1.5
	122046	AI560456	Hs.107319	ESTs	1.5
	122472	AA448609	Hs.128652	ESTs	1.5
50	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	1.5
	131714	AA642831	Hs.31016	putative DNA binding protein	1.5
	101233	AL135173	Hs.878	sorbitol dehydrogenase	1.5
	109501	AF047437	Hs.90436	sperm associated antigen 7	1.5
	126984	AA213820	Hs.256533	ESTs, Weakly similar to S11998 finger pr	1.5
55	125765	BE243877	Hs.76941	ATPase, Na+K+ transporting, beta 3 poly	1.5
	127693	AA676727		gb:zj68b11.s1 Soares_fetal_liver_spleen_	1.5
	128453	X02761	Hs.287820	fibronectin 1	1.5
	119418	T97590	Hs.221711	ESTs, Weakly similar to ALU1_HUMAN ALU	1.5
	132669	W38586	Hs.293981	guanine nucleotide binding protein (G pr	1.5
60	116708	F10528	Hs.70001	ESTs, Moderately similar to JC6169 nucl	1.5
	122420	AA446971		gb:zw85f11.s1 Soares_total_fetus_Nb2HF8_	1.5
	100238	L24959	Hs.348	calcium/calmodulin-dependent protein kin	1.5
	109710	D20044	Hs.12929	hypothetical protein FLJ20721	1.5
	105704	AI282341	Hs.75431	fibrinogen, gamma polypeptide	1.5
65	112712	R91060	Hs.330761	ESTs	1.5
	100098	AF003743		gb:Homo sapiens delayed rectifier potass	1.5
	114122	R46128	Hs.12751	ESTs	1.5
	132397	AA021160	Hs.4750	hypothetical protein DKFZp564K0822	1.5
	107881	AI568350	Hs.61273	hypothetical protein MGC2650	1.5
70	106302	AA398859	Hs.18397	hypothetical protein FLJ23221	1.5
	125898	AK001823	Hs.92287	Homo sapiens mRNA; cDNA DKFZp564C2478 (f	1.5
	104957	AI359009	Hs.10026	mitochondrial ribosomal protein L17	1.5
	102909	NM_005269	Hs.2693	glioma-associated oncogene homolog (zinc	1.5
	125559	BE297488	Hs.279877	cell division protein FtsJ	1.5
75	109634	H17083	Hs.183646	ESTs	1.5
	116607	W05238	Hs.94316	ESTs, Weakly similar to T31613 hypotheti	1.5
	127175	R11937		gb:yt54b08.r1 Soares infant brain 1NIB H	1.5
	110617	W93231	Hs.285901	Homo sapiens, clone IMAGE:3948563, mRNA,	1.5
	125988	W27648		gb:37e10 Human retina cDNA randomly prim	1.5
80	115093	AI241932	Hs.3542	hypothetical protein FLJ11273	1.5
	121207	AA705799	Hs.183714	ESTs	1.5
	112652	BE269699	Hs.235782	solute carrier family 21 (organic anion	1.5
	125213	AB014564	Hs.109299	protein tyrosine phosphatase, receptor t	1.5
	125912	AW867467	Hs.278712	eukaryotic translation initiation factor	1.5
	133046	R96881	Hs.63609	HpaII tiny fragments locus 9C	1.5
	122791	AL122055	Hs.129836	KIAA1028 protein	1.5

Table 26B

5	Pkey:		Unique Eos probe set identifier number
	CAT number:		Gene cluster number
10	Accession:		Genbank accession numbers
	Pkey	CAT number	Accession
10	108451	13766_27	AA079195 AA084955 AA126308 AA084956
	124195	2606_3	H83034 H52379
	123619	371681_1	AA602964 AA609200
	125165	1852047_1	W45350 W45406
	125324	1692163_1	R07785 T85948 T86972
15	126053	1601238_1	H64450 H64464
	126086	1606216_1	H75681 H70975
	126098	1629789_1	M79088 N88221
	125464	168460_1	N71807 AA2033399
	125499	1562851_1	H10543 R11878
20	126127	1205826_1	N95428 W24040 AW751366 H81987
	125546	356478_1	H09950 R18413 AA570553 AW973425
	125549	1702179_1	R20215 R18767
	125558	1703083_1	R59305 R19748
	125575	1566885_1	H14983 R21554
25	125743	5025_5	H17151 H11956
	125761	1744008_1	R68351 R68364
	126426	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017
			AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119 AA085208 AA085045
			AA284993 AA478122 AA477923
30	127155	200358_1	R11937 Z45532
	127175	1695805_1	Z24895 AW891336 R01294
	126528	1276201_1	H41694 H45213
	125957	1583542_1	AA436760 AW237453 BE327496 N47347 N56967
	125976	296453_1	R98091 W92898
35	125982	1766315_1	W27648 R99193 BE090398
	125988	1365728_1	AA323958 AA370268
	127245	226662_1	AA364195 AA325029 AW962050
	127248	227560_1	AA828125 AA834883 AA330555
	127262	231725_1	T16245 R19694 F13545 H10299 T66048 T65279 H18006
40	126659	1541209_1	C05723 AA018342
	126693	87363_1	AF116622 AJ114507 AA640834 AA377999
	127315	37938_1	AA442429 T19477
	126730	297653_1	AA248884
	103898	187213_3	F13008 T75435
45	127446	16001_2	AA099764 AA112950
	126826	127356_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073, BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
	126872	142696_1	BE011368 BE011362 BE011215 BE011365 BE011363
			AA225632 AJ820970 AJ820952 AA226472 AJ732140 AJ732059 AA226307
			AA225500
50	127523	351071_1	AA617637 AA554963
	126982	171753_1	AA211419 AA211566
	128215	530345_1	AA973310
	127704	405690_1	AA679609 AA694592
	127705	966283_2	AJ003322 AJ003324
55	128422	1811283_1	T77794 T85681
	127897	446527_1	AA773681 AA773857
	120734	208882_1	AA299948 AA299949
	100098	25117_-13	AF003743
	114620	32062_8	AA642974 AA084223
60	122652		26401_30 AA454641
	100842		tigr_HT4398 U05597
	123783		genbank_AA610112
	125032		genbank_T74884
	123808		genbank_AA620552
65	123864		genbank_AA620882
	118049		genbank_N53145
	102406		entrez_U43177
	116962		genbank_H79677
	134076	40321_1	AF086215 W02702 AA284288 W25655
70	125888	266863_1	H18298 H46830
	127271	321389_1	H96820 H79463
	113119		genbank_T47910 T47910
	104799		genbank_AA029703 AA029703
	127693	790317_1	AA576727 AA704704
75	120415		genbank_AA235810 AA235810
	127964	135151_1	F06298 R18057
	122359		681003_1 AA523486 AW026780 AJ821660 AA443898
	122420		genbank_AA446971
	124276		genbank_H83465
80	101447		entrez_M21305
	124540		genbank_N63232
	124554		genbank_N65961
	117357		genbank_N24829
	103305		entrez_X82279

103392	entrez_X94563
119416	genbank_T97186
105225	genbank_AA211777
121292	genbank_AA401807
112853	genbank_T02843
121387	genbank_AA405854
114501	genbank_AA075566
100221	entrez_D28383
130339	genbank_AA435746
100554	tigr_HT2241
123423	genbank_AA598484
123474	genbank_AA599209
123489	genbank_AA599708

TABLE 27A: ABOUT 895 GENES UP-REGULATED IN COMBINED LUNG FIBROSIS COMPARED TO NORMAL BODY

Table 27A lists about 895 genes that are upregulated in lung fibrosis (collection of IPF, HP, and NSIP) samples as compared with the normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" fibrosis sample expression level to "average" normal adult tissues was greater than or equal to about 2.0. The "average" fibrosis sample expression level was set to the 90th percentile amongst fibrosis samples. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of fibrosis to normal body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	56.0
424917	AI636208	Hs.96901	Homo sapiens cDNA: FLJ23049 fis, clone L	26.5
453310	X70697	Hs.553	solute carrier family 6 (neurotransmitter)	25.5
457200	U33749	Hs.197764	thyroid transcription factor 1	22.2
414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	21.1
429272	W25140	Hs.110667	ESTs	19.4
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial)	19.1
442006	AW975183	Hs.292663	ESTs	18.8
445885	AI734009	Hs.127699	KIAA1603 protein	18.0
440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	17.8
422426	W79117	Hs.58559	ESTs, Weakly similar to rholekin [M.musc]	17.4
444929	AI685841	Hs.161354	ESTs	16.5
440807	AW269421	Hs.128093	ESTs	16.3
408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	14.2
446967	AI699629	Hs.156781	ESTs	13.3
417801	AA417383	Hs.82582	Integrin, beta-like 1 (with EGF-like rep	12.3
437119	AI379921	Hs.177043	ESTs	12.3
451103	R52804	Hs.25956	DKFZP564D206 protein	11.5
443450	N56045	Hs.133529	ESTs	11.4
411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	11.3
432519	AI221311	Hs.130704	ESTs	11.3
414142	AW368397	Hs.150042	ESTs	11.0
433283	BE041135	Hs.175622	ESTs	10.1
441082	AW444804	Hs.202655	ESTs	10.1
452039	AI922988	Hs.172510	ESTs	10.0
417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	9.9
421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	9.8
412372	R65998	Hs.118615	ESTs	9.8
426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfamily	9.7
431007	AF039564	Hs.248211	retinoblastoma-binding protein 9	9.4
443709	AI082692	Hs.134662	ESTs	9.3
446232	AI281848	Hs.165547	ESTs	9.2
448253	H25899	Hs.201591	ESTs	9.2
432133	AB033088	Hs.272567	KIAA1262 protein	9.1
409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	9.0
431353	AA828032	Hs.189076	ESTs	8.8
450050	AI681268	Hs.257883	ESTs	8.8
458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	8.8
414958	C16096	Hs.297777	ESTs	8.7
425664	AJ006276	Hs.159003	transient receptor potential channel 6	8.7
408562	AI436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	8.6
453672	U73531	Hs.34526	G protein-coupled receptor	8.5
429420	AK001679	Hs.202289	hypothetical protein FLJ10376	8.5
421478	AI683243	Hs.97258	ESTs	8.4
404916				8.4
444396	T65213	Hs.4257	ESTs	8.3
442275	AW449467	Hs.54795	ESTs	8.3
437479	R61866	Hs.101277	ESTs	8.2
432203	AA305746	Hs.49	macrophage scavenger receptor 1	8.2
431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	7.9
406747	AI925153	Hs.217493	annexin A2	7.8

	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	7.7
	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	7.6
	421798	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	7.5
	421155	H87879	Hs.102267	lysyl oxidase	7.5
5	446917	AI347863	Hs.156572	ESTs	7.5
	422798	R92347	Hs.34574	ESTs	7.4
	426830	AA385751	Hs.160392	ESTs	7.4
	437157	BE048860	Hs.120655	ESTs	7.4
10	433231	AB040926	Hs.143552	KIAA1493 protein	7.3
	451561	N52812	Hs.177403	ESTs	7.1
	430656	AA482900	Hs.162080	ESTs	7.1
	448206	BE622585	Hs.3731	ESTs	7.1
	420209	AA256444	Hs.32295	Homo sapiens cDNA FLJ12604 fis, clone NT	7.0
15	426803	AA362568	Hs.179747	ecotropic viral integration site 5	6.9
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	6.9
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	6.8
	443324	R44013	Hs.164225	ESTs	6.8
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	6.8
20	427356	AW023482	Hs.97849	ESTs	6.7
	418735	N48769	Hs.44609	ESTs	6.7
	429945	NM_005729	Hs.226483	diaphanous (Drosophila, homolog) 2	6.6
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	6.6
	430099	AW194988	Hs.20537	Homo sapiens cDNA FLJ13942 fis, clone Y7	6.6
25	441835	AB036432	Hs.184	advanced glycosylation end product-speci	6.5
	428508	BE252383	Hs.184668	SBBI31 protein	6.5
	438202	AW169287	Hs.22588	ESTs	6.5
	441233	AA972965	Hs.135568	ESTs	6.4
	433384	AI021992	Hs.124244	ESTs	6.3
	427043	AA397679	Hs.298460	ESTs	6.3
30	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	6.3
	438909	AF085839		gb:Homo sapiens full length insert cDNA	6.3
	433365	AF026944	Hs.293797	ESTs	6.3
	456964	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	6.2
35	445186	AW614544	Hs.123641	protein tyrosine phosphatase, receptor t	6.2
	431337	N48107	Hs.292593	ESTs	6.1
	434819	AA650099	Hs.291541	ESTs	6.0
	458219	H22195	Hs.31874	ESTs	6.0
	434377	AW137148	Hs.136348	osteoblast specific factor 2 (fascidin	5.9
40	435933	AA805520	Hs.192075	ESTs	5.9
	436954	AA740151	Hs.130425	ESTs	5.9
	445424	AB028945	Hs.12695	cortactin SH3 domain-binding protein	5.8
	449108	AI140683	Hs.98328	ESTs	5.8
	410334	AW979261	Hs.291993	ESTs	5.7
	447112	H17800	Hs.7154	ESTs	5.7
45	447700	AI420183	Hs.171077	ESTs, Weakly similar to similar to serin	5.7
	449208	AW263635	Hs.48643	ESTs	5.7
	445657	AW612141	Hs.279575	ESTs	5.7
	421554	AW137676	Hs.97775	ESTs, Weakly similar to Testis-specific	5.7
50	435299	AI745458	Hs.122614	ESTs, Weakly similar to apoptotic protea	5.6
	416769	AI339257	Hs.115436	ESTs	5.6
	433527	AW235613	Hs.133020	ESTs	5.6
	452771	T05477		gb:EST03366 Fetal brain, Stralagene (cat	5.6
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	5.5
55	411514	AW850178	Hs.18995	KIAA1304 protein	5.5
	424084	AI940575	Hs.20914	Homo sapiens cDNA: FLJ23056 fis, clone L	5.5
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.4
	429710	AI337113	Hs.146025	Homo sapiens cDNA: FLJ23594 fis, clone L	5.4
	432113	AA935065	Hs.152385	ESTs	5.4
	447997	H00656	Hs.29792	ESTs	5.4
60	449328	AI962493	Hs.197647	ESTs	5.3
	416575	W02414	Hs.38383	ESTs	5.3
	432009	AL137424		gb:Homo sapiens mRNA; cDNA DKFZp761G2123	5.3
	434088	AF116677	Hs.249270	hypothetical protein PRO1986	5.3
65	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	5.2
	414299	AA142989	Hs.71730	ESTs	5.2
	431041	AA490967	Hs.105276	ESTs	5.2
	448104	AI674818	Hs.178391	ribosomal protein L44	5.2
	445279	R41900	Hs.22245	ESTs	5.1
70	408978	AL133617	Hs.49421	Homo sapiens mRNA; cDNA DKFZp434M0728 (f	5.1
	415094	D59513		gb:HUM042H108 Clontech human fetal brain	5.1
	428244	AI564123	Hs.42500	ADP-ribosylation factor-like 5	5.1
	452784	BE463857	Hs.151258	Homo sapiens cDNA: FLJ21062 fis, clone C	5.1
	455431	AW938484	Hs.80738	sialophorin (gpL115, leukosialin, CD43)	5.1
75	449416	AI651016	Hs.246311	ESTs	5.1
	421659	NM_014459	Hs.106511	protocadherin 17	5.1
	407638	AJ404672	Hs.288593	Homo sapiens cDNA FLJ11667 fis, clone HE	5.0
	446164	AW273539	Hs.199329	Homo sapiens cDNA: FLJ23577 fis, clone L	5.0
	413048	M93221	Hs.75182	mannose receptor, C type 1	5.0
80	446608	N75217	Hs.257846	ESTs	4.9
	419807	R77402		gb:Y75F11.1.s1 Soares placenta Nb2HP Homo	4.9
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	4.9
	442652	AI005163	Hs.201378	ESTs, Weakly similar to KIAA0944 protein	4.9
	429496	AA453800	Hs.192793	ESTs	4.8

	429859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor l	4.8
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	4.8
	425509	AF079363	Hs.158213	sperm associated antigen 6	4.8
5	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	4.8
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	4.8
	444218	AF070641	Hs.10584	Homo sapiens clone 24421 mRNA sequence	4.7
	453382	AA709285	Hs.5997	Homo sapiens cDNA FLJ13078 fis, clone NT	4.7
	447033	AI357412	Hs.157601	ESTs	4.7
10	417235	AA810278	Hs.24250	ESTs	4.7
	418200	AW629751	Hs.206654	ESTs, Weakly similar to alternatively sp	4.7
	427652	AI673025	Hs.43874	ESTs	4.7
	431255	AA497043	Hs.115685	ESTs	4.7
	441143	AI027604	Hs.159550	ESTs	4.7
15	452293	AI871833		gb:wm51h09.x1 NCI_CGAP_UI2 Homo sapiens	4.7
	443903	AI220547	Hs.135223	ESTs	4.7
	422352	AA766296	Hs.99200	ESTs	4.7
	424105	AI142336	Hs.43977	ESTs	4.6
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	4.6
20	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.6
	430510	AW162916	Hs.241576	hypothetical protein PRO2577	4.6
	425804	BE501698	Hs.258189	ESTs	4.6
	435347	AW014873	Hs.116963	ESTs	4.6
	446002	AI346468	Hs.145789	ESTs	4.6
25	452883	X80031	Hs.150318	ESTs	4.6
	442176	AA983764	Hs.128910	ESTs	4.6
	443253	AI041212	Hs.132117	ESTs	4.5
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	4.5
	439920	H05430	Hs.144455	ESTs	4.5
30	421502	AF111856	Hs.106039	solute carrier family 34 (sodium phospho	4.5
	434424	AI811202	Hs.125365	Homo sapiens cDNA: FLJ23523 fis, clone L	4.4
	408525	AW243323	Hs.266785	ESTs	4.4
	449299	AA299919		gb:EST12592 Uterus tumor I Homo sapiens	4.4
	450656	AA010539	Hs.18912	ESTs	4.4
35	433815	AI696602	Hs.112757	ESTs	4.4
	416879	H98899	Hs.42599	ESTs	4.3
	432182	AW607789	Hs.293119	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.3
	445386	AI422005	Hs.160380	ESTs	4.3
	450478	AW451709	Hs.271200	ESTs	4.3
40	453080	AI423056	Hs.23921	Homo sapiens cDNA FLJ12482 fis, clone NT	4.3
	436496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	4.3
	443257	AI334040	Hs.11614	Homo sapiens cDNA: FLJ23555 fis, clone L	4.3
	453921	AI824009	Hs.44577	ESTs	4.3
	419721	NM_001650	Hs.288650	aquaporin 4	4.2
45	432316	AW973235	Hs.293697	ESTs	4.2
	435202	AI971313	Hs.170204	KIAA0551 protein	4.2
	440320	AA879294		gb:nw86e09.s1 NCI_CGAP_Pr12 Homo sapiens	4.2
	438796	W67821	Hs.109590	genethonin 1	4.2
	400269				4.2
50	447724	AW298375	Hs.24477	ESTs	4.1
	446509	AF169693	Hs.132892	protocadherin 20	4.1
	451620	AW449888	Hs.257224	ESTs	4.1
	451963	AI825440	Hs.224952	ESTs	4.1
	456408	AI288348	Hs.23450	mRNA for FLJ00023 protein	4.1
55	425895	AI269484	Hs.161427	zinc finger protein 215	4.1
	447048	AW393080	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone L	4.1
	454024	AA993527	Hs.16281	hypothetical protein FLJ23403	4.0
	415929	AA724373	Hs.295306	ESTs, Highly similar to unnamed protein	4.0
	426625	T78300	Hs.171409	serologically defined colon cancer anti	4.0
60	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	4.0
	437138	AI935622	Hs.271245	ESTs	4.0
	455024	AW851309		gb:IL3-CT0220-170200-067-C11 CT0220 Homo	4.0
	436246	AW450963	Hs.119991	ESTs	4.0
	416030	H15261	Hs.21948	ESTs	4.0
65	459267	AI003631		gb:AJ003631 Selected chromosome 21 cDNA	3.9
	445122	AW241632	Hs.147377	Homo sapiens cDNA: FLJ23598 fis, clone L	3.9
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.9
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f	3.9
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	3.9
70	429208	AA447990	Hs.190478	ESTs	3.9
	442957	AI949952	Hs.49397	ESTs	3.9
	444050	AW138295	Hs.135024	ESTs	3.9
	444078	BE246919	Hs.10290	US snRNP-specific 40 kDa protein (hPp8-	3.9
	451024	AA442176		gb:zw63b08.r1 Soares_talal_fetus_Nb21F8_	3.9
75	442832	AW206560	Hs.253569	ESTs	3.9
	423377	AL049377		gb:Homo sapiens mRNA; cDNA DKFZp586H0718	3.9
	451895	T93573	Hs.16970	ESTs	3.9
	442353	BE379594	Hs.49136	ESTs	3.8
	421464	AA291553	Hs.190086	ESTs	3.8
80	404043				3.8
	407055	X89211		gb:H.sapiens DNA for endogenous retrovir	3.8
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (93720	3.8
	410247	AF181721	Hs.61345	RU2S	3.8
	417461	R38403	Hs.13305	ESTs	3.8

5	423609	AA328348	Hs.218289	ESTs	3.8
	440444	AA885221	Hs.156984	ESTs	3.8
	446254	BE179829	Hs.178852	Homo sapiens cDNA FLJ12832 fis, clone NT	3.8
	447505	AL049266	Hs.18724	Homo sapiens mRNA: cDNA DKFZp564F093 (tr	3.8
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	3.8
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	3.8
	444271	AW452569	Hs.149804	ESTs	3.8
	434217	AW014795	Hs.23349	ESTs	3.8
10	452571	W31518	Hs.34665	ESTs	3.7
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	3.7
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	3.7
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	3.7
	445034	AW293376	Hs.160323	ESTs	3.7
15	438842	AA827176	Hs.124316	ESTs	3.7
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7
	415025	AW207091	Hs.72307	ESTs	3.7
	420313	AB023230	Hs.96427	KIAA1013 protein	3.7
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone CO	3.7
20	433492	AW605849		gb:MR0-HT0241-200100-006-g02 HT0241 Homo	3.7
	434636	AA083764	Hs.241334	ESTs	3.7
	435747	AI079519	Hs.134398	ESTs	3.7
	458158	AW296778	Hs.300357	ESTs, Highly similar to dJ416F21.2 [H.s.a	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
25	410060	NM_001448	Hs.58367	glypican 4	3.7
	426116	AA868729	Hs.144694	ESTs	3.7
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	3.7
	414259	W44633	Hs.25044	Homo sapiens cDNA: FLJ23131 fis, clone L	3.7
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	3.6
30	431889	AA521277	Hs.124946	ESTs	3.6
	430414	AW365665	Hs.120388	ESTs	3.6
	433426	H69125	Hs.133525	ESTs	3.6
	421764	AI681535	Hs.99342	ESTs, Weakly similar to KCC1_HUMAN CALCI	3.6
	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	3.6
35	455235	AW675951		gb:CM1-PT0013-131299-067-109 PT0013 Homo	3.6
	408399	NM_005426	Hs.44585	tumor protein p53-binding protein, 2	3.6
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.6
	436982	AB018305	Hs.5378	spodin 1, (f-spondin) extracellular mat	3.6
	432231	AA339977	Hs.274127	CLST 11240 protein	3.6
40	432837	AA310693	Hs.279512	HSPC072 protein	3.6
	452166	AI948607	Hs.264580	ESTs	3.5
	458154	AW816379		gb:QV4-ST0234-181199-035-g01 ST0234 Homo	3.5
	420362	U79734	Hs.97206	huntingtin interacting protein 1	3.5
	424202	BE350295	Hs.15032	ESTs, Weakly similar to RAN binding prot	3.5
45	410658	AW105231	Hs.192035	ESTs	3.5
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	419503	AA243642	Hs.137422	ESTs	3.5
	439479	AI734258	Hs.245367	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	448404	BE089973		gb:RC6-BT0709-310300-021-G07 BT0709 Homo	3.5
50	424268	AA397653	Hs.144339	Human DNA sequence from clone 495010 on	3.5
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	3.5
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	3.5
	428927	AA441837	Hs.90250	ESTs	3.5
	422544	AB018259	Hs.118140	KIAA0716 gene product	3.4
55	431207	AA495925	Hs.9394	ESTs	3.4
	424508	AL080103	Hs.149770	Homo sapiens cDNA FLJ13658 fis, clone PL	3.4
	441484	AA935481	Hs.58972	ESTs	3.4
	425916	NM_006786	Hs.162200	urotensin 2	3.4
	401793				3.4
60	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	3.4
	438038	AI732629	Hs.194161	ESTs, Weakly similar to TA2R HUMAN, BETA	3.4
	439619	AW975998	Hs.58595	ESTs	3.4
	446577	AB040933	Hs.15420	KIAA1500 protein	3.4
	450445	AW974636	Hs.194563	ESTs	3.4
65	459482	AA625339	Hs.237052	EST, Weakly similar to ALU1_HUMAN ALU SU	3.4
	445495	BE622641	Hs.38489	ESTs	3.4
	428743	AL080060	Hs.301549	Homo sapiens mRNA: cDNA DKFZp564H172 (tr	3.4
	426320	W47595	Hs.169300	transforming growth factor, beta 2	3.4
	432859	AW974094		gb:EST386197 MAGE resequences, MAGM Homo	3.3
70	419235	AW470411	Hs.288433	neurotrophin	3.3
	429703	T93154	Hs.28705	ESTs	3.3
	413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	3.3
	406182				3.3
	417307	N99673	Hs.3585	ESTs, Weakly similar to AF126743 1 DNAJ	3.3
75	430140	AW296771	Hs.221999	ESTs	3.3
	436111	AI803082	Hs.157212	ESTs	3.3
	449729	R72032	Hs.29235	ESTs	3.3
	457620	AA602711		gb:np03h08.s1 NCI_CGAP_Pr2 Homo sapiens	3.3
80	428434	AW363590	Hs.65551	ESTs, Weakly similar to AF172993 1 PLUNC	3.3
	406554				3.3
	451381	BE241831		gb:TCAAPZE0011 Pediatric acute myelogeno	3.3
	443113	AI040686	Hs.132908	ESTs	3.3
	421470	R27496	Hs.1378	annexin A3	3.3
	446428	AW082270	Hs.210617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3

	435031	AI632091	Hs.116877	ESTs	3.3
	413136	BE066941		gb:PM0-BT0340-091299-002-a11 BT0340 Homo	3.2
	429228	AI553633	Hs.104985	ESTs	3.2
5	420252	AW270404	Hs.193161	ESTs	3.2
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	3.2
	444339	T96555	Hs.31562	ESTs	3.2
	434164	AW207019	Hs.148135	ESTs	3.2
	404599				3.2
10	426920	AA393351	Hs.132121	ESTs	3.2
	453736	AL118674	Hs.34871	KIAA0569 gene product	3.2
	408923	H73881	Hs.255436	ESTs	3.2
	430919	AA489041	Hs.295448	ESTs	3.2
	431622	AW979271	Hs.293184	ESTs	3.2
15	433584	AW295399		gb:U1-H-B12-zhv-h-03-0-UI.s1 NCI_CGAP_Su	3.2
	437073	AI885608	Hs.94122	ESTs	3.2
	438394	BE379623	Hs.27693	CGI-124 protein	3.2
	446242	N66336	Hs.7360	ESTs	3.2
	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	3.2
20	454009	AW015927	Hs.233071	ESTs	3.2
	449765	N92293	Hs.205832	EST, Moderately similar to ALU8_HUMAN AL	3.2
	415652	T79213	Hs.272073	ESTs	3.2
	453931	AL121278	Hs.25144	ESTs	3.2
	439382	BE247684	Hs.103070	ESTs	3.2
25	420077	AW512260	Hs.87767	ESTs	3.2
	430437	AI768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	3.2
	446745	AW118189	Hs.156400	ESTs	3.1
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	3.1
	450320	AW291775	Hs.213793	ESTs	3.1
30	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	3.1
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.1
	451110	AI955040	Hs.301584	ESTs	3.1
	431745	AW972448	Hs.163425	ESTs	3.1
	410781	AI375572	Hs.165028	ESTs	3.1
35	419546	AA244199		gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens	3.1
	444330	AI597655	Hs.49265	ESTs	3.1
	408761	AA057264	Hs.238936	ESTs	3.1
	409026	AL137554	Hs.49927	Homo sapiens mRNA; cDNA DKFZp434H1720 (f	3.1
	432055	AW972359	Hs.293334	ESTs	3.1
40	432441	AW292425	Hs.163484	ESTs	3.1
	408045	AW138959	Hs.245123	ESTs	3.1
	427191	BE221825	Hs.97691	ESTs	3.1
	416965	N26223	Hs.160436	ESTs	3.1
	441594	AL041080	Hs.208765	ESTs	3.1
45	406992	S82472		gb:beta-pol=DNA polymerase beta (exon a	3.0
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.0
	438323	AI986394	Hs.123369	ESTs	3.0
	427698	AW972594	Hs.294140	ESTs	3.0
	424296	AI631874	Hs.169391	ESTs	3.0
50	450522	AI698839		gb:wd31f02.x1 Soares_NFL_T_GBC_S1 Homo s	3.0
	407942	AA378608	Hs.5894	hypothetical protein FLJ10305	3.0
	417991	AA731452	Hs.190008	ESTs	3.0
	422589	AA312735	Hs.179725	ESTs	3.0
	437583	AA761190	Hs.244627	ESTs	3.0
55	452019	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.0
	449494	AW237014	Hs.288650	aquaporin 4	3.0
	444168	AI393165	Hs.19175	ESTs	3.0
	400297	AI127076	Hs.288381	hypothetical protein DKFZp564O1278	3.0
	410811	AW805687	Hs.300648	ESTs	3.0
60	450584	AA040403	Hs.60371	ESTs	3.0
	428043	T92248	Hs.2240	uteroglobin	3.0
	436120	AI248193	Hs.119860	ESTs	3.0
	442324	R63578	Hs.28426	ESTs	2.9
	448693	AW004854	Hs.228320	Homo sapiens cDNA: FLJ23537 fis, clone L	2.9
65	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	2.9
	431385	BE178536	Hs.11090	high affinity immunoglobulin epsilon rec	2.9
	408427	AW194270	Hs.177236	ESTs	2.9
	459587	AA031956		gb:zk15e04.s1 Soares_pregnant_uterus_NbH	2.9
	438128	AA904430	Hs.122049	ESTs, Weakly similar to U4U6 small nucl	2.9
70	408938	AA056013	Hs.22607	ESTs	2.9
	419276	BE165909	Hs.134682	Homo sapiens cDNA: FLJ23161 fis, clone L	2.9
	422022	AA302420	Hs.200442	ESTs	2.9
	426890	AA393167	Hs.41294	ESTs	2.9
	427374	AI150033	Hs.143686	ESTs	2.9
75	434208	T92641	Hs.127648	hypothetical protein PRO2176	2.9
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	2.9
	451229	AW967707	Hs.48473	ESTs	2.9
	415511	AJ732617	Hs.182362	ESTs	2.9
	408776	AA057365	Hs.63356	ESTs	2.9
80	421110	AJ250717	Hs.1355	cathepsin E	2.9
	453636	R67837	Hs.169872	ESTs	2.9
	436578	AI091435	Hs.134859	ESTs	2.9
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	2.9
	419231	AL046294	Hs.136245	ESTs, Weakly similar to dJ20221.4 [H.sa	2.8

5	408171	AA301228	Hs.43299	Homo sapiens cDNA FLJ12890 fis, clone NT	2.8
	445189	AJ936450	Hs.147482	ESTs	2.8
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	2.8
	427457	AW779105	Hs.164682	ESTs, Weakly similar to ORF2 consensus s	2.8
	435082	AA664273	Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone TH	2.8
10	446932	AA961459	Hs.125644	ESTs	2.8
	439140	W85737	Hs.290830	ESTs	2.8
	405041				2.8
	421306	AA806207	Hs.125889	ESTs	2.8
	427514	AA640773	Hs.209224	ESTs	2.8
15	427939	T92459	Hs.16886	ESTs	2.8
	429127	AA749382	Hs.107233	ESTs	2.8
	429590	AI219490	Hs.44445	ESTs, Weakly similar to Kelch motif cont	2.8
	433163	R40468	Hs.163582	ESTs	2.8
	439635	AA477288	Hs.94891	Homo sapiens cDNA: FLJ22729 fis, clone H	2.8
20	448015	AI458065	Hs.23196	ESTs	2.8
	456761	D69899	Hs.127842	CGI-142	2.8
	457112	AW772449	Hs.268081	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
	449540	AA001713		gb:zh86e08.s1 Soares_fetal_liver_spleen_	2.8
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	2.8
25	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.8
	433515	AA595800	Hs.190246	ESTs	2.8
	424450	AL137526	Hs.147472	dynein Intermediate chain 2	2.8
	438122	AI620270	Hs.129837	ESTs	2.8
	424086	AI351010	Hs.102267	lysyl oxidase	2.8
30	438885	AI886558	Hs.184987	ESTs	2.8
	412903	BE007967	Hs.155795	ESTs	2.8
	454111	AW081681	Hs.269064	ESTs	2.8
	439398	AA284267	Hs.221504	ESTs	2.8
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	2.8
35	434812	AA649860	Hs.189496	ESTs	2.8
	432583	AW023624	Hs.162282	ESTs	2.8
	428104	AA421350	Hs.191604	ESTs	2.8
	408217	AI433201	Hs.279860	hypothetical protein FLJ20030	2.8
	438016	AI949638	Hs.109150	SH3-domain binding protein 5 (BTK-associ	2.8
40	436396	AI683487	Hs.299112	Homo sapiens cDNA FLJ11441 fis, clone HE	2.7
	430887	N66801	Hs.260287	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
	446311	AW007294	Hs.149795	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	416185	AW975861	Hs.291995	ESTs	2.7
	408613	AW242086	Hs.253967	ESTs	2.7
45	442510	AF150179	Hs.249690	ESTs	2.7
	433293	AF007835	Hs.32417	ESTs	2.7
	413875	BE176776		gb:RC3-HT0586-110300-011-g09 HT0586 Homo	2.7
	404488				2.7
	408936	AL138043	Hs.293549	ESTs	2.7
50	431980	AA523696	Hs.222695	Homo sapiens cDNA: FLJ20986 fis, clone C	2.7
	436738	AW102613	Hs.152913	ESTs	2.7
	451797	AW663858	Hs.56120	ESTs	2.7
	452163	AI863140		gb:tz43h12.x1 NCI_CGAP_Bm52 Homo sapien	2.7
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.7
55	459366	AA129703		gb:zn92b05.r1 Stratagene lung carcinoma	2.7
	431448	AL137517	Hs.288381	hypothetical protein DKFZp564O1278	2.7
	430733	AW975920	Hs.283361	ESTs	2.7
	453652	AW009640	Hs.28368	ESTs	2.7
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	2.7
60	411905	BE265067		gb:601193893F1 NIH_MGC_7 Homo sapiens cD	2.7
	408729	AA195764	Hs.72639	ESTs	2.7
	450726	AW204600	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.7
	447720	AL038765	Hs.161304	ESTs	2.7
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	2.7
65	442074	C17511	Hs.128430	ESTs	2.7
	424115	AA335497	Hs.293965	ESTs	2.7
	417728	AW138437	Hs.24790	KIAA1573 protein	2.7
	433803	AI823593	Hs.27688	ESTs	2.7
	419247	S65791	Hs.89764	fragile X mental retardation 1	2.7
70	424310	AA338648	Hs.50334	ESTs	2.6
	439504	AW665281	Hs.224625	ESTs	2.6
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	2.6
	430417	AA461045	Hs.50701	ESTs	2.6
	438297	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN A	2.6
75	422505	AL120862	Hs.124165	ESTs	2.6
	457285	AI038858	Hs.228780	ESTs, Highly similar to AF199597 1 A-tyr	2.6
	428667	AI375550	Hs.74407	nucleolar protein p40; homolog of yeast	2.6
	431750	AA514986	Hs.283705	ESTs	2.6
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	2.6
80	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	2.6
	403903				2.6
	407910	AA650274	Hs.41295	fibronectin leucine rich transmembrane p	2.6
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	2.6
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	2.6
	436645	AW023424	Hs.156520	ESTs	2.6
	408380	AF123050	Hs.44532	diubiquitin	2.6
	402629				2.6

	406594			2.6
	415122	D60708	Hs.22245	ESTs
	416747	AW876523	Hs.15929	Homo sapiens cDNA FLJ12910 fis, clone NT
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C
5	444361	W76027	Hs.23920	Homo sapiens cDNA FLJ13124 fis, clone NT
	446509	BE395090	Hs.15535	Human gene from PAC 886K2, chromosome 1
	449260	AA741180	Hs.29879	ESTs
	452311	AW304029	Hs.252744	ESTs
10	413802	AW954490	Hs.32241	ESTs
	417318	AW953937	Hs.12891	ESTs
	440028	AW473875	Hs.125843	ESTs
	437960	AI669586	Hs.222194	ESTs
	433687	AA743991	gb:ny57g01.s1 NCL_CGAP_Pr18	Homo sapiens
15	430573	AA744550	Hs.136345	ESTs
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN
	453204	R10799	Hs.191990	ESTs
	436751	AA732217	Hs.294054	ESTs
	408165	AL137573	Hs.43143	Homo sapiens mRNA: cDNA DKFZp564A2463 (f
20	431120	AA492588	gb:ng99c08.s1 NCL_CGAP_Thy1	Homo sapiens
	446638	AL133063	Hs.15783	Homo sapiens mRNA: cDNA DKFZp434P1115 (f
	438458	AW975186	Hs.162875	ESTs, Weakly similar to ALU1_HUMAN ALU S
	446063	AI720140	Hs.151079	ESTs
	430499	AW969408	Hs.231991	ESTs
	450496	AW449251	Hs.257131	ESTs
25	441330	AI692984	Hs.129354	ESTs
	424433	H04507	Hs.9218	ESTs
	434677	AW444575	Hs.130834	ESTs
	445779	AI253104	Hs.189267	ESTs
30	444649	AW207523	Hs.197628	ESTs
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A
	432222	AI204995	gb:an03c03.x1 Stratagene schizo brain S1	
	404288			ESTs, Moderately similar to ALU4_HUMAN A
35	408572	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A
	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912
	410095	AW589638	Hs.258947	ESTs
	410947	AK000305	Hs.67055	hypothetical protein FLJ20298
	418343	AA216372	Hs.159501	ESTs
40	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto
	426637	AW979268	gb:EST391378 MAGE resequences, MAGP	Homo
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy
	432507	BE391093	gb:601286042F1 NIH_MGC_44	Homo sapiens c
	433859	N69243	Hs.192974	Homo sapiens cDNA FLJ12735 fis, clone NT
45	439651	H64500	Hs.123646	ESTs
	443830	AI142095	Hs.143273	ESTs
	446800	AI341635	Hs.156486	ESTs
	450262	AW409872	Hs.271166	ESTs, Moderately similar to ALU7_HUMAN A
	451343	AW975057	Hs.293353	ESTs
50	451539	AA059467	Hs.218933	ESTs
	452412	AA029608	Hs.61373	ESTs
	454288	BE222648	Hs.279458	ESTs, Highly similar to c380A1.1b (H.sap
	445745	AB007924	Hs.13245	KIAA0455 gene product
	424943	AU077260	Hs.153924	death-associated protein kinase 1
55	440106	AA864968	Hs.127699	KIAA1603 protein
	458429	AV646559	Hs.12346	Homo sapiens cDNA: FLJ21399 fis, clone C
	415261	T40928	Hs.8346	ESTs
	420026	AI831190	Hs.166676	ESTs
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam
60	458722	AA741545	Hs.282832	ESTs
	419449	H18417	Hs.57483	Homo sapiens cDNA FLJ14294 fis, clone PL
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S
	433644	AW342028	Hs.256112	ESTs
	419172	AW338625	Hs.22120	ESTs
65	437982	N93466	Hs.121764	ESTs, Weakly similar to testicular teld
	443348	AW873595	Hs.57572	ESTs
	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE
	448030	N30714	Hs.20161	HDCME31P protein
70	417203	AA406341	Hs.269908	Homo sapiens cDNA FLJ11991 fis, clone HE
	449275	AW450848	Hs.205457	KIAA1620 protein
	436198	AK001125	Hs.300922	Homo sapiens cDNA FLJ10263 fis, clone HE
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL
	442191	W95186	Hs.8136	endothelial PAS domain protein 1
75	428571	NM_008531	Hs.2291	Probe hTg737 (polycystic kidney disease,
	453142	AA033648	Hs.7473	ESTs
	425657	T89839	Hs.119471	ESTs
	452822	X85689	Hs.288617	Homo sapiens cDNA: FLJ22621 fis, clone H
	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf
80	458332	AI000341	Hs.220491	ESTs
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor
	459644			
	429125	AA446854	Hs.271004	ESTs
	448337	AW206453	Hs.3782	ESTs

	427778	AA412323	Hs.105323	ESTs	2.4
	425371	D49441	Hs.155981	mesothelin	2.4
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.4
5	447610	AW296286	Hs.255534	ESTs	2.4
	409519	AA075368		gbzm86h10.r1 Stratagene ovarian cancer	2.4
	441006	AW605267	Hs.7627	CGI-60 protein	2.4
	440817	AJ341423	Hs.270165	ESTs	2.4
	420020	BE295866	Hs.94382	adenosine kinase	2.4
10	435395	AA729235	Hs.117907	ESTs	2.4
	424144	AA454033	Hs.41644	Homo sapiens cDNA: FLJ23003 fis, clone L	2.4
	405494				2.4
	458145	AJ239457	Hs.130794	ESTs	2.4
	408547	AA574291	Hs.57837	ESTs	2.4
15	408941	AA52469	Hs.165221	ESTs	2.4
	409457	AW818081		gb:CM4-ST0276-101299-059-b09 ST0276 Homo	2.4
	417137	U46265	Hs.81281	hypothetical protein	2.4
	418950	T78517	Hs.13941	ESTs	2.4
	420756	AA411800	Hs.189900	ESTs	2.4
20	428316	AJ860775	Hs.98506	ESTs	2.4
	432896	NM_014097	Hs.279778	PRO1693 protein	2.4
	436148	BE005252		gb:CM1-BND116-030400-171-g02 BN0116 Homo	2.4
	436284	AA708016	Hs.190389	ESTs	2.4
	437327	AL353942		gb:Homo sapiens mRNA; cDNA DKFZp761L2312	2.4
25	442611	BE077155	Hs.177537	ESTs	2.4
	456062	AJ866286	Hs.71962	ESTs	2.4
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.4
	401335				2.4
	428771	AB028992	Hs.193143	KIAA1069 protein	2.4
30	419140	AJ982647	Hs.215725	ESTs	2.4
	454693	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	2.4
	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.4
	407339	AA777542	Hs.132670	ESTs	2.4
	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	2.4
35	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	2.4
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	2.4
	452561	AJ692181	Hs.49169	KIAA1634 protein	2.4
	427878	C05766	Hs.181022	CGI-07 protein	2.4
	419752	AA249573	Hs.152618	ESTs	2.4
40	430073	U88136	Hs.232070	telomerase-associated protein 1	2.4
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	2.4
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.3
	407905	AW103655	Hs.252905	ESTs	2.3
	427660	AJ741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	2.3
45	422355	AW403724	Hs.140	immunoglobulin heavy constant gamma 3 (G	2.3
	453049	BE537217	Hs.30343	ESTs	2.3
	438568	R98865	Hs.11135	major histocompatibility complex, class	2.3
	453445	AL036532	Hs.91453	ESTs	2.3
	424711	NM_005795	Hs.152175	calcitonin receptor-like	2.3
50	446346	AJ290205		gb:q79g06.x1 Soares_NhHMPu_S1 Homo sapi	2.3
	441974	AJ683782	Hs.128245	ESTs	2.3
	444805	AB007899	Hs.12017	KIAA0439 protein; homolog of yeast ubiq	2.3
	424027	AW337575	Hs.201591	ESTs	2.3
	419606	AW294795	Hs.198529	ESTs, Weakly similar to similar to acyl-	2.3
55	428613	AB037749	Hs.186928	KIAA1328 protein	2.3
	434340	AJ193043	Hs.128685	ESTs	2.3
	450297	AW901347	Hs.38592	Homo sapiens cDNA: FLJ23342 fis, clone H	2.3
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	2.3
	433650	AA603472	Hs.28456	ESTs	2.3
60	419086	NM_000216	Hs.89591	Kellmann syndrome 1 sequence	2.3
	428758	AA433988	Hs.98502	Homo sapiens cDNA FLJ14303 fis, clone PL	2.3
	430153	AW968128		gb:EST380338 MAGE resequences, MAGJ Homo	2.3
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.3
	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	2.3
65	400610				2.3
	402222				2.3
	407162	N63855	Hs.142634	zinc finger protein	2.3
	415250	F02614	Hs.27319	ESTs	2.3
	421751	AW813731	Hs.159153	ESTs	2.3
70	428552	AW274560	Hs.129520	ESTs	2.3
	432658	AW973769	Hs.162319	ESTs	2.3
	434742	AA648302	Hs.291695	ESTs	2.3
	436586	AJ308862	Hs.167028	ESTs	2.3
	441675	AJ914329	Hs.5461	ESTs	2.3
75	442039	AW276240	Hs.128352	ESTs, Weakly similar to p80 [Rnorvegicu	2.3
	443160	AJ467915	Hs.36053	ESTs	2.3
	448764	AJ568607	Hs.182112	ESTs	2.3
	449579	AW207260	Hs.134014	prostate cancer associated protein 6	2.3
	439810	AL109710	Hs.85568	EST	2.3
80	413714	AJ560944	Hs.71428	ESTs	2.3
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	2.3
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	2.3
	438670	AJ275803	Hs.123428	ESTs	2.3
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	2.3

	459702				2.3
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	2.3
	438474	AW655818	Hs.6232	KIAA0764 gene product	2.3
5	453037	AA045175	Hs.177552	ESTs	2.3
	428467	AK002121	Hs.184465	hypothetical protein FLJ111259	2.3
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	2.3
	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapie	2.3
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	2.3
10	417015	M83772	Hs.80876	flavin containing monooxygenase 3	2.3
	405506				2.3
	448330	AL036449	Hs.207163	ESTs	2.3
	409719	AJ769160	Hs.108681	ESTs	2.3
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	2.3
15	425188	AK002052	Hs.155071	hypothetical protein FLJ111190	2.3
	427961	AW293165	Hs.143134	ESTs	2.3
	447357	AJ375922	Hs.159367	ESTs	2.3
	412642	BE244598	Hs.809	hepatocyte growth factor (hepatopoietin A;	2.3
	453716	AA037675	Hs.152675	ESTs	2.3
20	437370	AL359587	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.3
	407949	W21874	Hs.247057	ESTs	2.2
	427972	AA864870	Hs.181304	pulative gene product	2.2
	453313	BE005771	Hs.153746	Homo sapiens cDNA: FLJ22490 fis, clone H	2.2
	426476	NM_003296	Hs.2042	testis specific protein 1 (probe H4-1 p3	2.2
25	424238	AA337401	Hs.137635	ESTs	2.2
	452930	AW195285	Hs.194097	ESTs	2.2
	424527	AW138558	Hs.267158	ESTs	2.2
	453095	AW295660	Hs.252756	ESTs	2.2
	449161	N53431	Hs.47647	ESTs, Weakly similar to KIAA0423 [H.sapi	2.2
30	429586	T73510	Hs.209153	angiotensin-like 3	2.2
	423782	AK72209	Hs.288359	ESTs	2.2
	458124	AW005548	Hs.124590	ESTs	2.2
	450109	AI539295	Hs.17957	ESTs	2.2
	421461	AW291023	Hs.97255	ESTs	2.2
35	412222	AA528283	Hs.292737	ESTs	2.2
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.2
	441736	AW292779	Hs.169799	ESTs	2.2
	401049				2.2
	440727	AI073991	Hs.134268	ESTs	2.2
40	419751	AW195581	Hs.93121	KIAA0761 protein	2.2
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.2
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.2
	410292	AA843087	Hs.124194	ESTs	2.2
45	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23069 fis, clone L	2.2
	449695	AA164569	Hs.34550	ESTs	2.2
	429399	AA452244	Hs.16727	ESTs	2.2
	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	2.2
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.2
50	436772	AW975688	Hs.250867	zona pellucida glycoprotein 3A (sperm re	2.2
	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	2.2
	445268	AI218358	Hs.175048	ESTs	2.2
	402481				2.2
55	412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.2
	416521	H60929	Hs.44197	hypothetical protein DKFZp564D0462	2.2
	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen	2.2
	419780	AA713522	Hs.87752	ESTs	2.2
	421211	AA284966	Hs.266308	ESTs, Weakly similar to AF216312 1 type	2.2
	427541	AI798983	Hs.97961	ESTs	2.2
60	432013	AI796879	Hs.162102	ESTs	2.2
	436461	AW511956	Hs.293261	ESTs	2.2
	438002	AI560246	Hs.201648	ESTs, Weakly similar to ZN42_HUMAN ZINC	2.2
	440312	AW614597	Hs.72475	ESTs	2.2
	440479	AA886461	Hs.208161	ESTs	2.2
65	441178	W90789	Hs.153976	ESTs	2.2
	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fis, clone C	2.2
	443314	AW771701	Hs.54646	ESTs	2.2
	422165	AL041199	Hs.1481	histidine decarboxylase	2.2
70	450696	AI654223	Hs.16026	Homo sapiens cDNA: FLJ23191 fis, clone L	2.2
	432974	BE348793		gb:ht70g02.x1 NCI_CGAP_Lu24 Homo sapiens	2.2
	404200				2.2
	435990	AI015862	Hs.131793	ESTs	2.2
	421309	AI222086	Hs.270449	ESTs, Moderately similar to ALU1_HUMAN A	2.2
75	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.2
	416642	T96118	Hs.226313	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	406672	M26041	Hs.198253	major histocompatibility complex, class	2.2
	417819	AI253112	Hs.133540	ESTs	2.2
	417355	D13168	Hs.82002	endothelin receptor type B	2.2
80	459574	AI741122	Hs.101810	Homo sapiens cDNA FLJ14232 fis, clone NT	2.2
	404274				2.2
	415086	AI597963	Hs.118726	ESTs	2.2
	418210	R54575	Hs.13337	ESTs, Weakly similar to unnamed protein	2.2
	419220	AA811938	Hs.291759	ESTs	2.2
	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	2.2

	451050	AW937420	Hs.69662	ESTs	2.2
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	2.2
	428414	AL049980	Hs.184216	DKFZP564C152 protein	2.2
5	412925	AI089319	Hs.179243	ESTs	2.2
	438192	AI859065	Hs.16808	ESTs, Weakly similar to paraplegin-like	2.2
	410976	R36207	Hs.25092	ESTs	2.2
	406673	M34996	Hs.198253	major histocompatibility complex, class	2.2
	449677	AA002071		gb:zh85d01.s1 Soares_fetal_liver_spleen_	2.2
10	449321	AA001150	Hs.132937	ESTs	2.2
	418557	BE140602	Hs.246645	ESTs	2.2
	416320	H47867	Hs.34024	ESTs	2.2
	426384	AI472078		gb:ij85h03.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.2
	414140	AA281279	Hs.23317	ESTs	2.2
15	419520	AB009303	Hs.297790	Human clone 23734 mRNA sequence	2.2
	446999	AA151520	Hs.279525	hypothetical protein PRO2605	2.2
	457447	X78261	Hs.272177	H.sapiens mRNA for TRE17 5' extremity an	2.2
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.1
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	2.1
20	410048	W76467	Hs.274550	proline oxidase homolog	2.1
	400880				2.1
	418092	R45154	Hs.106604	ESTs	2.1
	428780	AI478578	Hs.50536	ESTs	2.1
	431067	AW574823	Hs.200413	ESTs	2.1
25	432803	AA565398		gb:nk41f01.s1 NCI_CGAP_GC2 Homo sapiens	2.1
	412104	AW205197	Hs.240951	ESTs	2.1
	422819	AL122084	Hs.121073	hypothetical protein FLJ10466	2.1
	454359	N71277		gb:za36e03.s1 Soares fetal liver spleen	2.1
	424806	AA382523	Hs.105689	ESTs	2.1
30	434445	AI349306	Hs.11782	ESTs	2.1
	442994	AI026718	Hs.16954	ESTs	2.1
	410371	AA084482	Hs.115850	ESTs	2.1
	450232	BE300815	Hs.201326	ESTs	2.1
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	2.1
35	430899	BE018217	Hs.183528	ESTs, Weakly similar to Bem46-like prote	2.1
	431814	BE256242	Hs.270847	della-tubulin	2.1
	417543	AA203620	Hs.110153	ESTs, Weakly similar to BCGF_HUMAN B-CEL	2.1
	444542	AI61293	Hs.146862	ESTs, Weakly similar to KIAA0525 protein	2.1
	404593				2.1
40	434803	AW974640		gb:EST386744 MAGE resequences, MAGM Homo	2.1
	451623	H77818	Hs.268991	ESTs	2.1
	452466	N84635	Hs.29664	Human DNA sequence from clone 682J15 on	2.1
	402046				2.1
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.1
45	436192	W93847	Hs.24139	Homo sapiens cDNA: FLJ23137 tis, clone L	2.1
	401987				2.1
	423119	AA322201	Hs.131976	EST	2.1
	427112	Z32887	Hs.290951	ESTs	2.1
	414464	AI870175	Hs.13957	ESTs	2.1
50	447829	AI433029	Hs.164104	ESTs	2.1
	449679	AI823951	Hs.296668	Homo sapiens cDNA FLJ11846 tis, clone HE	2.1
	405472				2.1
	413621	AI808648	Hs.184156	ESTs	2.1
	432212	AW137742	Hs.293451	ESTs	2.1
	404289				2.1
55	415362	F06735		gb:HSC1JB091 normalized infant brain cDN	2.1
	427739	AW196755	Hs.98105	ESTs	2.1
	427772	AA412289	Hs.98123	ESTs	2.1
	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.1
60	434335	AA630107	Hs.213220	ESTs	2.1
	436052	AI021983	Hs.271432	ESTs	2.1
	442773	AB037722	Hs.8707	Homo sapiens mRNA: cDNA DKFZp434N1131 (f	2.1
	446799	AW978373	Hs.49221	ESTs, Weakly similar to zinc finger prot	2.1
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	2.1
65	455673	BE065939		gb:RC3-BT0319-100100-012-c11 BT0319 Homo	2.1
	458624	AI362790	Hs.181801	ESTs	2.1
	405095				2.1
	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	2.1
	433589	AA886530	Hs.188912	ESTs	2.1
70	438398	AA806526	Hs.130277	ESTs	2.1
	447233	AW246333	Hs.17901	Homo sapiens cDNA: FLJ21974 tis, clone H	2.1
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.1
	431087	H12723	Hs.290791	ESTs	2.1
	409064	AA062954	Hs.141883	ESTs	2.1
75	427558	D49493	Hs.2171	growth differentiation factor 10	2.1
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	2.1
	438118	AW753311	Hs.259415	ESTs	2.1
	427621	BE621182	Hs.179882	Homo sapiens cDNA FLJ12437 tis, clone NT	2.1
	452114	N22687	Hs.8236	ESTs	2.1
80	448782	AL050295	Hs.301550	KIAA0758 protein	2.1
	403937				2.1
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	2.1
	452416	AA026115	Hs.114777	ESTs	2.1
	451609	AL046019	Hs.209276	ESTs	2.1

	435934	R19382	Hs.117859	ESTs	2.1
	445158	AI992108	Hs.127206	ESTs	2.1
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	2.1
5	439335	AA742697	Hs.62492	ESTs, Weakly similar to S59856 collagen	2.1
	443949	AW827419	Hs.235070	ESTs	2.1
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.1
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	2.1
	438676	AA813745	Hs.123446	ESTs	2.1
	405848				2.1
10	416940	N75620	Hs.43157	ESTs	2.1
	442381	AI185136	Hs.48650	ESTs	2.1
	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586l1823 (f	2.1
	436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	2.1
15	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	2.1
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	2.1
	439425	AF086244	Hs.114659	ESTs	2.1
	421168	AF182277	Hs.1360	cytochrome P450, subfamily IIB (phenobar	2.1
	449611	AI970394	Hs.197075	ESTs	2.1
	404548				2.1
20	416734	H81213	Hs.14825	ESTs	2.1
	435865	AA883552	Hs.16810	ESTs	2.1
	439072	AF085930	Hs.269123	ESTs	2.1
	447482	AB033059	Hs.18705	KIAA1233 protein	2.1
25	457292	AI921270	Hs.214178	Homo sapiens cDNA FLJ14251 fis, clone OV	2.1
	444974	AI203500	Hs.151612	ESTs	2.1
	456034	AW450979		gb:U1-H-B13-ala-a-12-0-U1.s1 NC1_CGAP_Su	2.1
	430634	AI860651	Hs.26685	ESTs	2.1
	426782	R14614	Hs.191254	ESTs	2.0
30	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	2.0
	445326	AI220072	Hs.165893	ESTs	2.0
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.0
	409994	D86864	Hs.57735	acetyl LDL receptor; SREC	2.0
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	2.0
35	455226	AW902103		gb:QV0-NN1022-120500-220-c07 NN1022 Homo	2.0
	417321	N68722	Hs.191368	ESTs	2.0
	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.0
	404323				2.0
	448133	AA723157	Hs.73769	folate receptor 1 (adult)	2.0
40	421047	AW514772	Hs.104473	ESTs	2.0
	425497	AA524596	Hs.188844	ESTs	2.0
	444623	AI183829	Hs.202111	ESTs	2.0
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.0
	433563	AI732637	Hs.277901	ESTs	2.0
	406495				2.0
45	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	2.0
	455807	BE141140		gb:MR0-HT0075-021299-006-d07 HT0075 Homo	2.0
	425465	L18964	Hs.1904	protein kinase C, iota	2.0
	449424	AW448937	Hs.197030	ESTs	2.0
50	427940	AA417812	Hs.38775	ESTs	2.0
	411502	AW946605	Hs.250154	Homo sapiens cDNA FLJ12973 fis, clone NT	2.0
	411365	M76477	Hs.278242	tubulin, alpha, ubiquitous	2.0
	412369	H80456	Hs.285243	Homo sapiens cDNA: FLJ22029 fis, clone H	2.0
	452959	AI933416	Hs.189674	ESTs	2.0
55	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	2.0
	428775	AA434579	Hs.143691	ESTs	2.0
	420000	AB036063	Hs.180726	Homo sapiens cDNA FLJ13543 fis, clone PL	2.0
	408321	AW405882	Hs.44205	cortistatin	2.0
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	2.0
60	411050	AW814902		gb:MR1-ST0206-120400-022-08 ST0206 Homo	2.0
	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	2.0
	428978	AA442784	Hs.125445	ESTs	2.0
	458562	N34128	Hs.145268	ESTs	2.0
	425527	AL162032	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (f	2.0
	403760				2.0
65	424368	AB037766	Hs.146085	KIAA1345 protein	2.0
	421229	AI056590	Hs.7086	Homo sapiens cDNA: FLJ23000 fis, clone L	2.0
	436304	AA339622	Hs.108887	ESTs	2.0
	453498	BE181412	Hs.23245	Homo sapiens cDNA FLJ11767 fis, clone HE	2.0
70	439018	AW300887	Hs.26638	ESTs, Weakly similar to unnamed protein	2.0
	453280	AL157476	Hs.32913	Homo sapiens mRNA; cDNA DKFZp761C082 (fr	2.0
	420193	AI460080	Hs.202869	ESTs	2.0
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.0
	401575				2.0
75	419092	J05581	Hs.89603	mucin 1, transmembrane	2.0
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	2.0
	410763	AF279145	Hs.8966	tumor endothelial marker 8	2.0
	414783	AW069569	Hs.75839	zinc finger protein 6 (ZMPX1)	2.0
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.0
80	405963				2.0
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.0
	420831	AA280824	Hs.190035	ESTs	2.0
	424152	AL133591	Hs.301405	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.0
	424641	AB001106	Hs.151413	glia maturation factor, beta	2.0

5	427616	AI698584	Hs.98028	ESTs	2.0
	435115	AI821726	Hs.116603	ESTs	2.0
	437636	AA764781	Hs.291844	ESTs	2.0
	438295	AI394151	Hs.37932	ESTs	2.0
	439430	AF124250	Hs.6564	breast cancer anti-estrogen resistance 3	2.0
10	445388	AI925280	Hs.236842	EST	2.0
	447101	N72185	Hs.44189	ESTs	2.0
	448796	AA147829	Hs.33193	ESTs, Highly similar to AC007228 3 BC372	2.0
	449623	C00719	Hs.120440	ESTs	2.0
	450159	AI702416	Hs.200771	ESTs, Weakly similar to CAN2_HUMAN CALPA	2.0
15	456613	R19992	Hs.106620	Homo sapiens clone 23950 mRNA sequence	2.0
	457233	AI355009	Hs.221698	ESTs	2.0
	457384	AA501760	Hs.18075	chromosome 9 open reading frame 3	2.0
	457471	AW971364	gb:EST383453	MAGE resequences, MAGL Homo	2.0
					2.0

TABLE 27B

20	Pkey:	Unique Eos probeset identifier number			
	CAT number:	Gene cluster number			
	Accession:	Genbank accession numbers			
25	Pkey	CAT number	Accession		
	409457	1132521_1	AW818081 AW392887 AW514700 AW392881		
	409519	113722_1	AA075368 AA075369		
30	410008	116812_1	AA079552 BE142525 BE142527		
	410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355		
	411050	1230330_1	AW814902 BE156656 BE156667 BE156590 BE156441 BE156447		
35	411880	1263110_1	AW872477 BE088101 T05990		
	411905	1265181_1	BE265067 BE264978 AW875420		
	412303	1288130_1	AW936336 AW936339		
40	413135	1350379_1	BE066941 BE066911 BE066979 BE066929 BE066925		
	413499	1373910_1	BE144884 H97942		
	413875	1396766_1	BE176776 H85072		
45	415094	1522103_1	D59513 D59515 D80174 D59514		
	415362	1534980_1	F06735 R55896 R12110 H08697		
	416624	1604694_1	H69044 T47567 H75691 T50292		
50	418378	174656_1	AW962081 AA218925 AA354237		
	419546	185766_1	AA244199 AA244272 H57440		
	419807	188252_1	R77402 AA262462 AA250988 RD6794		
55	420537	195241_1	AW976153 AA278945 AA747691		
	422429	216469_1	AA310527 AW962295 Z44865 H06641		
	423377	22769_1	AL049377 AL079930 AL047223 AW865968 AA385235		
60	426384	256211_1	AJ472078 AA377209 AA865807		
	428637	293660_1	AW979268 AA878419 AA431342 AA431628		
	430153	313709_1	AW968128 AA468102 AA468165		
65	430844	324570_1	T94960 AA487679 T95013		
	431120	328264_1	AA492588 AA492498 AA492571		
	431169	328799_1	AW971240 AA493843 AA493723		
70	431322	331543_1	AW970622 AA503009 AA502998 AA502805 T92188		
	432009	34025_1	AL137424 BE007148 T52277		
	432222	343347_1	AI204995 AW827539 AW959908 AW440776 AA528756		
75	432507	348711_1	BE391093 AA551334 BE389643		
	432779	354024_1	AW979241 AA565006 AA847102		
	432803	354267_1	AA565398 AW894072 H97930		
80	432869	355475_1	AW974094 AA569074 AA602574		
	432974	356950_1	BE348793 AA573118 N79366		
	433492	367934_1	AW605849 AW262898 N41060 AA594852		
85	433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600958 AA778832		
	433687	373061_1	AA743991 AA604852 AW272737		
	434803	393471_1	AW974540 AA649516 N75526		
90	436148	41500_1	BE005252 AK000786		
	437327	43610_1	AL353942 AW994305		
	438909	46684_1	AF085839 R69137 AW188788 R69254		
95	440320	491930_1	AA879294 N67538 AJ474541		
	444314	600867_1	AI140497 AW749625 AW749626 AW749644		
	444610	612257_1	AI174783 R83589 R12271		
100	446346	673545_1	AI290205 AW235762 AI651268		
	447197	711623_1	R36075 AI366546 R36167		
	448404	761515_1	BE089973 AI498612 AW805032		
105	449299	80436_1	AA299919 AW957012 AA001107 T83631 BE156389		
	449540	80945_2	AA001713 H63836		
	449677	81270_1	AA002071 AA002232 T99209		
110	450522	837264_1	AI698839 AI909260 AI909259		
	451024	85565_1	AA442176 AA259181		
	451381	867770_1	BE241831 AW249135 BE548847 AW250245		
115	452163	902067_1	AJ863140 W80703 R43474		
	452293	909195_1	AJ871833		
	452453	918300_1	AI902519 AI902518 AI902516		
120	452542	921410_1	AW812256 AW812257 AI906423 AI906422		
	452771	930983_1	T05477 T07855 AI917711		
	454359	1130674_1	N71277 AW390764		

5	454693	1229132_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
	455024	1249196_1	AW851308 AW850888 AW851419 AW851412 AW851299
	455226	1262534_1	AW902103 AW869012 AW869139
	455235	1265634_1	AW875951 AW875950 AW875936 AW875948 AW875939 AW875957
	455673	1349656_1	BE065939 BE066079 BE065956
	455807	1370914_1	BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108
		456034	142696_1 AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
			BE011368 BE011362 BE011215 BE011365 BE011363
10	457471	340916_1	AW971364 AA525021 AA570759
	457620	371514_1	AA602711 BE078290
	458154	491768_1	AW816379 AAB88282 AA879046 AA879195
	459267	966605_1	AJ003631 AJ003650 AJ003651

TABLE 27C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source: 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

25	Pkey	Ref	Strand	NL_position
	400610	9887671	Minus	117606-117928,124040-124147
	400880	9931121	Plus	29235-29336,36363-36580
	401049	7232177	Plus	149157-150692
30	401335	9884881	Plus	15736-16352
	401575	7229804	Minus	76253-76364
	401793	7263888	Minus	102945-103083
	401987	4406829	Minus	72893-73021,76938-77049
	402046	8072415	Plus	166394-166556,168167-168395
	402222	9958106	Plus	3261-3834,3939-4269
35	402481	9797406	Plus	87891-88991
	402629	9931216	Plus	33641-33775,34182-34372,36003-36084,40343-40612
	403760	7712202	Minus	45910-46260,47563-47824
	403903	7710671	Minus	101165-102597
40	403937	7711761	Minus	12609-12773
	404043	9558573	Plus	29042-29135,46597-46699
	404200	6010176	Minus	7066-7210
	404274	9885189	Plus	104127-104318
	404288	2769644	Plus	3512-3691
45	404289	2769644	Plus	15049-15286,30267-30457
	404323	9719753	Minus	31913-32219
	404488	8113286	Minus	64835-64994
	404548	8570305	Minus	83896-84162
	404593	9944086	Minus	74922-75788
50	404599	8705107	Plus	110443-110733
	404916	7341826	Plus	91057-91188
	405041	7547195	Plus	121230-121714
	405095	8072599	Plus	138877-139066
	405472	8439781	Plus	106297-106447,108462-108596
55	405494	8050952	Minus	70284-70518
	405848	7651809	Minus	28135-28244
	405963	8247786	Plus	4056-4699
	406182	5923650	Minus	28256-28935
	406485	7711305	Plus	125036-125422
60	406506	7711374	Minus	6843-8077
	406554	7711566	Plus	106956-107121
	406594	8248611	Minus	35543-35845

TABLE 28A: ABOUT 796 GENES DOWN-REGULATED IN LUNG FIBROSIS COMPARED TO NORMAL BODY

Table 28A lists of about 796 genes that are downregulated in lung fibrosis (collection of IPF, HP, and NSIP) samples as compared with normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" fibrosis sample expression level to "average" normal adult tissues sample expression was less than or equal to 0.1. The "average" normal lung tissue level was set to the 75th percentile amongst normal lung tissues. The "average" fibrosis expression level was set to the 95th percentile amongst fibrosis samples. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of normal lung to fibrosis

80	Pkey	ExAccn	Unigene ID	Unigene Title	R1
	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	18.18
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	9.39
	404518	AJ815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	8.30
	404795				5.56

	403211				5.46
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	5.43
	400489				5.19
5	425571	AJ007292	Hs.158306	ephrin-A2	5.19
	406357				5.08
	407979	AA046306	Hs.62927	ESTs	5.08
	452378	AA025855	Hs.19597	ESTs	4.78
	408053	AW139474	Hs.246862	ESTs	4.62
10	421770	AA374192	Hs.108124	ribosomal protein L41	4.52
	425126	N32759	Hs.172944	chorionic gonadotropin, beta polypeptide	4.49
	402386				4.39
	402448				4.37
	448245	AI923551	Hs.170843	ESTs	4.31
15	413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	4.29
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	4.24
	447768	X86400	Hs.19520	FXD domain-containing ion transport reg	4.21
	405163				4.19
	437120	AI356125	Hs.157767	ESTs, Weakly similar to human HOXA2 [Hs	4.19
20	409020	AA062549	Hs.21162	ESTs	4.09
	431073	BE254470	Hs.249186	cone-rod homeobox	4.07
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	4.05
	403716				3.99
	424969	AW950928	Hs.153998	creatine kinase, mitochondrial 1 (ubiqui	3.94
25	404348				3.90
	407070	Y10209		gb:H.sapiens mRNA for CD30L protein	3.82
	412919	AI368680	Hs.816	SRY (sex determining region Y)-box 2	3.81
	402409				3.80
	456150	Z42308		gb:HSC0FB121 normalized infant brain cDN	3.79
30	427030	AA397600	Hs.97531	ESTs	3.76
	426328	AW631296		gb:hh83c09.y1 NCI_CGAP_GU1 Homo sapiens	3.74
	429307	AU076592	Hs.198951	jun B proto-oncogene	3.71
	400172				3.70
	431227	X63755	Hs.2743	keratin, cuticle, ultrahigh sulphur 1	3.68
35	433883	AI925688	Hs.222312	ESTs, Weakly similar to B24264 proline-r	3.68
	446850	R71245	Hs.174303	ESTs	3.67
	405147				3.64
	406821	AA977896	Hs.128873	ESTs, Highly similar to ALFA_HUMAN FRUCT	3.57
	402762				3.55
40	401496				3.50
	421201	AW241940	Hs.102500	hypothetical protein FLJ20481	3.50
	402911				3.49
	425330	D25216	Hs.155650	KIAA0014 gene product	3.49
	438004	AA774984	Hs.220649	ESTs, Weakly similar to FCE2 MOUSE LOW A	3.46
45	448185	AI633040	Hs.172730	ESTs	3.46
	433367	AA584930	Hs.269451	ESTs, Weakly similar to XAP-5-like prote	3.43
	416596	H67669	Hs.38564	ESTs	3.41
	400645				3.39
	418464	R87580		gb:ym89h07.r1 Soares adult brain N2b4HB5	3.37
50	426507	AA380285		gb:EST93491 Supt cells Homo sapiens cDNA	3.35
	403479				3.34
	406082	S47833	Hs.82927	adenosine monophosphate deaminase 2 (iso	3.34
	401919				3.33
	449031	AI867502	Hs.271462	ESTs	3.33
55	400116				3.31
	401590				3.29
	401007				3.28
	404610	H58589	Hs.35156	Homo sapiens cDNA FLJ11027 fis, clone PL	3.25
60	408641	AW245207	Hs.5555	Homo sapiens cDNA FLJ13170 fis, clone NT	3.25
	407196	D11747	Hs.177415	Finkel-Biskis-Reilly murine sarcoma viru	3.23
	410258	X52638	Hs.739	6-phosphofructo-2-kinase/fructose-2,6-bi	3.23
	433232	AI658621	Hs.127769	ESTs	3.23
	457937	AW976930	Hs.128760	ESTs	3.23
	406101				3.18
65	407080	Z38133	Hs.113973	myosin, heavy polypeptide 8, skeletal mu	3.18
	419947	AW298744	Hs.118894	ESTs	3.16
	421905	AI660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H	3.16
	454019	D31846	Hs.37025	aquaporin 2 (collecting duct)	3.16
	428674	AA431734	Hs.104915	ESTs	3.14
70	402056				3.06
	425182	AF041259	Hs.155040	zinc finger protein 217	3.06
	425393	NM_000218	Hs.156115	potassium voltage-gated channel, KQT-lik	3.06
	433657	AI244368	Hs.8124	PH domain containing protein in retina 1	3.05
	402158				3.03
75	404938				3.02
	403376				3.01
	418828	AF020774	Hs.88844	Homo sapiens hair and skin epidermal-ty	3.00
	402423				2.99
	416253	BE250659	Hs.15463	ESTs	2.99
80	435265	AA779958	Hs.185932	ESTs	2.99
	425655	BE614551	Hs.158675	ribosomal protein L14	2.98
	428704	AA432007	Hs.249484	ESTs	2.98
	425439	D38024	Hs.157425	double homeobox, 2	2.97
	445613	BE550889	Hs.158491	ESTs	2.97

	402714			2.96	
	403526			2.96	
	403605			2.95	
5	441852	AB028968	Hs.7989	KIAA1045 protein	2.95
	417629	T76945	Hs.64211	ESTs, Weakly similar to similar to acyl-	2.94
	447744	AA313230	Hs.19413	S100 calcium-binding protein A12 (calgr	2.91
	419821	AW967486	Hs.189119	ESTs	2.90
	446993	AI570964	Hs.164257	ESTs	2.89
10	414580	BE386918		gb:601275386F1 NIH_MGC_20 Homo sapiens c	2.88
	423379	AI985349	Hs.157492	Homo sapiens cDNA FLJ14079 fis, clone HE	2.88
	440206	AI762232	Hs.46794	ESTs	2.88
	402212	AW502761	Hs.30909	KIAA0430 gene product	2.87
	406059				2.85
15	423548	AF007194	Hs.129782	mucin 3A, intestinal	2.86
	402051				2.85
	415196	AK000150	Hs.78185	MAX-like bHLHZIP protein	2.85
	455446	AW947749		gb:RCO-MT0005-130300-031-b01 MT0005 Homo	2.85
	442428	BE464988	Hs.298302	ESTs	2.84
20	403247				2.83
	404825				2.83
	459184	L35001	Hs.95669	ESTs	2.83
	402968				2.82
	417575	R00382	Hs.191199	ESTs	2.82
25	404668				2.81
	420619	AF130255	Hs.99430	testis zinc finger protein	2.81
	447241	BE382838	Hs.19322	ESTs	2.80
	448793	AI864581	Hs.215477	ESTs	2.79
	453014	AI937242	Hs.176590	ESTs	2.79
30	446775	AI792836	Hs.232273	ESTs	2.78
	455075	AW854850		gb:QV2-CT0261-201099-011-h03 CT0261 Homo	2.78
	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	2.75
	457546	AA568484	Hs.153632	ESTs	2.75
	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	2.74
35	433677	AI791912	Hs.190885	ESTs, Moderately similar to ALU1_HUMAN A	2.74
	405703				2.73
	408840	AW277132	Hs.254880	ESTs	2.73
	413958	BE277913	Hs.172364	Homo sapiens mRNA for FLJ00086 protein,	2.73
	454421	BE409759	Hs.59563	Homo sapiens mRNA for FLJ00007 protein,	2.73
40	406702	ZZ0656	Hs.278432	myosin, heavy polypeptide 6, cardiac mus	2.72
	408664	R56362		gb:yg93c07.r1 Soares infant brain 1N1B H	2.72
	402457				2.71
	403612				2.71
	407049	X72632		(NONE)	2.71
45	415423	AA164743	Hs.187617	Homo sapiens cDNA FLJ13941 fis, clone Y7	2.70
	402862				2.69
	403540				2.69
	431465	AW293178	Hs.180086	ESTs	2.69
	406563				2.68
50	417003	AL038170	Hs.80756	betaine-homocysteine methyltransferase	2.68
	426220	AI383475	Hs.171697	ESTs, Weakly similar to immunoglobulin s	2.68
	446707	AI591214	Hs.156336	ESTs	2.68
	447557	AW028809	Hs.229570	ESTs	2.68
	413529	U11874	Hs.846	Interleukin 8 receptor, beta	2.67
	403997				2.66
55	408704	AA056635	Hs.5366	Homo sapiens cDNA: FLJ21522 fis, clone C	2.66
	407005	U20230		gb:Human guanyl cyclase C gene, partial	2.65
	405075				2.64
	430728	AW968522		gb:EST380598 MAGE resequences, MAGJ Homo	2.64
60	405327				2.63
	409419	BE207219	Hs.20474	ESTs, Highly similar to S17112 interfero	2.63
	434300	AA740944	Hs.116295	ESTs	2.63
	405895				2.62
	431929	AW294163	Hs.146127	ESTs	2.61
	405217				2.60
65	437569	AA760849	Hs.294052	ESTs	2.60
	419822	AW968884	Hs.255780	ESTs	2.59
	445918	AW014139	Hs.145656	ESTs	2.59
	446149	BE242950	Hs.203181	ESTs	2.59
70	457829	AI742291	Hs.210843	ESTs, Weakly similar to dJ1039K5.2 [Hsa	2.58
	404282				2.53
	409778	AW499705		gb:U1-HF-BR0p-ajk-b-05-0-U1.r1 NIH_MGC_5	2.53
	445353	BE561465	Hs.175211	ESTs	2.53
	458764	BE619386		gb:601473204F1 NIH_MGC_68 Homo sapiens c	2.53
	402195				2.52
75	404247				2.52
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	2.52
	402588				2.50
	432301	U34249	Hs.167075	ring finger protein 9	2.50
80	424958	AA984420	Hs.283659	ESTs	2.49
	442197	AW837912		gb:QV3-LT0048-260100-068-c02 LT0048 Homo	2.49
	415003	M11437	Hs.77741	kininogen	2.48
	420767	AF072711	Hs.99918	carboxyl ester lipase (bile salt-stimula	2.48
	422885	BE244068	Hs.121544	interleukin 12 receptor, beta 1	2.47

	440424	AJ991125	Hs.189109	Homo sapiens cDNA: FLJ21458 fis, clone C	2.47
	402153				2.46
	432152	AK000245	Hs.272790	Homo sapiens cDNA FLJ20238 fis, clone CO	2.46
	454414	R55574	Hs.164675	ESTs	2.45
5	401603				2.44
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.44
	408513	AW206468	Hs.103118	ESTs	2.43
	409826	AW501112	Hs.34487	hypothetical protein FLJ23412	2.42
	400672				2.41
10	430713	AA351647	Hs.2542	eukaryotic translation elongation factor	2.41
	449748	H23963	Hs.32043	ESTs	2.41
	453756	AW139415	Hs.61906	ESTs	2.41
	400624				2.40
	403125				2.40
15	406118				2.39
	402155				2.38
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarcom	2.38
	425515	W26609		gb:35f12 Human retina cDNA randomly prim	2.38
	402951				2.37
20	427886	AA417083	Hs.104789	ESTs	2.37
	447173	AW449385	Hs.157294	ESTs	2.37
	448703	BE613942	Hs.170890	Homo sapiens cDNA: FLJ21129 fis, clone C	2.37
	426344	H41821	Hs.169393	transcriptional activator of the c-fos p	2.36
	401840				2.35
25	403731				2.34
	405378				2.34
	405555	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	2.34
	416559	AI039195	Hs.128060	ESTs, Weakly similar to cDNA EST yk481g5	2.34
	438216	ZB3952	Hs.252815	ESTs	2.34
30	448427	BE395260		gb:601311130F1 NIH_MGC_44 Homo sapiens c	2.34
	451588	AW072057		gb:ws58g05.x1 NCI_CGAP_Bm25 Homo sapien	2.34
	423011	NM_000683	Hs.299847	ESTs, Highly similar to A2AD_HUMAN ALPHA	2.33
	451172	AW206465	Hs.207423	ESTs	2.33
	401015				2.32
35	414705	BE464157	Hs.281455	ESTs	2.32
	438894	AA853077		gb:NHTBCae03a05f1 Normal Human Trabecula	2.31
	446305	AW270149	Hs.254515	ESTs, Moderately similar to AF248953 1 g	2.31
	453512	AL040160	Hs.209542	ESTs, Weakly similar to B cell linker pr	2.29
	418556	T02850		gb:FB12A9 Fetal brain, Stratagene Homo s	2.28
40	457197	AB016092	Hs.197114	RNA binding protein; AT-rich element bin	2.28
	457275	AA463422	Hs.209431	ESTs	2.28
	458766	AW183518	Hs.188417	ESTs, Weakly similar to ZnT-3 [H.sapiens	2.28
	414075	U11862	Hs.75741	amiloride binding protein 1 (amine oxida	2.27
	430210	AL157426	Hs.235390	Homo sapiens mRNA; cDNA DKFZp761B101 (tr	2.27
45	442614	AI269030		gb:qj73c12.x1 NCI_CGAP_Kd3 Homo sapiens	2.27
	402538				2.26
	438891	AL389940	Hs.109968	ESTs	2.26
	440056	BE294828	Hs.13323	hypothetical protein FLJ22059	2.26
	406150				2.25
50	426880	AA453482		gb:zx47a11.r1 Soares_testis_NHT Homo sap	2.25
	447129	AW014123	Hs.161402	ESTs	2.25
	458893	BE161733	Hs.97283	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.25
	456778	AI458309	Hs.117406	ESTs	2.24
	401728				2.23
55	404139				2.23
	414095	BE293546		gb:601186671F1 NIH_MGC_15 Homo sapiens c	2.23
	432037	AW450592	Hs.300459	ESTs	2.23
	451965	AA021163	Hs.22287	ESTs	2.23
60	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	2.22
	427586	AA609661	Hs.190592	ESTs	2.22
	454108	AA161071	Hs.71465	squalene epoxidase	2.22
	429749	AI685174	Hs.22293	ESTs	2.21
	434507	AW511138	Hs.256581	ESTs	2.21
	436652	AA724543	Hs.168824	ESTs	2.21
65	437433	R74016	Hs.121581	ESTs	2.21
	401688				2.20
	441748	R14439	Hs.209194	ESTs	2.19
	453072	BE251845	Hs.221516	ESTs, Weakly similar to tetraspan TM4SF	2.19
	400635				2.18
70	417176	AW974475	Hs.143467	ESTs	2.18
	427858	NM_001971	Hs.21	elastase 1, pancreatic	2.18
	454886	AW837063		gb:QV1-LT0037-150200-069-g08 LT0037 Homo	2.18
	458232	BE217872	Hs.279537	ESTs	2.18
75	408922	R87388		gb:ym88g04.r1 Soares adult brain N2b4HB5	2.17
	423568	Y10148	Hs.131138	neurotensin receptor 2	2.17
	440338	R62431	Hs.12758	ESTs	2.17
	403115				2.16
	409125	R17268	Hs.301560	ESTs	2.16
	426887	AI971975	Hs.212892	ESTs	2.16
80	413811	BE168828		gb:QV1-HT0517-020400-145-#04 HT0517 Homo	2.15
	442962	AI025315	Hs.131615	ESTs	2.15
	403921				2.14
	413140	T06607	Hs.6846	hypothetical protein FLJ13055	2.14

	421996	AW583807	Hs.1460	glucagon	2.14
	436130	AA341497	Hs.31408	ESTs	2.14
	407243	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	2.13
	407708	AF019968	Hs.37936	suppressor of variegation 3-9 (Drosophil	2.13
5	442792	AI352340	Hs.131194	ESTs	2.12
	454406	AA213605	Hs.267861	ESTs	2.12
	424648	AA344576		gb:EST50478 Gall bladder I Homo sapiens	2.11
	433963	AI218808	Hs.187778	ESTs	2.11
	400736				2.10
10	406343				2.10
	409702	AI752244	Hs.285749	Human DNA from chromosome 19-specific co	2.10
	432092	AF135026		gb:Homo sapiens kallikrein-like protein	2.10
	441915	AI566116	Hs.207066	ESTs, Weakly similar to FOG [M.musculus]	2.10
	453147	AA733098	Hs.279909	CGI-05 protein	2.10
15	415604	Z44177	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	2.08
	422927	AW247388	Hs.301423	calcium binding protein 1 (calbrain)	2.08
	401211	AJ004832	Hs.5038	neuropathy target esterase	2.07
	413808	J00287	Hs.182183	caldesmon 1	2.07
	414433	BE407755	Hs.169100	Homo sapiens cDNA FLJ12529 fis, clone NT	2.07
20	421978	AJ243662	Hs.110195	NICE-1 protein	2.07
	431204	F28841	Hs.250760	cytochrome c oxidase subunit Via polypep	2.07
	433605	AJ378012	Hs.147953	ESTs	2.06
	449383	AW444712	Hs.196573	ESTs	2.06
	455652	BE064675		gb:RC1-BT0313-301299-012-h11 BT0313 Homo	2.05
25	402382				2.04
	407282	AI345597	Hs.254727	ESTs	2.04
	457273	AJ167145	Hs.165538	ESTs	2.04
	459073	AW968616	Hs.296234	ESTs, Highly similar to mitogen-activate	2.04
	402394				2.03
30	426875	AW451624	Hs.178202	ESTs	2.03
	456634	AA609911	Hs.109012	ESTs	2.03
	434352	AF129505	Hs.86492	small muscle protein, X-linked	2.02
	439281	AA100768	Hs.48485	ESTs	2.02
	444153	AK001610	Hs.10414	hypothetical protein FLJ10748	2.02
35	401122				2.01
	444340	AI143198	Hs.143561	ESTs	2.01
	455104	BE064863		gb:RC1-BT0313-110300-015-406 BT0313 Homo	2.01
	415011	AW963085		gb:EST375158 MAGE resequences, MAGH Homo	2.00
	440144	AW082297	Hs.88523	ESTs	2.00
40	403183				1.99
	409802	AW500732		gb:UH-HF-BN0-akm-h-07-0-UI.r1 NIH_MGC_50	1.98
	430144	AI732722	Hs.187694	ESTs	1.98
	444580	AI168365	Hs.268663	ESTs	1.98
	401704				1.97
45	401810				1.97
	424473	AK001405	Hs.148584	Homo sapiens cDNA FLJ10543 fis, clone NT	1.97
	438573	AW135084	Hs.299865	ESTs	1.97
	412921	BE009345	Hs.128942	ESTs	1.96
	422233	AB002058	Hs.113275	purinergic receptor P2X-like 1, orphan r	1.96
50	425352	NM_000939	Hs.1897	proopiomelanocortin (adrenocorticotropin	1.96
	410285	AA083609		gb:zm63d05.r1 Stratagene fibroblast (937	1.95
	414323	NM_014759	Hs.239500	KIAA0273 gene product	1.94
	428119	AW298211	Hs.255737	ESTs	1.94
	424510	AK001841	Hs.149797	hypothetical protein FLJ10979	1.92
55	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	1.92
	429785	HB2114	Hs.301769	ESTs	1.92
	437344	R90921	Hs.5846	hypothetical protein FLJ13055	1.92
	451819	AI819096	Hs.249260	ESTs	1.92
	459080	H89244	Hs.79625	heterogeneous nuclear ribonucleoprotein	1.92
60	422664	AA315933	Hs.120879	ESTs	1.91
	432247	AA531287	Hs.105805	ESTs	1.91
	453820	R77494	Hs.75416	DAZ associated protein 2	1.91
	400675				1.90
	405556	Y09305	Hs.30148	homeodomain-interacting protein kinase 3	1.90
65	407099	M94891	Hs.278423	pregnancy specific beta-1-glycoprotein 4	1.90
	440297	BE560553	Hs.205450	Homo sapiens cDNA: FLJ22570 fis, clone H	1.90
	443104	AA088470	Hs.83135	p53-responsive gene 6	1.90
	444329	W73753	Hs.58330	ESTs	1.90
	402690				1.89
70	432354	AW137262	Hs.192713	ESTs	1.89
	427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	1.88
	443322	AI825817	Hs.143272	ESTs	1.88
	458185	AI762757	Hs.129869	ESTs, Weakly similar to AF113685 1 PRO09	1.88
	459072	AI815978	Hs.160427	ESTs	1.88
75	402534				1.87
	409689	AA078492		gb:7P04D11 Chromosome 7 Placental cDNA L	1.87
	416931	D45371	Hs.80485	adipose most abundant gene transcript 1	1.87
	430176	AL161995	Hs.234775	neurturin	1.87
	430631	AJ003147	Hs.278464	olfactory receptor, family 1, subfamily	1.87
80	433114	AA121579		gb:zn77f02.r1 Stratagene NT2 neuronal pr	1.87
	439254	U57352	Hs.6517	amiloride-sensitive cation channel 1, ne	1.87
	448461	AW166358	Hs.124979	ESTs	1.87
	450675	AA010662	Hs.188639	ESTs	1.87

	401767			1.86	
	449891	N64867	Hs.37848	ESTs	1.85
	400527				1.84
5	428581	AA430570	Hs.104881	ESTs	1.84
	443647	AV653846	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	1.84
	444785	AV651441	Hs.282475	ESTs	1.84
	449566	AA001778	Hs.288155	Homo sapiens cDNA: FLJ21819 fis, clone H	1.84
	436752	AW298529	Hs.255774	ESTs	1.83
10	437405	AA338837	Hs.42547	Homo sapiens cDNA FLJ13975 fis, clone Y7	1.83
	449174	T66136	Hs.12880	ESTs	1.83
	449887	AW080843	Hs.200275	ESTs	1.83
	453261	AA034116	Hs.118494	ESTs	1.83
	454243	AW241901	Hs.250683	ESTs	1.83
15	459188	AA216382	Hs.30002	SH3-containing protein SH3GLB2	1.83
	424334	AA393460		gb:z171e05.r1 Soares_testis_NHT Homo sap	1.82
	432150	AK000224	Hs.272789	hypothetical protein FLJ20217	1.82
	408123	AW163377		gb:au94e02.y1 Schneider fetal brain 0000	1.81
	428722	U76456	Hs.190787	tissue inhibitor of metalloproteinase 4	1.80
20	442196	AI902646	Hs.31844	Homo sapiens cDNA FLJ12586 fis, clone NT	1.80
	421419	M99587	Hs.104134	homeo box (H6 family) 1	1.79
	405420				1.78
	405737				1.78
	414016	AA134594	Hs.71528	ESTs	1.78
25	415744	AW964850	Hs.279307	ESTs	1.78
	420375	AF182077	Hs.97244	glioma tumor suppressor candidate region	1.78
	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	1.78
	421592	AF009801	Hs.105941	bagpipe homeobox (Drosophila) homolog 1	1.77
	401743				1.75
30	405187				1.75
	442763	AI017037	Hs.131121	ESTs	1.75
	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	1.75
	413248	T64858	Hs.21433	ESTs	1.74
	423913	NM_016436	Hs.301055	hepatocellular carcinoma-associated anti	1.74
35	439999	AA115811	Hs.6838	ras homolog gene family, member E	1.74
	440185	AW104546	Hs.270929	ESTs	1.74
	450482	AI697844	Hs.221720	ESTs	1.74
	413972	BE279548	Hs.162717	ESTs, Weakly similar to HPPD_HUMAN 4-HYD	1.73
	420476	AW575863	Hs.136232	ESTs	1.73
40	428748	AW593206	Hs.98785	ESTs	1.73
	431148	AA502653	Hs.28821	ESTs	1.73
	447205	BE617015	Hs.11006	ESTs	1.73
	455994	BE179190		gb:RC0-HT0613-210300-032-f07 HT0613 Homo	1.73
	401039				1.72
	403251				1.72
45	409762	AW498884	Hs.257970	ESTs	1.72
	440914	AA909562	Hs.143884	ESTs	1.72
	448507	AL133109	Hs.21333	Homo sapiens mRNA; cDNA DKFZp566N1047 (f	1.72
	409605	AW444477	Hs.258507	ESTs	1.71
50	441212	AW242447	Hs.146182	ESTs, Weakly similar to lactase phlorizi	1.71
	445624	AW140103	Hs.78880	ivB (bacterial acetolactate synthase)-I	1.71
	458619	AA872064	Hs.301218	ESTs, Weakly similar to Unknown gene pro	1.71
	401969				1.70
	403327				1.70
55	407245	X90568	Hs.172004	titin	1.70
	417361	NM_000275	Hs.82027	oculocutaneous albinism II (pink-eye dil	1.70
	436034	AF282693	Hs.150185	inflammation-related G protein-coupled r	1.70
	442682	AI014545	Hs.231027	EST	1.70
	458494	AI380906	Hs.158436	ESTs	1.70
	404682				1.69
60	407402	AF035303		gb:Homo sapiens clone 23943 mRNA sequenc	1.69
	409368	AA071069		gb:zm68e10.r1 Stratagene neuroepithelium	1.69
	440352	AA883812	Hs.125508	ESTs	1.69
	448866	BE297743	Hs.284203	myogenic factor 3	1.69
	402201				1.68
65	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.68
	403186				1.67
	409543	AW410200		gb:rh05b12.x1 NIH_MGC_17 Homo sapiens cD	1.67
	443672	AA323352	Hs.9567	butyrobetaine (gamma), 2-oxoglutarate di	1.67
70	450391	AI694522	Hs.202280	ESTs	1.67
	408919	AW295352	Hs.251836	ESTs	1.66
	416136	H45027	Hs.181770	ESTs	1.66
	416865	H97863	Hs.42456	ESTs	1.66
	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	1.66
75	437237	BE513073		gb:601171435F1 NIH_MGC_15 Homo sapiens c	1.66
	429134	AA446953	Hs.99004	ESTs	1.65
	445041	T64183	Hs.11398	ESTs	1.65
	453240	AI969564	Hs.284249	Homo sapiens cDNA: FLJ22334 fis, clone H	1.65
	405243				1.64
80	426039	BE265133	Hs.217493	annexin A2	1.64
	430135	NM_000035	Hs.234234	aldolase B, fructose-bisphosphate	1.64
	435942	R06285	Hs.191215	ESTs	1.64
	448106	AI800470	Hs.171941	ESTs	1.64
	408591	AF015224	Hs.46452	mammaglobin 1	1.63

	410881	AW809157		gb:RCO-ST0118-041099-031-c07_1 ST0118 Ho	1.63
	417743	R14738	Hs.8312	ESTs, Weakly similar to AF170723 1 prote	1.62
	430632	AC004597	Hs.248088	olfactory receptor, family 10, subfamily	1.62
5	448651	BE246440	Hs.93728	pre-B-cell leukemia transcription factor	1.62
	453718	AL119317	Hs.120350	phospholipase A2, group VI (cytosolic, c	1.62
	459499	AW402653	Hs.28355	Homo sapiens cDNA: FLJ22402 fis, clone H	1.62
	412374	X01388	Hs.73849	apolipoprotein C-III	1.61
	419113	AA446586	Hs.21835	ESTs	1.61
10	426795	AI810474	Hs.196945	ESTs	1.61
	426998	BE274360		gb:601121068F1 NIH_MGC_20 Homo sapiens c	1.61
	428407	NM_003963	Hs.184194	transmembrane 4 superfamily member 5	1.61
	444475	C75571		gb:C75571 Human pancreatic islet Homo sa	1.61
	453399	Z70295	Hs.32966	guanylate cyclase activator 2B (uroguany	1.61
15	456275	AW976183	Hs.88414	ESTs, Weakly similar to dJ512E2.1 [H.sap	1.61
	414050	BE246327		gb:TCBAP1E1957 Pediatric pre-B cell acut	1.60
	418004	U37519	Hs.87539	aldehyde dehydrogenase 8	1.60
	428651	AF196478	Hs.188401	annexin A10	1.60
	443853	AI089064	Hs.250644	ESTs	1.60
20	407007	U22961		gb:Human mRNA clone with similarity to L	1.59
	412067	N45697		gb:yy78d01.r1 Soares_multiple_sclerosis_	1.59
	419080	AW150835	Hs.18878	hypothetical protein FLJ21620	1.59
	448619	AI867182	Hs.202255	ESTs	1.59
	403665				1.58
25	407524	X64985		gb:H.sapiens mRNA HTPCRX11 for olfactory	1.58
	424286	AA338285	Hs.90744	proteasome (prosome, macropain) 26S subu	1.58
	412055	T28160	Hs.778	guanylate cyclase activator 1B (retina)	1.57
	430218	AW998865	Hs.186703	ESTs	1.57
	431882	NM_001426	Hs.271977	engrailed homolog 1	1.57
30	450797	AI761930	Hs.205127	ESTs	1.57
	455366	AW947563		gb:RCO-MT0004-140300-031-g11 MT0004 Homo	1.57
	408421	AW193734	Hs.253067	ESTs	1.56
	421907	BE018556	Hs.109358	ATPase, Class V, type 10B	1.56
	432742	AA564453	Hs.162339	ESTs	1.56
35	436624	T64297	Hs.5241	fatty acid binding protein 1, liver	1.56
	439543	W75935	Hs.146083	ESTs	1.56
	443317	AI051601	Hs.200191	ESTs	1.56
	449097	BE271708	Hs.95110	ESTs, Weakly similar to PIP6_HUMAN 1-PHO	1.56
	457127	AA194554	Hs.183434	ATPase, H+ transporting, lysosomal (vacu	1.56
40	407387	AB000896		gb:Homo sapiens mRNA for cadherin FIB1,	1.55
	418837	U48263	Hs.89040	prepronociceptin	1.55
	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	1.55
	458475	AI650322	Hs.143249	ESTs	1.55
	402561				1.54
45	411187	AW821291		gb:PM3-ST0307-241299-002-03 ST0307 Homo	1.54
	419224	NM_012189	Hs.252716	fibrousheathin II	1.54
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	1.53
	415426	Z41991	Hs.23197	ESTs	1.53
	421428	U26726	Hs.1376	hydroxysteroid (11-beta) dehydrogenase 2	1.53
50	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	1.53
	428489	AI807459	Hs.98582	ESTs	1.53
	437728	AA766719		gb:aa39c09.s1 NCI_CGAP_GCB1 Homo sapiens	1.53
	407124	R08160	Hs.268857	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.52
	414932	C14577	Hs.194517	ESTs	1.52
55	433500	AF064255	Hs.111401	very long-chain acyl-CoA synthetase homo	1.52
	439688	AW445181	Hs.209637	Homo sapiens cDNA FLJ12921 fis, clone NT	1.52
	453391	AW600302	Hs.232655	ESTs	1.52
	424688	AA216287	Hs.1815	myosin, light polypeptide 3, alkali; ven	1.51
	436895	AF037335	Hs.5338	carbonic anhydrase XII	1.51
60	443012	AI566813	Hs.132278	ESTs	1.51
	415824	D42039	Hs.78871	mesoderm development candidate 2	1.50
	445152	AI214667	Hs.283597	ESTs	1.50
	455941	BE160011	Hs.129998	Homo sapiens cDNA FLJ14267 fis, clone PL	1.50
	457889	AL035864	Hs.69517	ESTs, Highly similar to differentially e	1.50
65	458503	AL133933	Hs.64310	interleukin 11 receptor, alpha	1.50
	400694				1.49
	420937	AW966719	Hs.1340	collpase, pancreatic	1.49
	426752	X69490	Hs.172004	titin	1.49
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	1.49
70	428874	W32133	Hs.194366	transferrin (prealbumin, amyloidosis I	1.49
	444287	AI033077	Hs.10755	dihydropyrimidinase	1.49
	450684	AA872605	Hs.25333	interleukin 1 receptor, type II	1.49
	425747	AA57620	Hs.205360	ESTs	1.48
	432378	AI493046	Hs.146133	ESTs	1.48
75	447999	AW138840	Hs.201778	ESTs	1.48
	453888	AW450670	Hs.252819	ESTs	1.48
	406667	M12523	Hs.75442	albumin	1.47
	418129	X52997	Hs.1144	glycoprotein IX (platelet)	1.47
	426309	AI912555	Hs.157195	peptide YY, 2 (seminaplasmin)	1.47
80	426755	BE253469		gb:601108143F1 NIH_MGC_16 Homo sapiens c	1.47
	414258	AA203285	Hs.294141	ESTs, Weakly similar to dJ73D15.1 [H.sa	1.46
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	1.46
	420562	AI345569	Hs.190046	ESTs	1.46
	425011	T51986	Hs.283108	hemoglobin, gamma G	1.46

	443050	AI612788	Hs.132348	ESTs, Weakly similar to diaphanous 1 (H.	1.46
	411074	X60435	Hs.68137	adenylate cyclase activating polypeptide	1.45
	434680	T11738	Hs.127574	ESTs	1.45
	454771	AW819939	Hs.273629	ESTs	1.45
5	415672	N53097	Hs.193579	ESTs	1.44
	418141	AW845738	Hs.171118	Homo sapiens mRNA for FLJ00026 protein,	1.44
	406706	X03740	Hs.231581	myosin, heavy polypeptide 1, skeletal mu	1.43
	418197	AA214253		gb:zn58g02.r1 Stratagene muscle 937209 H	1.43
10	431821	AW452256	Hs.271221	hypothetical protein FLJ20064	1.43
	455433	AW939463		gb:QV1-DT0072-310100-056-g02 DT0072 Homo	1.43
	407743	AW814118		gb:MR3-ST0203-151199-011-d09 ST0203 Homo	1.42
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	1.42
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	1.42
	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	1.42
15	452456	BE080763		gb:QV1-BT0631-150200-071-f09 BT0631 Homo	1.42
	456535	AA305079	Hs.1342	cytochrome c oxidase subunit Vb	1.42
	408349	BE546947	Hs.44276	homeo box C10	1.41
	420391	AA456891	Hs.79123	KIAA0084 protein	1.41
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	1.41
20	449329	AW752783		gb:IL3-CT0219-221199-029-F03 CT0219 Homo	1.41
	453615	AA195712	Hs.132696	ESTs	1.41
	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	1.40
	420287	AA740907	Hs.88297	ESTs	1.40
	427583	M82952	Hs.179704	maprin A, alpha (PABA peptide hydrolase)	1.40
25	418787	AW296134	Hs.86999	ESTs	1.39
	422072	AB018255	Hs.111138	KIAA0712 gene product	1.39
	425988	BE045897	Hs.274454	ESTs	1.39
	428087	AA100573	Hs.182421	tropoin C2, fast	1.39
30	438136	NM_002390	Hs.6088	a disintegrin and metalloproteinase doma	1.39
	455579	BE011320		gb:PM3-BN0218-090500-002-d09 BN0218 Homo	1.39
	402316				1.38
	417084	H08370	Hs.33067	ESTs	1.38
	423276	AC003034	Hs.126261	Homo sapiens Chromosome 16 BAC clone CIT	1.38
35	433787	AI472951	Hs.173688	ESTs	1.38
	413830	BE263439	Hs.13144	HSPC160 protein	1.37
	423576	NM_000383	Hs.129829	autoimmune regulator (autoimmune polyen	1.37
	401886				1.36
	412688	AW583062	Hs.74502	chymotrypsinogen B1	1.36
40	401238				1.34
	421511	AA488940	Hs.105216	hypothetical protein FLJ11125	1.34
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B11	1.34
	425450	U14755	Hs.157449	UIM homeobox protein 1	1.34
	427333	AF067797	Hs.176658	aquaporin 8	1.34
45	430937	X53463	Hs.2704	glutathione peroxidase 2 (gastrointestin	1.34
	445204	AW135523	Hs.245853	ESTs	1.34
	452030	AL137578	Hs.27607	Homo sapiens mRNA; cDNA DKFZp564N2464 (f	1.34
	456379	W22208		gb:63E10 Human retina cDNA Tsp5091-claav	1.34
	457416	BE142052		gb:CM3-HT0137-150999-011-b05 HT0137 Homo	1.34
50	415741	AI902761	Hs.272087	ESTs	1.33
	422260	AA315993	Hs.105484	ESTs, Weakly similar to LITB_HUMAN LITBO	1.33
	429188	AB011171	Hs.198037	KIAA0599 protein	1.33
	442776	AW959498	Hs.8709	chymotrypsin C (caldecrin)	1.33
	454748	AW862014		gb:RC3-CT0347-160200-013-d09 CT0347 Homo	1.33
55	437744	AW290905	Hs.300288	ESTs, Weakly similar to CGHJ2E collagen	1.32
	451997	AA021351	Hs.158497	KIAA0724 gene product	1.32
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	1.32
	411879	BE145354	Hs.273758	Homo sapiens cDNA: FLJ23112 fis, clone L	1.31
	424304	NM_001395	Hs.144879	dual specificity phosphatase 9	1.31
60	401442				1.30
	403942				1.30
	443687	F13040	Hs.182937	peptidylprolyl isomerase A (cyclophilin	1.30
	401624				1.29
	411885	AA452636	Hs.131057	ESTs, Moderately similar to CRGD_HUMAN G	1.29
65	418575	AA225313	Hs.222886	ESTs	1.29
	419818	AI657122	Hs.301931	ESTs	1.29
	429845	AB020337	Hs.225943	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	1.29
	447586	AI081980	Hs.285829	solute carrier family 25 (mitochondrial	1.29
	407013	U35637		gb:Human nebulin mRNA, partial cds	1.28
70	428470	AC002301	Hs.184507	Homo sapiens Chromosome 16 BAC clone CIT	1.28
	429780	AL137518	Hs.300388	ESTs	1.28
	453539	AW731886	Hs.95196	ESTs, Weakly similar to T20B12.3 [C.sleg	1.28
	400846				1.27
75	420257	AA257035	Hs.190042	ESTs	1.27
	429184	AF095735	Hs.198003	sarcosine dehydrogenase	1.27
	437389	AL359587	Hs.271586	hypothetical protein DKFZp762M115	1.27
	444412	AI147652	Hs.216381	Homo sapiens clone HH409 unknown mRNA	1.27
	451139	AW293316	Hs.205558	ESTs	1.27
	431284	AA570148	Hs.126783	Homo sapiens cDNA: FLJ22610 fis, clone H	1.26
80	431969	AA366217	Hs.2879	carboxypeptidase A1 (pancreatic)	1.26
	406158				1.25
	419648	T73661	Hs.91877	ESTs, Highly similar to THIH_HUMAN THYRO	1.25
	430681	AW969675	Hs.291232	ESTs	1.25
	434880	U02388	Hs.101	cytochrome P450, subfamily IVF, polypept	1.25

	436217	T53925	Hs.107	fibrinogen-like 1	1.25
	440089	AA864468	Hs.135646	ESTs	1.25
	446787	U67167	Hs.315	mucin 2, intestinal/tracheal	1.25
5	448207	AI475490	Hs.170577	ESTs	1.25
	454869	AW836004		gb:PM0-LT0019-170200-001-d11 LT0019 Homo	1.25
	413271	AA127873	Hs.114949	ESTs	1.24
	422619	AA313322		gb:EST185218 Colon carcinoma (HCC) cell	1.24
	422796	AW897265		gb:CM0-NN0057-150400-335-a04 NN0057 Homo	1.24
10	427530	AA405093	Hs.126519	ESTs	1.24
	437727	AA766707	Hs.153039	ESTs	1.24
	426435	AI827946	Hs.189118	ESTs	1.23
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	1.22
	407964	AW130334	Hs.281111	ESTs	1.21
15	430828	AI763257	Hs.86327	Homo sapiens cDNA: FLJ22431 fs, clone H	1.21
	432029	D31628	Hs.2899	4-hydroxyphenylpyruvate dioxygenase	1.21
	457843	AW138211	Hs.128746	ESTs	1.21
	413242	BE074165		gb:PM3-BT0564-030300-002-e12 BT0564 Homo	1.20
	446057	AI420227	Hs.149358	ESTs	1.20
20	447198	D61523	Hs.283435	ESTs	1.20
	449513	AI653232	Hs.195059	EST	1.20
	415566	F12119		gb:HSC35H091 normalized infant brain cDN	1.19
	423315	R54109	Hs.26096	ESTs	1.19
	455817	BE142384		gb:CM2-HT0144-210999-011-d04 HT0144 Homo	1.19
25	459354	BE514778		gb:601317094F1 NIH_MGC_9 Homo sapiens cD	1.19
	408432	AW195262		gb:cn67b05.x1 NCI_CGAP_CML1 Homo sapiens	1.18
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	1.18
	419251	NM_001486	Hs.89771	glucokinase (hexokinase 4) regulatory pr	1.18
	456702	AI684534		gb:wa72f10.x1 Soares_NFL_T_GBC_S1 Homo s	1.18
30	458009	AI221409	Hs.144983	ESTs	1.18
	410193	AJ132592	Hs.59757	zinc finger protein 281	1.17
	417779	AA829526	Hs.124977	ESTs	1.17
	435101	AI743156	Hs.131064	ESTs	1.17
	445360	AI798776	Hs.156029	ESTs	1.17
35	414160	BE257021		gb:601117426F1 NIH_MGC_16 Homo sapiens c	1.15
	418078	AA521268	Hs.86508	ESTs	1.15
	425133	NM_002613	Hs.154729	3-phosphoinositide dependent protein kin	1.15
	437935	AW939591	Hs.5940	hypothetical protein FLJ20063	1.15
	446377	AW014022	Hs.170953	ESTs	1.15
40	420097	AA700127	Hs.190504	ESTs	1.13
	446591	H44186	Hs.15456	PDZ domain containing 1	1.13
	451477	AI798425	Hs.42710	ESTs	1.13
	459197	BE244587		gb:TCBAP2E0851 Pediatric pre-B cell acut	1.13
45	428934	AF039401	Hs.194659	chloride channel, calcium activated, fam	1.12
	431191	AW972118	Hs.100002	HSPC162 protein	1.12
	424403	F05183	Hs.1799	CD1D antigen, d polypeptide	1.11
	433546	AI075877	Hs.125461	Homo sapiens cDNA FLJ11539 fis, clone HE	1.11
	451179	W05469	Hs.31818	ESTs	1.11
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	1.10
50	420774	AA280209	Hs.165270	ESTs	1.10
	428887	AA437009	Hs.98984	ESTs	1.10
	430582	AI215509	Hs.143964	ESTs	1.10
	453642	AI370936	Hs.34074	dipeptidylpeptidase VI	1.10
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	1.09
55	417998	AW967420		gb:EST379495 MAGE resequences, MAGJ Homo	1.09
	456387	W28876		gb:52h7 Human retina cDNA randomly prime	1.09
	427965	D00306	Hs.183864	elastase 3B	1.08
	447388	AW630534	Hs.76277	ESTs, Weakly similar to TB2 [H.sapiens]	1.08
	413841	M34276	Hs.75576	plasminogen	1.07
60	429201	X03178	Hs.198246	group-specific component (vitamin D bind	1.07
	433313	W20128	Hs.296039	ESTs	1.07
	439450	R51613	Hs.125304	ESTs	1.07
	458963	AI701393	Hs.278728	Rad and Gem-related 2 (rat homolog)	1.07
	405161				1.06
65	406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	1.06
	424294	BE299311		gb:601119256F1 NIH_MGC_17 Homo sapiens c	1.06
	424544	M88700	Hs.150403	dopa decarboxylase (aromatic L-amino aci	1.06
	444687	AW972109	Hs.135107	ESTs	1.06
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	1.06
70	421243	AW873803	Hs.102876	pancreatic lipase	1.05
	444290	AA262496	Hs.29280	ESTs	1.05
	407984	AW134708	Hs.243569	ESTs	1.04
	439706	AW872527	Hs.59761	ESTs	1.04
	402194				1.03
75	427506	AK000134	Hs.179100	hypothetical protein FLJ20127	1.03
	428819	AL135623	Hs.193914	KIAA0575 gene product	1.03
	434590	T47232		gb:yg64b08.s1 Stratagene ovary (937217)	1.03
	416378	AW044467	Hs.73708	ESTs, Weakly similar to A57291 cytokine	1.02
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abi subst	1.02
80	443316	AI478463	Hs.18443	ESTs	1.02
	428585	AB007863	Hs.185140	KIAA0403 protein	1.01
	400440	X83957	Hs.83870	nebulin	1.00
	404619	BE514535	Hs.77171	minichromosome maintenance deficient (S	1.00
	407168	R45175		gb:yg40f01.s1 Soares infant brain 1NIB H	1.00

	408052	AW501117	Hs.283585	ESTs	1.00
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	1.00
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	1.00
5	410234	NM_003837	Hs.81255	fructose-1,6-bisphosphatase 2	1.00
	410319	R23413	Hs.71935	putative zinc finger protein from EUOIM	1.00
	411000	N40449	Hs.201619	ESTs, Weakly similar to SEB4B [H.sapiens	1.00
	412098	AI493054	Hs.158968	ESTs	1.00
	412446	AI768015	Hs.92127	ESTs	1.00
10	412637	AA115097	Hs.261313	ESTs	1.00
	413147	BE067271		gb:PM2-BT0349-161299-001-b05 BT0349 Homo	1.00
	413597	AW302885	Hs.117183	ESTs	1.00
	414117	W88559	Hs.1787	proteolipid protein (Pelizaeus-Merzbache	1.00
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibitor	1.00
15	417074	Z49878	Hs.81131	guanidinoacetate N-methyltransferase	1.00
	418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo	1.00
	419768	T72104	Hs.93194	apolipoprotein A-I	1.00
	420182	Z44245	Hs.22999	ESTs	1.00
	420923	AF097021	Hs.273321	differentially expressed in hematopoietic	1.00
20	421100	AW351839	Hs.124660	Homo sapiens cDNA: FLJ21763 fis, clone C	1.00
	421204	AW081587	Hs.165051	ESTs	1.00
	422189	AF252292	Hs.112933	Tax interaction protein 40	1.00
	422792	AI951548	Hs.135163	ESTs	1.00
	423371	AU076819	Hs.1650	solute carrier family 25, member 3	1.00
25	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	1.00
	424922	BE386547	Hs.217112	ESTs, Weakly similar to Similarity to Ye	1.00
	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	1.00
	425545	N98529	Hs.158295	Human mRNA for myosin light chain 3 (MLC	1.00
	425983	AK000226	Hs.165619	mucin and cadherin-like	1.00
30	426004	AW600300	Hs.124123	ESTs, Weakly similar to synectin [R.nor	1.00
	427627	R87582	Hs.179915	guanine nucleotide binding protein (G pr	1.00
	428848	NM_000230	Hs.194236	leptin (murine obesity homolog)	1.00
	429027	AL022314	Hs.194750	Human DNA sequence from clone 1170K4 on	1.00
	429231	AAB13214		gb:zj32e09.s1 Soares_testis_NHT Homo sap	1.00
35	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	1.00
	429930	AI580809	Hs.99569	ESTs	1.00
	429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	1.00
	430418	R98852	Hs.36029	heart and neural crest derivatives expe	1.00
	431845	AA516469	Hs.270554	ESTs	1.00
40	433084	M18079	Hs.282265	fatty acid binding protein 2, intestinal	1.00
	433839	F35430	Hs.146070	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.00
	434452	AA634333	Hs.116822	ESTs	1.00
	435499	R89344	Hs.14148	ESTs	1.00
	438433	AB018274	Hs.6214	KIAA0731 protein	1.00
45	442403	AW207724	Hs.129516	ESTs	1.00
	442803	AI675298	Hs.199917	ESTs	1.00
	443266	AI277101	Hs.25890	ESTs, Weakly similar to transducin [H.sa	1.00
	444656	AI277924	Hs.145199	ESTs	1.00
	445573	AI439646	Hs.157494	ESTs, Weakly similar to KIAA0676 protein	1.00
50	446163	AA026880	Hs.25252	Homo sapiens cDNA FLJ13603 fis, clone PL	1.00
	447359	NM_012093	Hs.18268	adenylate kinase 5	1.00
	447551	BE066634	Hs.929	myosin, heavy polypeptide 7, cardiac mus	1.00
	448657	BE147857	Hs.293841	ESTs, Weakly similar to KIAA0672 protein	1.00
	449238	AA428229	Hs.85524	muscle-specific RING-finger protein homo	1.00
55	450085	AW293791	Hs.60162	Homo sapiens cDNA: FLJ21528 fis, clone C	1.00
	450390	N93227	Hs.98403	ESTs	1.00
	451681	Z28564	Hs.255950	ESTs, Weakly similar to AA64_HUMAN 64 KD	1.00
	452093	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	1.00
	452528	AA742457	Hs.291479	ESTs	1.00
60	452624	AU076606	Hs.30054	coagulation factor V (proaccelerin, labi	1.00
	453754	AW972580	Hs.172753	ESTs	1.00
	453991	AW014915	Hs.273741	ESTs	1.00
	454517	AW903340		gb:IL2-UM0079-090300-050-D02 UM0079 Homo	1.00
	459367	BE148877		gb:CM4-HT0244-111199-040-h12 HT0244 Homo	1.00
65	408021	AW137133	Hs.245857	ESTs	0.99
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	0.99
	437206	AW975934	Hs.283382	ESTs, Weakly similar to Protein sequence	0.99
	422890	Z43784	Hs.78713	solute carrier family 25 (mitochondrial	0.98
	425878	AW964806	Hs.38085	ESTs, Weakly similar to putative glycine	0.98
70	441888	AI733306	Hs.128071	hypothetical protein FLJ21302	0.98
	423068	M25629	Hs.123107	kallikrein 1, renal/pancreas/salivary	0.97
	453534	NM_014796	Hs.33187	KIAA0748 gene product	0.97
	457787	AA683268		gb:ae92b04.s1 Stratagene schizo brain S1	0.97
	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	0.96
75	422069	AJ010063	Hs.111110	titin-cap (teletin)	0.96
	425260	L47726	Hs.1870	phenylalanine hydroxylase	0.96
	418406	X73501	Hs.84905	cytokeratin 20	0.95
	425670	AW968536	Hs.190146	ESTs	0.95
	416373	AA195845	Hs.73680	ESTs, Weakly similar to AF198455 1 epith	0.94
80	452243	AL355715	Hs.28555	programmed cell death 9	0.94
	411908	L27943	Hs.72924	cytidine deaminase	0.93
	415067	AI264969	Hs.929	myosin, heavy polypeptide 7, cardiac mus	0.93
	437156	AI916600	Hs.121194	Homo sapiens cDNA: FLJ21569 fis, clone C	0.93
	450685	L15533	Hs.423	pancreatitis-associated protein	0.92

5	427450	AB014526	Hs.178121	KIAA0626 gene product	0.91
	432440	X63597	Hs.2996	sucrase-isomaltase	0.91
	426651	AU076646	Hs.171683	nuclear receptor subfamily 1, group H, m	0.90
	414910	X12662	Hs.29679	cofactor required for Sp1 transcription	0.89
	423317	AJ272204	Hs.64616	chromosome 12 open reading frame 3	0.89
	424735	U31875	Hs.152677	Homo sapiens cDNA FLJ20338 fis, clone HE	0.89
	439751	AA196090	Hs.50794	Homo sapiens mRNA full length insert cDN	0.89
	452689	F33868	Hs.284176	transferrin	0.89
10	446240	AI535736	Hs.170165	ESTs	0.88
	449110	H56112	Hs.277053	ESTs	0.88
	453817	AW755253	Hs.61920	ESTs	0.88
	428221	U96781	Hs.183075	ESTs, Highly similar to Ca2+ ATPase of f	0.87
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	0.87
15	446525	AW967069	Hs.211556	Homo sapiens cDNA: FLJ23378 fis, clone H	0.87
	453341	AI758912	Hs.295341	adenylyl cyclase-associated protein 2	0.87
	403740				0.86
	420156	AW449258	Hs.6187	ESTs	0.86
	430304	AL122071	Hs.238927	Homo sapiens mRNA; cDNA DKFZp434H1235 (f	0.86
20	421142	AW503944	Hs.130822	ESTs	0.85
	444107	T46839	Hs.10319	UDP glycosyltransferase 2 family, polype	0.85
	419415	AW451692	Hs.192036	ESTs	0.84
	423321	AB013885	Hs.126926	beta-ureidopropionase	0.84
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	0.84
25	433447	U29195	Hs.3281	neuronal pentraxin II	0.84
	403047				0.83
	406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	0.81
	407782	AA608956	Hs.112619	ESTs, Weakly similar to PQ0109 Purkinje	0.81
	405232				0.80
30	437776	AA768037	Hs.291671	ESTs	0.80
	415505	R39870	Hs.12548	ESTs	0.79
	444436	N25871	Hs.177337	ESTs	0.78
	409096	AA194412	Hs.50550	sarcomeric muscle protein	0.77
	432134	AI816782	Hs.122583	Homo sapiens cDNA: FLJ21934 fis, clone H	0.76
35	437066	AA743570	Hs.200935	ESTs	0.76
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	0.75
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	0.73
	413333	M74028	Hs.75297	fibroblast growth factor 1 (acidic)	0.71
	420567	AK000812	Hs.98874	similar to proline-rich protein 48	0.71
40	447145	AA761073	Hs.192943	ESTs	0.71
	452103	R42764	Hs.3248	mutS (E. coli) homolog 6	0.71
	410929	H47233	Hs.30643	ESTs	0.70
	400301	X03635	Hs.1657	estrogen receptor 1	0.69
	415702	F28877		gb:HSPD18414 HM3 Homo sapiens cDNA clone	0.67
45	411396	C04646	Hs.85428	ESTs	0.65
	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	0.65

TABLE 28B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

55	Pkey	CAT number	Accession
	407743	1012151_1	AW814118 AW814257 AW072376
	408123	1040435_1	AW163377 AW160398
	408432	1058667_1	AW195262 R27868 AW811262
60	408664	1073340_1	R56362 AW248096 R07152 R07285
	408922	109017_1	R87388 R84328 AA058916
	409368	112377_1	AA071059 AA085201 AA085020
	409543	1138723_1	AW410200 AW409705 AW411433 BE296786 BE270309
	409689	114833_1	AA078492 AA078333 AA077450 AA077746 AA076896
65	409778	1154206_1	AW499705 AW502537 AW503016
	409802	1155179_1	AW500732 AW504061
	410285	119128_1	AA083609 AA083790 AA112048
	410881	1225682_1	AW809157 AW812181 AW812172 AW812161 AW812165
	411187	1235092_1	AW821291 AW821264 AW821287 AW821290 AW821285 AW821280 AW821259
70	412067	1275641_1	N45697 N45540 AW890595
	413147	1350637_1	BE067271 BE067266 BE067286 BE067278 BE067299 BE067285
	413242	1355323_1	BE074165 BE075001 BE075009
	413811	1391117_1	BE168828 BE168830 BE168823 BE168928 BE168820 BE168826
	414060	1413697_1	BE246327 BE244704
	414095	1416521_1	BE293546 BE249848
75	414160	1422273_1	BE257021 BE258316 BE257099
	414580	1453848_1	BE386918 BE408833 BE385437
	415011	151328_1	AW963085 AA159005 AW963073
	415566	1539861_1	F12119 Z45475 T64832
80	415702	1547874_1	F28877 F35687
	417998	171375_1	AW967420 AA210915 AA236991 AA210916
	418197	172864_1	AA214253 AA214259 Z28472 Z28881 Z17828
	418464	1759038_-2	R87580
	418556	1767866_-1	T02850

	422619	218670_1	AA313322 BE408282 AA465612 BE073382
	422796	221500_1	AW897265 AW897274 AL119504 AW897275 AW897270 AW897312 AW897318 AW897317 AA317240 AW951361 T06241 AA326794 AL138130
			AW407975 AW999277
5	424294	237907_1	BE299311 AA338954 AA338468 AW960907
	424334	238221_1	AA393460 AA338940 AW966277 AA419006
	424648	241947_1	AA344576 AA732430 AA344601
	425515	252721_1	W26609 W27360 AA358818
	426328	264901_1	AW631296 AA375484
	426507	268382_1	AA380285 AW934727 AW934914
10	426755	271382_1	BE253469 BE176417 BE176415 AA384133
	426880	273277_2	AA453482 AF012388
	426998	274259_1	BE274360
	429231	301463_1	AA813214 AI936567 AI743529 AA448279 AA994476 AI807452 AI218180 AA972858
	430728	322706_1	AW968522 AA485112 AA485162 AW968698
15	432092	34124_1	AF135026 AA583908
	433114	35904_1	AA121579 AB005217
	434590	38931_1	T47232 AF147365 T47231
	437237	43506_2	BE513073
	437728	441520_1	AA766719 AA767041 AW977440
20	439894	478738_1	AA853077 AA852175
	442197	535550_1	AW837912 AW837934 AA984475 AW997490
	442614	547073_1	AI269030 AI204085 AI004047
	444475	607874_1	C75571 AI150469 T10778
	448427	762970_1	BE395260 AW291036 AI500420
25	449329	80484_1	AW752783 H38266 AA001166
	451588	87667_1	AW072057 AI225096 AA018702
	452456	918391_1	BE080763 T96599 BE081135 AI902630 H49182 AI904021 AI902697
	454517	1221063_1	AW803340 AW803280 AW803275 AW803415 AW803343 AW803422
	454748	1233013_1	AW862014 AW858740 AW858735 AW818542 AW858765 AW862027 AW858775 AW858771 AW858763
30	454869	1238137_1	AW836004 AW836087 AW836163 AW836162 AW836085 AW836084 AW836079 AW836083 AW836082 AW836086 AW836088 AW836166 AW836164
			AW836002 AW836078 AW836161 AW862135 AW836165 AW836003
	454886	1238987_1	AW837063 AW935882 AW935957
	455075	1252389_1	AW854850 AW854848
35	455104	1253737_1	BE064863 BE153698 AW856751 BE153820 BE064737 BE153674 BE064730 BE065062 BE153536 AW856622 BE155079 BE064651 BE153665
			BE084650 BE064691
	455366	1284685_1	AW947563 AW947543 AW947553 AW947549 AW947717 AW902659 AW902927 BE011032
	455433	1290311_1	AW939463 AW939484 AW939480 AW939459 AW939546 AW939593 AW939548 AW939595 AW939106
	455446	1291969_1	AW947749 AW947746 AW947754 AW946636 AW946674
40	455579	1333944_1	BE011320 BE006381 BE006361 BE011180 BE011328 BE011325 BE011157 BE006384 BE006387 BE006385 BE011160 BE011319 BE011346
			BE006370 BE006386 BE011173 BE006389 BE006376 BE006375 BE006364 BE011321 BE006379
	455652	1348736_1	BE064675 BE064761 BE064809 BE064673 BE064672 BE064674
	455817	1371986_1	BE142384 BE142387
	455994	1398737_1	BE179190 BE179206 BE179182 BE179185 BE179186 BE179194
45	456150	1574395_1	Z42308 H23514
	456379	1839113_2	W22206 W22498 W26922
	456387	1842730_1	W28876 W26158
	456702	219191_1	AI684534 BE262411 AA314031 AW752724
	457416	334503_1	BE142052 AW265588 AA506741
	457787	407235_1	AA683268 BE002903 BE002672
50	458764	73207_1	BE619386 AA300687
	459197	924229_1	BE244587 AW938684 AW176490 AI940102 AW844995 AW938670 AI909850 AI909885 AI940079 AI909873
55	TABLE 28C		
	Pkey:	Unique number corresponding to an Eos probelet	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.	
60	Strand:	Indicates DNA strand from which exons were predicted.	
	NL_position:	Indicates nucleotide positions of predicted exons.	
	Pkey	Ref	Strand NL_position
65	400489	8954013	Plus 131475-131652
	400627	9796886	Plus 160750-161007
	400545	9800107	Minus 124618-124881
	400624	7228177	Minus 94097-94756
	400635	8567750	Minus 102800-102932,107482-107689
	400672	8118724	Minus 148067-148503
70	400675	8118750	Plus 11223-11816
	400694	8118802	Plus 94288-94442
	400736	8118985	Plus 143447-143851
	400846	9188605	Plus 39310-39474
	401007	8117333	Minus 140821-141050
75	401015	8117441	Plus 72260-72369
	401039	7232177	Plus 6588-6884
	401122	8570296	Plus 68258-68444
	401238	9954455	Minus 49473-49644
	401442	8346725	Minus 85674-85910
80	401496	7381769	Minus 82790-83002
	401590	9956320	Minus 33547-33649
	401603	7689963	Minus 116559-116780
	401624	8575907	Plus 168318-168444,172964-173647

	401688	2347081	Plus	22016-22624
	401704	3097841	Plus	24712-25374
	401728	8134856	Minus	82117-82920
5	401743	2865207	Plus	115475-115640
	401767	9958312	Plus	156823-156921,157364-157554
	401810	7342191	Plus	129063-129476
	401840	7684597	Plus	56283-56439
	401866	7229913	Minus	79215-79393
10	401919	9502466	Plus	67536-67666
	401969	3126777	Plus	44863-45366
	402051	8082020	Minus	19346-19480,20041-20119
	402056	8084234	Plus	207002-207288
	402153	8247879	Minus	122580-122987
	402158	8516165	Minus	148298-148429,148566-148677
15	402165	8569830	Minus	65064-65979
	402194	8576113	Plus	70917-71191
	402195	7689778	Minus	147901-148884
	402201	8576119	Plus	655-951
	402316	7527774	Minus	10751-10919,18817-19052,22131-22328
20	402382	9690314	Minus	155331-155528
	402386	9799769	Plus	22069-22303
	402394	9929690	Plus	33308-33482
	402409	9796255	Minus	8571-10061
	402423	9796344	Minus	62487-62664
25	402448	9796640	Plus	112942-113069,114303-114521
	402457	9796782	Minus	15513-15577,16838-16926
	402534	9801061	Plus	58989-59457
	402538	9801137	Minus	96314-96539
	402561	9864675	Plus	72967-73163
30	402588	9908948	Minus	33027-33183,59060-59198
	402690	8348058	Plus	13368-13998
	402714	8969253	Minus	18811-18886,19105-19328,19525-19764
	402762	9230904	Minus	123298-124035
	402862	2956660	Minus	18518-18656
35	402911	7263904	Plus	142689-142979
	402951	9408717	Plus	73252-73329,73718-73877,76217-76299,78195-78401
	402968	9581763	Minus	58658-58924
	403047	3540153	Minus	59793-59968
40	403115	7331404	Minus	142952-143094,145474-145653,146269-146445,152816-152998
	403125	9180936	Minus	197548-197712
	403183	9838273	Plus	109930-110074
	403186	9838287	Minus	117513-117856
	403211	7630841	Minus	159211-159369
	403247	7656833	Minus	76626-77140
45	403251	7677983	Plus	100391-100652
	403327	8440025	Minus	174311-174451,174587-174705,175523-175592
	403376	9369545	Minus	108698-108830
	403479	7329292	Minus	148369-148533,150678-150809
50	403526	8017144	Plus	55367-55483
	403540	8077057	Minus	56315-56450
	403605	6862654	Plus	91614-91718
	403612	8469060	Minus	94723-94859
	403665	7249278	Plus	69027-69375
	403716	7239669	Plus	86899-87122
55	403731	7543752	Minus	144000-144618
	403740	7630882	Plus	86504-87227
	403921	7711590	Minus	3297-3536
	403942	7711825	Minus	99606-99767
	403997	7708819	Plus	134427-134593
60	404139	9838113	Plus	76707-76891
	404247	7406725	Minus	83949-84214,84312-84415,84499-84677,84878-85114
	404282	2276311	Plus	61503-62205
	404348	7630858	Minus	28895-29062
	404668	9797204	Minus	11332-11546,12584-12718
65	404682	9797231	Minus	40977-41150
	404795	4826439	Plus	147501-147780
	404825	6478944	Plus	210382-210494
	404938	7381808	Minus	165838-165950
	405075	7770506	Minus	124680-125321
70	405147	9438278	Minus	158996-159557
	405161	9966260	Plus	157607-157785
	405163	9966267	Minus	161171-161299
	405187	7229826	Plus	117025-117170,118567-118736
	405217	7239551	Plus	32646-33138
75	405232	7249042	Plus	125904-126063
	405243	7249201	Minus	22312-23197
	405327	6094661	Minus	120550-120750
	405378	6491714	Plus	91139-91440
	405420	7211837	Minus	13428-13582
80	405703	4240388	Minus	15850-16061
	405737	9943984	Minus	104275-104508,104755-104877
	405895	7677903	Minus	66990-67484
	406059	9103984	Minus	13856-14004

5	406101	9124019	Plus	125325-125831
	406118	9143818	Plus	53997-54629
	406150	9886026	Minus	59331-59701
	406158	7144874	Plus	62393-63016,65012-65578
	406343	9255974	Plus	17284-17440,18489-18546,18917-19004,19384-19538
	406357	9256093	Minus	77181-77415
	406563	7711604	Plus	34401-34538

10

TABLE 29A: 2286 GENES UP-REGULATED IN IDIOPATHIC PULMONARY FIBROSIS (IPF) COMPARED TO NORMAL BODY

15 Table 29A lists about 2286 genes that are up regulated in idiopathic pulmonary fibrosis samples as compared with normal "body map" samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" idiopathic pulmonary fibrosis expression level to "average" normal adult tissues sample expression was greater than or equal to about 2.0. The "average" fibrosis sample expression level was set to the 90th percentile amongst idiopathic pulmonary fibrosis samples. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

20 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of IPF to normal body tissue

25	Pkey	ExAccn	Unigene ID	Unigene Title	R1
30	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	211.8
	442275	AW449467	Hs.54795	ESTs	189.7
	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	134.1
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	130.4
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	116.8
	421798	N74880	Hs.264330	N-acylsphingosine amidohydrolase (acid c	92.1
	406964	M21305		gb:Human alpha satellite and satellite 3	80.7
35	443709	AI082692	Hs.134662	ESTs	67.1
	431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	61.4
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	57.4
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	54.6
	457200	U33749	Hs.197764	thyroid transcription factor 1	44.9
	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	42.7
	443324	R44013	Hs.164225	ESTs	39.8
40	414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	27.3
	442006	AW975183	Hs.292663	ESTs, Weakly similar to S72482 hypothei	27.1
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	27.1
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	26.9
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	22.2
	421659	NM_014459	Hs.106511	protocadherin 17	21.0
	450478	AW451709	Hs.271200	ESTs	20.2
45	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	19.7
	447033	AI357412	Hs.157601	ESTs	19.4
	445885	AI734009	Hs.127699	KIAA1603 protein	18.9
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	17.9
	432437	W07088	Hs.293685	ESTs	17.8
	424105	AI142336	Hs.43977	Human DNA sequence from clone RP11-195N1	17.3
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	17.2
50	440807	AW269421	Hs.128093	ESTs	16.7
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	16.4
	433365	AF026944	Hs.293797	ESTs	16.4
	445279	R41900	Hs.22245	ESTs	16.4
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	16.4
	405654				16.1
	449328	AI962493	Hs.197647	ESTs	16.1
55	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	15.7
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	15.5
	417728	AW138437	Hs.24790	KIAA1573 protein	15.0
	440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	14.8
	452039	AI922988	Hs.172510	ESTs	14.4
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	14.3
	421464	AA291553	Hs.190086	ESTs	14.1
60	421554	AW137676	Hs.97775	ESTs	13.8
	431889	AA521277	Hs.124946	ESTs, Weakly similar to A46010 X-linked	13.2
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	13.2
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	12.9
	459702				12.7
	421110	AJ250717	Hs.1355	cathepsin E	12.6
	407638	AJ404672	Hs.334483	hypothetical protein FLJ23571	12.6
65	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	12.5
	423244	AL039379	Hs.209502	ESTs, Weakly similar to ubiquitous TPR m	12.2
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	12.1
	436882	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular mat	12.1
	451551	N52812	Hs.177403	ESTs	12.0
	424086	AJ351010	Hs.102267	lysyl oxidase	12.0
	435299	AI745458	Hs.122614	ESTs, Weakly similar to T20593 hypothei	12.0
80	429496	AA453800	Hs.192793	ESTs	11.9

	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
	403637				11.2
	436061	AI248584	Hs.190745	Homo sapiens cDNA: FLJ21326 fis, clone C	11.2
5	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	10.9
	421470	R27496	Hs.1378	annexin A3	10.8
	440209	H05049	Hs.22269	neurexin 3	10.8
	428927	AA441837	Hs.90250	ESTs	10.7
	448693	AW004854	Hs.228320	hypothetical protein FLJ23537	10.5
10	424717	H03754	Hs.152213	wingless-type MMTV integration site fami	10.4
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	10.4
	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	10.4
	442176	AA983764	Hs.128910	ESTs	10.4
	439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
15	452883	X80031	Hs.530	collagen, type IV, alpha 3 (Goodpasture	10.3
	417015	M83772	Hs.80876	flavin containing monooxygenase 3	10.3
	422022	AA302420	Hs.200442	ESTs	10.3
	447724	AW298375	Hs.24477	ESTs	10.2
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	10.0
20	458194	AW383618	Hs.265459	ESTs, Moderately similar to ALU2_HUMAN A	9.9
	446232	AI281848	Hs.194691	retinoic acid induced 3	9.9
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	9.9
	453382	AA709285	Hs.5997	hypothetical protein FLJ13078	9.8
	412372	R55998	Hs.285243	hypothetical protein FLJ22029	9.8
25	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 (H	9.8
	407568	AA740964	Hs.62699	ESTs	9.8
	414259	W44633	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	9.6
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	9.5
	441484	AA935481	Hs.58972	ESTs	9.5
30	422426	W79117	Hs.58559	ESTs	9.4
	406747	AI925153	Hs.217493	annexin A2	9.4
	450050	AI681268	Hs.257883	ESTs	9.4
	431337	N48107	Hs.292593	ESTs	9.3
	408427	AW194270	Hs.177236	ESTs	9.3
35	447048	AW393080	Hs.228320	hypothetical protein FLJ23537	9.3
	453636	R67837	Hs.169872	ESTs	9.3
	443450	N66045	Hs.133529	ESTs	9.2
	418735	N48769	Hs.44609	ESTs	9.2
	421160	AL080215	Hs.102301	Homo sapiens mRNA; cDNA DKFZp586J0323 (f	9.1
40	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	9.1
	441233	AA972965	Hs.135568	ESTs	9.1
	459587	AA031956		gbzrk15e04.s1 Soares_pregnant_uterus_NbH	9.0
	436245	AW450963	Hs.119991	ESTs	9.0
	445189	AI936450	Hs.147482	ESTs	8.9
45	410781	AI375672	Hs.165028	ESTs	8.9
	446868	AV660737	Hs.135100	ESTs	8.8
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	8.8
	425564	AI006276	Hs.159003	transient receptor potential channel 6	8.8
	414968	C16096	Hs.22826	tropomodulin 3 (ubiquitous)	8.8
50	410334	AW979261	Hs.291993	ESTs	8.8
	442510	AF150179	Hs.249890	ESTs	8.8
	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	8.7
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	8.7
	444929	AI685841	Hs.161354	ESTs	8.7
55	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	8.6
	444218	AF070641	Hs.10684	Homo sapiens clone 24421 mRNA sequence	8.6
	412719	AW016610	Hs.129911	ESTs	8.6
	453445	AL036532	Hs.91453	ESTs	8.5
	419261	X07876	Hs.89791	wingless-type MMTV integration site faml	8.5
60	451110	AI955040	Hs.265398	ESTs, Weakly similar to transformation-r	8.5
	433815	AI696602	Hs.112757	ESTs	8.3
	432203	AA305746	Hs.49	macrophage scavenger receptor 1	8.3
	451103	R52804	Hs.25956	DKFZP564D206 protein	8.3
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	8.3
65	424989	AA985520	Hs.23575	ESTs	8.3
	433231	AB040926	Hs.143552	KIAA1493 protein	8.2
	408217	AA433201	Hs.279860	tumor protein, translationally-controlled	8.1
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	8.1
	436751	AA732217	Hs.294054	ESTs	8.0
70	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	8.0
	413048	M93221	Hs.75182	mannose receptor, C type 1	8.0
	426803	AA362568	Hs.179747	ecotropic viral integration site 5	7.9
	409718	D66640	Hs.56045	src homology three (SH3) and cysteine ri	7.8
	423424	AF150241	Hs.128433	prostaglandin D2 synthase, hematopoietic	7.8
75	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.7
	421013	M62397	Hs.1345	mutated in colorectal cancers	7.7
	437479	R61866	Hs.101277	ESTs	7.6
	416778	M16505	Hs.79876	steroid sulfatase (microsomal), arylsulf	7.6
	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	7.6
80	444395	T65213	Hs.4257	ESTs	7.6
	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H	7.6
	450715	AI266484	Hs.31570	ESTs, Weakly similar to KIAA1324 protein	7.6
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	7.6
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	7.6

5	449108	AJ140683	Hs.98328	hypothetical protein MGC13040	7.5
	422798	R92347	Hs.34574	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.5
	416030	H15261	Hs.21948	ESTs	7.5
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	7.4
	424906	AI566085	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	7.4
10	448206	BE622585	Hs.3731	ESTs, Moderately similar to I38022 hypot	7.3
	432133	AB033088	Hs.272567	KIAA1262 protein	7.3
	447112	H17800	Hs.7154	ESTs	7.3
	446917	AI347863	Hs.156672	ESTs	7.3
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	7.3
15	431761	AW002846	Hs.105468	hypothetical protein FLJ22690	7.3
	426743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (fr	7.2
	413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	7.2
	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	7.2
	438122	AI620270	Hs.129837	ESTs, Weakly similar to Z263_HUMAN ZINC	7.2
20	449511	AI970394	Hs.197075	ESTs	7.2
	453616	NM_003462	Hs.33846	dynein, axonemal, light intermediate pol	7.2
	410060	NM_001448	Hs.58367	glypican 4	7.2
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	7.2
	452571	W31518	Hs.34665	ESTs	7.2
25	453736	AL118674	Hs.34871	zinc finger homeobox 1B	7.2
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	7.2
	405494				7.2
	442832	AW206560	Hs.253569	ESTs	7.1
	420193	AI460080	Hs.202869	ESTs	7.1
30	434217	AW014795	Hs.23349	ESTs	7.0
	427356	AW023482	Hs.97849	ESTs	7.0
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.9
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	6.9
	442377	AA993807	Hs.167367	ESTs	6.9
35	441143	AI027604	Hs.159650	ESTs	6.9
	445122	AW241632	Hs.147377	hypothetical protein FLJ23598	6.9
	431353	AA828032	Hs.189076	ESTs	6.9
	407510	U96191		gb:Human trophoblast hypoxia-regulated f	6.8
	426753	T89832	Hs.170278	ESTs	6.8
40	445186	AW614544	Hs.123541	protein tyrosine phosphatase, receptor t	6.8
	451963	AI825440	Hs.224952	ESTs	6.8
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	6.8
	433426	H69125	Hs.133525	ESTs	6.8
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	6.8
45	415236	R41400		gb:Y94b12.s1 Soares Infant brain 1N1B H	6.8
	409031	AA376836	Hs.76728	ESTs	6.7
	427558	D49493	Hs.2171	growth differentiation factor 10	6.7
	437259	AJ377755	Hs.120595	ESTs	6.7
	421952	AA300900	Hs.98849	ESTs, Moderately similar to AF161511 1 H	6.7
50	447081	Y13896	Hs.17287	potassium inwardly-rectifying channel, s	6.7
	430099	AW194988	Hs.20537	hypothetical protein FLJ13942	6.7
	422475	AL359938	Hs.117313	Meis (mouse) homolog 3	6.7
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	6.7
	424750	D29956	Hs.152818	ubiquitin specific protease 8	6.6
55	403574				6.6
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	6.6
	415025	AW207091	Hs.72307	ESTs	6.5
	448104	AI674818	Hs.316433	Homo sapiens cDNA FLJ11375 fis, clone HE	6.5
	444271	AW452569	Hs.149804	ESTs	6.5
60	437157	BE048860	Hs.120655	ESTs	6.5
	444050	AW138295	Hs.135024	ESTs	6.5
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	6.5
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	6.5
	424433	H04607	Hs.9218	ESTs	6.4
65	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	6.4
	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	6.4
	422544	AB018259	Hs.118140	KIAA0716 gene product	6.4
	449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	6.3
	413930	M86153	Hs.75618	RAB11A, member RAS oncogene family	6.3
70	417246	AI760098	Hs.21411	ESTs	6.3
	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	6.3
	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	6.3
	438909	AF085839		gb:Homo sapiens full length insert cDNA	6.3
	446002	AI346468	Hs.145789	ESTs	6.3
75	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	6.3
	419150	T29518	Hs.89640	TEK tyrosine kinase, endothelial (venous	6.3
	424202	BE350295	Hs.15032	RAN binding protein 17	6.3
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	6.2
	415511	AI732617	Hs.182362	ESTs	6.2
80	430510	AW162916	Hs.241576	hypothetical protein PRO2577	6.2
	416879	H98899	Hs.42589	ESTs	6.2
	432603	AA565398		gb:nk41f01.s1 NCI_CGAP_GC2 Homo sapiens	6.2
	442852	BE080429	Hs.15738	ESTs	6.2
	435974	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	6.2
	441082	AW444804	Hs.202655	ESTs	6.2
	404599				6.1
	453931	AL121278	Hs.25144	ESTs	6.1

	420252	AW270404	Hs.193161	ESTs	6.1
	431622	AW979271	Hs.293184	ESTs	6.1
	456964	H59846	Hs.128355	ESTs, Moderately similar to ALU7_HUMAN A	6.1
5	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.0
	424693	BE169810	Hs.47557	ESTs	6.0
	419172	AW338625	Hs.22120	ESTs	6.0
	413384	NM_000401	Hs.75334	exostoses (multiple) 2	6.0
	453037	AA045175	Hs.177552	ESTs	6.0
10	444042	NM_004915	Hs.10237	ATP-binding cassette, sub-family G (WHIT	6.0
	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	6.0
	422352	AA766296	Hs.99200	ESTs	5.9
	433527	AW235613	Hs.133020	ESTs	5.9
	420077	AW512260	Hs.87767	ESTs	5.9
	429703	T93154	Hs.28705	ESTs	5.9
15	433098	AW190593	Hs.151143	ESTs	5.9
	451099	R52795	Hs.25954	Interleukin 13 receptor, alpha 2	5.9
	449416	A1651016	Hs.246311	ESTs	5.9
	459023	AW968226	Hs.60798	ESTs	5.9
20	450584	AA040403	Hs.60371	ESTs	5.9
	427660	A1741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	5.9
	429125	AA446854	Hs.271004	ESTs, Weakly similar to I38022 hypothet	5.9
	450025	AK001875	Hs.24321	Homo sapiens cDNA FLJ12028 fis, clone HE	5.9
	433479	AW511459	Hs.249972	ESTs	5.8
	443113	A1040686	Hs.132908	ESTs	5.8
25	430414	AW365665	Hs.120388	ESTs	5.8
	419752	AA249573	Hs.152618	ESTs, Moderately similar to ZN91_HUMAN Z	5.8
	435420	A1928513	Hs.59203	ESTs	5.8
	404916				5.8
30	424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.8
	448253	H25899	Hs.201591	ESTs	5.8
	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	5.8
	446967	A1699629	Hs.156781	ESTs	5.8
	435082	AA664273	Hs.186104	Homo sapiens cDNA FLJ13803 fis, clone TH	5.7
35	438842	AA827176	Hs.124316	ESTs	5.7
	437260	AA747807	Hs.149500	ESTs	5.7
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	5.7
	428043	T92248	Hs.22240	uteroglobin	5.7
	408045	AW138959	Hs.245123	ESTs	5.7
40	450568	AL050078	Hs.25159	Homo sapiens cDNA FLJ10784 fis, clone NT	5.7
	426508	BE252383	Hs.184668	SBB131 protein	5.7
	453393	AW956392	Hs.110376	ESTs	5.6
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	5.6
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.6
45	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	5.6
	433225	AW816515	Hs.173540	ATPase, Class V, type 10D	5.6
	416575	W02414	Hs.38383	ESTs	5.5
	404043				5.5
	415094	D59513	Hs.330778	ESTs	5.5
50	453049	BE537217	Hs.30343	ESTs	5.5
	430153	AW968128	Hs.336679	ESTs	5.5
	410811	AW805687	Hs.300648	ESTs	5.5
	443903	A1220547	Hs.135223	ESTs	5.5
	429420	AK001679	Hs.202289	hypothetical protein DKFP434P1735	5.5
55	444471	AB020684	Hs.11217	KIAA0877 protein	5.5
	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	5.5
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	5.5
	432113	AA935065	Hs.152385	ESTs	5.5
	446608	N75217	Hs.257846	ESTs	5.5
60	419945	AW290975	Hs.118923	ESTs	5.5
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	5.4
	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	5.4
	439382	BE247684	Hs.103070	ESTs	5.4
	428895	AA437124	Hs.187247	ESTs	5.4
	446577	AB040933	Hs.15420	KIAA1500 protein	5.4
65	419247	S65791	Hs.89764	fragile X mental retardation 1	5.4
	427778	AA412323	Hs.105323	ESTs	5.4
	437138	A1935622	Hs.271245	ESTs	5.4
	431322	AW970622		gb:EST382704 MAGE resequences, MAGK Homo	5.4
70	430437	A1768801	Hs.169943	Homo sapiens cDNA FLJ13569 fis, clone PL	5.4
	435202	A1971313	Hs.170204	KIAA0551 protein	5.4
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	5.3
	434992	AA658501	Hs.283358	ESTs	5.3
	454039	AW079064	Hs.245540	ESTs	5.3
75	456408	A1288348	Hs.23450	mitochondrial ribosomal protein S25	5.3
	406554				5.3
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFP566A1046 (f	5.3
	416769	A1339257	Hs.115435	ESTs, Moderately similar to I54374 gene	5.3
	414299	AA142989	Hs.71730	ESTs	5.3
80	420362	U79734	Hs.97206	huntingtin interacting protein 1	5.3
	459664				5.3
	425509	AF079363	Hs.158213	sperm associated antigen 6	5.3
	401497				5.3
	440727	A1073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	5.2

5	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	5.2
	408776	AA057365	Hs.63356	ESTs, Weakly similar to I38022 hypothe	5.2
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	5.2
	451050	AW937420	Hs.69662	ESTs	5.2
	400297	AJ127076	Hs.334473	hypothetical protein DKFZp564O1278	5.2
10	404957				5.2
	452771	T05477	Hs.333265	ESTs	5.2
	438885	A186558	Hs.184987	ESTs	5.2
	428244	A1564123	Hs.42500	ADP-ribosylation factor-like 5	5.2
	420481	U50525	Hs.99201	Human BRCA2 region, mRNA sequence CG029	5.2
15	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	5.2
	408729	AA195764	Hs.72639	ESTs	5.1
	457100	AA417878	Hs.48401	ESTs, Moderately similar to ALU8_HUMAN A	5.1
	426342	AF093419	Hs.169378	multiple PDZ domain protein	5.1
	417154	A1674701	Hs.21388	ESTs	5.1
20	411869	W20027	Hs.23439	ESTs	5.1
	427043	AA397679	Hs.3991	ESTs	5.1
	445635	A1769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.1
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ23156 fis, clone L	5.1
	422063	BE156476		gb:QV0-HT0368-040100-082-c05 HT0368 Homo	5.1
25	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	5.1
	408677	A1279892	Hs.46801	sorting nexin 14	5.0
	404097				5.0
	437636	AA764781	Hs.291844	ESTs	5.0
	452822	X85689	Hs.288617	hypothetical protein FLJ22621	5.0
30	410733	D84284	Hs.66052	CD38 antigen (p45)	5.0
	439140	W85737	Hs.290830	ESTs	5.0
	407366	AF026942		gb:Homo sapiens cig33 mRNA, partial sequ	5.0
	405547				5.0
	423377	AL049377		gb:Homo sapiens mRNA; cDNA DKFZp586H0718	5.0
35	449168	NM_016206	Hs.23142	colon carcinoma related protein	5.0
	455431	AW938484		gb:CM0-DT0057-290200-253-d06 DT0057 Homo	5.0
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.0
	411149	N68715	Hs.269128	ESTs	5.0
	432441	AW292425	Hs.163484	ESTs	5.0
40	419807	R77402		gb:y75f11.s1 Soares placenta Nb2HP Homo	5.0
	440615	A1733055	Hs.130806	ESTs	5.0
	450109	A1539295	Hs.115740	KIAA0210 gene product	5.0
	449695	AA164569	Hs.34550	ESTs	5.0
	421764	A1681535	Hs.148135	serine/threonine kinase 33	4.9
45	404593				4.9
	423607	AA328329	Hs.6591	ESTs	4.9
	432009	AL137424	Hs.306458	Homo sapiens mRNA; cDNA DKFZp761G2123 (f	4.9
	419235	AW470411	Hs.288433	neurotrophin	4.9
	436304	AA339622	Hs.108887	ESTs	4.9
50	434813	A1821826		gb:rs92b10.x5 NCL_CGAP_Pr3 Homo sapiens	4.9
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	4.9
	415245	N59650	Hs.27252	ESTs	4.9
	428780	A478578	Hs.50636	ESTs	4.9
	406333				4.9
55	445034	AW293376	Hs.143659	ESTs	4.8
	440202	AW516211	Hs.125300	ring finger protein 21, interferon-respo	4.8
	424538	A1472106	Hs.49303	Homo sapiens cDNA FLJ11663 fis, clone HE	4.8
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	4.8
	427652	A1673025	Hs.43874	ESTs, Moderately similar to I54374 gene	4.8
60	458722	AA741545	Hs.282832	ESTs, Weakly similar to T24961 hypothe	4.8
	407327	AA487182	Hs.269414	ESTs, Weakly similar to Z195_HUMAN ZINC	4.8
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	4.8
	415261	T40928	Hs.8346	ESTs	4.8
	453543	AA485425	Hs.48919	Homo sapiens cDNA FLJ11508 fis, clone HE	4.8
65	438014	N71183	Hs.121806	Homo sapiens cDNA FLJ11971 fis, clone HE	4.8
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	4.8
	441006	AW605267	Hs.7627	CGI-60 protein	4.8
	412222	AA528283	Hs.292737	ESTs	4.8
	424115	AA335497	Hs.293965	ESTs, Weakly similar to I38022 hypothe	4.8
70	453197	A1916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S	4.8
	439398	AA284267	Hs.221504	ESTs	4.8
	436397	AA715013	Hs.169835	ESTs	4.8
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	4.8
	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
75	425916	NM_006786	Hs.162200	urotensin 2	4.8
	447020	T27308	Hs.16986	hypothetical protein FLJ11046	4.8
	427457	AW779105	Hs.164682	ESTs	4.7
	451620	AW449888	Hs.257224	ESTs	4.7
	408938	AA059013	Hs.22607	ESTs	4.7
80	420036	R60336	Hs.52792	Homo sapiens mRNA; cDNA DKFZp586I1823 (f	4.7
	424508	AL080103	Hs.149770	Homo sapiens cDNA FLJ13658 fis, clone PL	4.7
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	4.7
	427669	AW451832	Hs.255938	ESTs, Moderately similar to KIAA1200 pro	4.7
	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	435347	AW014873	Hs.116963	ESTs	4.7
	425458	H89317	Hs.182889	ESTs	4.7
	432869	AW974094		gb:EST386197 MAGE resequences, MAGM Homo	4.7

	436594	AI419982	Hs.156189	ESTs	4.7
	421237	U25029	Hs.102761	Human glucocorticoid receptor alpha mRNA	4.7
	432731	R31178	Hs.287820	fibronectin 1	4.7
5	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	4.7
	426320	W47595	Hs.169300	transforming growth factor, beta 2	4.7
	419751	AW195581	Hs.93121	KIAA0761 protein	4.6
	433515	AA595800	Hs.190246	ESTs	4.6
	451381	BE241831	Hs.172330	hypothetical protein MGC2705	4.6
10	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	4.6
	438297	AW515196	Hs.258238	ESTs, Moderately similar to ALU1_HUMAN A	4.6
	406892	S82472		gb:beta-pol-DNA polymerase beta (exon a	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	435933	AA805520	Hs.192075	ESTs	4.6
15	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypothe	4.6
	445657	AW612141	Hs.279575	Homo sapiens G-protein coupled receptor	4.6
	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
	447700	AI420183	Hs.171077	ESTs, Weakly similar to T21259 hypothe	4.6
	423735	AA330259		gb:EST33963 Embryo, 12 week II Homo sapi	4.6
20	424144	AA454033	Hs.41644	AKAP-associated sperm protein	4.6
	416258	N45661	Hs.90011	adenylosuccinate synthase	4.6
	410011	AB020641	Hs.57856	PFTAIRE protein kinase 1	4.6
	454359	N71277		gb:za36e03.s1 Soares fetal liver spleen	4.5
	422977	AA631498		gb:np83h04.s1 NCI_CGAP_Thy1 Homo sapiens	4.5
25	433485	AI493076	Hs.201967	aldo-keto reductase family 1, member C2	4.5
	450192	AA263143	Hs.24596	RAD51-Interacting protein	4.5
	432015	AI157504	Hs.159115	Homo sapiens mRNA; cDNA DKFZp586O0724 (f	4.5
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	4.5
	409041	AB033025	Hs.50081	KIAA1199 protein	4.5
30	434265	AA846811	Hs.130554	Homo sapiens cDNA: FLJ23089 fis, clone L	4.5
	452526	W38537	Hs.280740	hypothetical protein MGC3040	4.5
	403271				4.5
	450656	AA010539	Hs.18912	ESTs	4.5
	446096	AI276454		gb:q71a12.x1 Soares_NhHMPu_S1 Homo sapi	4.5
35	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.5
	437950	AI669586	Hs.222194	ESTs	4.5
	440862	H39048	Hs.127432	ESTs	4.5
	410615	AW772721		gb:h195c01.x1 NCI_CGAP_Thy8 Homo sapiens	4.5
	413583	AL120806	Hs.5888	ESTs	4.5
40	419449	H18417	Hs.57483	Homo sapiens cDNA FLJ14294 fis, clone PL	4.5
	442324	R63578	Hs.28426	ESTs	4.4
	453080	AI423056	Hs.23921	hypothetical protein DKFZp547A023	4.4
	435747	AI079519	Hs.134398	ESTs	4.4
	446509	AF169693	Hs.132892	protocadherin 20	4.4
45	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	4.4
	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	4.4
	448089	AI467945	Hs.173696	ESTs	4.4
	434367	AB020700	Hs.3830	KIAA0893 protein	4.4
	434757	AI038997	Hs.132921	ESTs	4.4
50	413453	AA129640	Hs.128065	ESTs	4.4
	454438	AA224053	Hs.172405	cell division cycle 27	4.4
	458154	AW816379	Hs.335018	ESTs	4.4
	430417	AA461045	Hs.50701	ESTs	4.4
	434819	AA650099	Hs.291541	ESTs, Weakly similar to ALUB_HUMAN !!!!	4.4
55	438796	W67821	Hs.109590	genethonin 1	4.4
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.4
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.4
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.4
	451895	T93573	Hs.16970	ESTs	4.4
60	435434	AA680387	Hs.187850	ESTs	4.4
	449623	C00719	Hs.120440	EST	4.4
	433563	AI732637	Hs.277901	ESTs	4.3
	444649	AW207523	Hs.197628	ESTs	4.3
	441594	AL041080	Hs.208765	ESTs, Moderately similar to ALU7_HUMAN A	4.3
65	443314	AW771701	Hs.54646	ESTs	4.3
	400292	AA250737	Hs.72472	ESTs	4.3
	427972	AA864870	Hs.181304	putative gene product	4.3
	446932	AA961459	Hs.125644	ESTs	4.3
	445640	AW969626	Hs.31704	ESTs, Weakly similar to KIAA0227 [H.sapi	4.3
70	452393	H87398	Hs.99858	ribosomal protein L7a	4.3
	443204	AW205878	Hs.29643	Homo sapiens cDNA FLJ13103 fis, clone NT	4.3
	400508				4.3
	411155	AW819939	Hs.273629	ESTs	4.3
	435772	AA700019	Hs.132992	ATP-binding cassette, sub-family G (WHIT	4.3
75	439830	AA846666	Hs.151489	ESTs, Weakly similar to XE7_HUMAN PROTEI	4.3
	455511	BE144762		gb:CMO-HT0180-041099-055-b04 HT0180 Homo	4.3
	443257	AJ334040	Hs.11614	HSPC065 protein	4.3
	436033	H75391	Hs.255748	ESTs	4.3
	420214	AI146375	Hs.286073	ESTs, Moderately similar to ALU5_HUMAN A	4.3
80	410519	AW612264	Hs.131705	ESTs	4.3
	401189				4.3
	418852	BE537037	Hs.273294	hypothetical protein FLJ20069	4.3
	425733	F13287	Hs.159388	Homo sapiens clone Z3578 mRNA sequence	4.3
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3

	422429	AA310527		gb:EST181333 Jurkat T-cells V Homo sapie	4.3
	434677	AW444575	Hs.130834	ESTs	4.3
	403310				4.3
5	451830	H18433	Hs.21542	KIAA1035 protein	4.3
	422222	AI59372	Hs.193247	hypothetical protein DKFZp434A171	4.3
	435627	W88774	Hs.118370	ESTs	4.3
	436461	AW511956	Hs.293261	ESTs	4.3
	452166	AI948607	Hs.264680	ESTs	4.3
10	413998	AW103807	Hs.243933	ESTs	4.2
	416642	T96118	Hs.226313	ESTs	4.2
	452081	AW958859	Hs.7514	Homo sapiens cDNA FLJ12141 fis, clone MA	4.2
	452930	AW195285	Hs.194097	ESTs, Weakly similar to I38022 hypothei	4.2
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.2
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	4.2
15	424641	AB001106	Hs.151413	glia maturation factor, beta	4.2
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.2
	409629	AW449589	Hs.279724	ESTs	4.2
	458771	AW295151	Hs.163612	ESTs	4.2
20	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	4.2
	436645	AW023424	Hs.156520	ESTs	4.2
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	4.2
	445268	AI218358	Hs.175048	ESTs	4.2
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	4.2
25	431917	D16181	Hs.2868	peripheral myelin protein 2	4.2
	443348	AW873596	Hs.182278	calmodulin 2 (phosphorylase kinase, deli	4.2
	443151	AI827193	Hs.132714	ESTs	4.2
	419255	AA235672	Hs.87491	ESTs	4.2
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	4.2
30	452561	AI692181	Hs.49169	KIAA1634 protein	4.2
	421106	AA877124	Hs.172844	ESTs	4.2
	424268	AA397653	Hs.307438	Human DNA sequence from clone 495010 on	4.2
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	4.2
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	4.2
35	423045	AW967472	Hs.183302	PCTAIRE protein kinase 2	4.2
	428771	AB028992	Hs.193143	KIAA1069 protein	4.1
	445745	AB007924	Hs.13245	KIAA0455 gene product	4.1
	417009	AA191719	Hs.314714	ESTs	4.1
	436517	BE080932	Hs.135225	ESTs	4.1
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	4.1
	414083	AL121282	Hs.257786	ESTs	4.1
	452728	AI915676	Hs.239708	ESTs	4.1
	409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	4.1
	441802	AA968636	Hs.127877	ESTs	4.1
45	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	4.1
	413875	BE176776		gb:RC3-HT0586-110300-011-g09 HT0586 Homo	4.1
	444009	AI380792	Hs.135104	ESTs	4.1
	410785	AW803341		gb:IL2-UM0079-090300-050-D03 UM0079 Homo	4.1
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	4.1
50	438993	AA828995		gb:cd77b08.s1 NC1_CGAP_Ov2 Homo sapiens	4.1
	435256	AF193766	Hs.13872	cytokine-like protein C17	4.1
	428104	AA421350	Hs.191604	ESTs	4.1
	439648	AW780192	Hs.267596	ESTs	4.1
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	4.1
55	446364	AB006624	Hs.14912	KIAA0285 protein	4.1
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
	408369	R38438	Hs.182575	solute carrier family 15 (H+/peptide tra	4.0
	404561				4.0
	401575				4.0
60	419296	AA236115	Hs.120785	ESTs	4.0
	432055	AW972359	Hs.293334	ESTs	4.0
	439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	4.0
	450320	AW291775	Hs.213793	ESTs	4.0
65	447350	AI375572	Hs.172634	ESTs	4.0
	441974	AI683782	Hs.128245	ESTs	4.0
	453142	AA033648	Hs.7473	ESTs	4.0
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	4.0
	410292	AA843087	Hs.124194	ESTs	4.0
70	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	4.0
	420218	AW958037	Hs.286	ribosomal protein L4	4.0
	426625	T78300	Hs.300642	serologically defined colon cancer anti	4.0
	417708	N74392	Hs.50495	ESTs	4.0
	451024	AA442176		gb:zw63b08.r1 Soares_talal_fetus_Nb2HF8_	4.0
75	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0
	422058	AA862231	Hs.334443	ESTs	4.0
	439479	AI734258	Hs.245367	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.0
	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	4.0
	432222	AI204995		gb:an03c03.x1 Stralagene schizo brain S1	4.0
80	444188	AI393165	Hs.699	peptidylprolyl isomerase B (cyclophilin	4.0
	453096	AW294631	Hs.11325	ESTs	4.0
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	4.0
	421002	AF116030	Hs.100932	transcription factor 17	4.0
	445414	AV653692	Hs.146105	ESTs	4.0

	447207	AA442233	Hs.17731	hypothetical protein FLJ12892	4.0
	451353	N21043	Hs.42932	ESTs	4.0
	437075	AA743748	Hs.40758	ESTs	3.9
5	410505	AW752139	Hs.314323	ESTs	3.9
	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	3.9
	426116	AA868729	Hs.144694	ESTs	3.9
	415716	N59294	Hs.179562	nucleosome assembly protein 1-like 1	3.9
	435298	AW293496	Hs.180138	ESTs	3.9
10	417718	T86540	Hs.193981	ESTs	3.9
	436772	AW975688	Hs.74170	metallothionein 1E (functional)	3.9
	401045				3.9
	408767	AA057279	Hs.211928	ESTs	3.9
	407303	AA016296	Hs.165200	ESTs, Weakly similar to A56194 thromboxa	3.9
15	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	3.9
	451623	H77818	Hs.268991	ESTs	3.9
	450063	AI681509	Hs.277133	ESTs	3.9
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.9
	419276	BE165909	Hs.305881	MSTP043 protein	3.9
20	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.9
	436149	AI754308	Hs.159452	ESTs	3.9
	422667	H25642	Hs.133471	ESTs	3.9
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	3.9
	458219	H22195	Hs.31874	ESTs	3.9
25	443613	AI079356		gb:oz39b09.s1 Soares_NhHMPu_S1 Homo sapi	3.9
	439810	AL109710	Hs.85568	EST	3.9
	436578	AI091435	Hs.134859	ESTs	3.9
	415598	AI433165	Hs.9856	ESTs	3.9
	425087	R62424	Hs.126059	ESTs	3.9
30	454111	AW081681	Hs.269054	ESTs, Weakly similar to T42689 hypotheti	3.9
	409719	AI769160	Hs.108681	Homo sapiens brain tumor associated prot	3.9
	452466	N84635	Hs.29664	hypothetical protein DKFZp5648052	3.9
	424962	NM_012288	Hs.153954	TRAM-like protein	3.9
	435823	R07856	Hs.16355	ESTs	3.9
35	440633	AI140686	Hs.263320	ESTs	3.9
	429334	D63078	Hs.186180	Homo sapiens cDNA: FLJ23038 fis, clone L	3.9
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	3.9
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.9
	417461	R38403	Hs.13305	ESTs	3.9
40	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.8
	419140	AI982647	Hs.215725	ESTs	3.8
	415652	T79213	Hs.272073	ESTs	3.8
	430140	AW296771	Hs.221999	ESTs	3.8
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	3.8
45	422165	AL041199	Hs.1481	histidine decarboxylase	3.8
	417706	T90797	Hs.268623	ESTs	3.8
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.8
	450522	AI698839		gb:wd3102.x1 Soares_NFL_T_GBC_S1 Homo s	3.8
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	3.8
50	449729	R72032	Hs.29235	ESTs	3.8
	414700	H63202	Hs.38163	ESTs	3.8
	440899	AW449445	Hs.120021	DKFZP4341092 protein	3.8
	439335	AA742697	Hs.62492	ESTs, Weakly similar to B39066 prolins-r	3.8
	408625	AW243323	Hs.266785	ESTs	3.8
55	421987	AI133161	Hs.286131	CGI-101 protein	3.8
	418915	AI474778	Hs.118977	ESTs	3.8
	410224	M55513	Hs.150208	potassium voltage-gated channel, shaker-	3.8
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.8
	442849	R10099	Hs.269805	ESTs	3.8
60	427191	BE221825	Hs.97691	ESTs	3.8
	407942	AA378608	Hs.5894	hypothetical protein FLJ10305	3.8
	437030	AA742577	Hs.303781	EST	3.8
	427940	AA417812	Hs.38775	ESTs	3.7
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	3.7
65	449679	AI823951	Hs.129700	tolloid-like 1	3.7
	425937	NM_013240	Hs.163846	putative N6-DNA-methyltransferase	3.7
	458663	AV658444	Hs.280776	tankyrase, TRF1-interacting ankyrin-rela	3.7
	456443	AW967500	Hs.133543	ESTs	3.7
	439957	AI453184	Hs.66357	ESTs	3.7
	446999	AA151520	Hs.334822	hypothetical protein MGC4485	3.7
70	428414	AL049980	Hs.184216	DKFZP564C152 protein	3.7
	455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	3.7
	418379	AA218940	Hs.137516	fidgelin-like 1	3.7
	419720	AA249131	Hs.337778	hypothetical protein FLJ11068	3.7
75	443584	AI807036	Hs.267245	hypothetical protein FLJ14803	3.7
	416185	AW975861	Hs.47367	KIAA1785 protein	3.7
	417235	AA810278	Hs.24250	ESTs	3.7
	441720	AI346487	Hs.28739	ESTs	3.7
	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.7
80	417355	D13168	Hs.82002	endothelin receptor type B	3.7
	449321	AA001150	Hs.132937	ESTs	3.7
	424806	AA382523	Hs.105689	MSTP031 protein	3.7
	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	3.7
	409248	AB033035	Hs.51965	KIAA1209 protein	3.7

	421037	AI684808	Hs.197653	ESTs	3.7
	427088	AA398085	Hs.142390	ESTs	3.7
	420637	AW976153		gb:EST388262 MAGE resequences, MAGN Homo	3.7
5	420026	AI831190	Hs.166676	ESTs	3.7
	429419	AB023226	Hs.202276	KIAA1009 protein	3.7
	447410	AI470235	Hs.172698	EST	3.7
	404274				3.7
	416320	H47867	Hs.34024	ESTs	3.7
10	412642	BE244598	Hs.809	hepatocyte growth factor (hepatopoietin A;	3.7
	431716	D89053	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.7
	446025	AW305075	Hs.180948	KIAA0729 protein	3.7
	450458	AA009926		gb:z107e05.r1 Soares_fetal_liver_spleen_	3.7
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor l	3.6
	438257	AW474419	Hs.224794	ESTs	3.6
15	440887	AI799488	Hs.135905	ESTs	3.6
	454693	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	3.6
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	3.6
	408687	AL110280	Hs.301152	Homo sapiens mRNA; cDNA DKFZp434F053 (fr	3.6
	407726	AA435679	Hs.88594	ESTs	3.6
20	436026	AI349764	Hs.217081	ESTs	3.6
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	3.6
	452293	AI871833	Hs.304509	ESTs	3.6
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.6
	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	3.6
25	429208	AA447990	Hs.190478	ESTs	3.6
	458429	AV646559	Hs.12346	Homo sapiens cDNA: FLJ21399 fis, clone C	3.6
	404476				3.6
	405848				3.6
30	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	3.6
	403937				3.6
	437918	AI761449	Hs.121629	ESTs	3.6
	432408	N39127	Hs.332557	ESTs, Weakly similar to A46010 X-linked	3.6
	437641	AA811452	Hs.291911	ESTs	3.6
35	439635	AA477288	Hs.94891	hypothetical protein FLJ22729	3.6
	446102	AW168067	Hs.252956	ESTs	3.6
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	3.6
	425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	3.6
	432030	AI908400	Hs.143789	ESTs	3.6
40	446453	AV658469	Hs.188646	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	3.6
	440801	AA906366	Hs.190535	ESTs	3.6
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	3.6
	440886	AW511032	Hs.190516	ESTs	3.6
	401049				3.6
45	449424	AW448937	Hs.197030	ESTs	3.6
	418076	R61388	Hs.6724	ESTs	3.6
	423035	AW449679	Hs.156739	Hsapiens XG mRNA (clone PEP11)	3.6
	435463	AA682507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	3.6
50	438016	AI949638	Hs.336846	EST	3.6
	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	3.6
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	3.5
	456536	AW135986	Hs.257859	ESTs	3.5
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	3.5
55	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
	435344	AA700326	Hs.190599	ESTs	3.5
	445056	AB014530	Hs.12259	KIAA0630 protein	3.5
	449444	AW818436	Hs.23590	solute carrier family 16 (monocarboxylic	3.5
	442652	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	3.5
60	423121	AW684848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	449540	AA001713		gb:zh86e08.s1 Soares_fetal_liver_spleen_	3.5
	425734	AF056209	Hs.159396	peptidylglycine alpha-amidating monooxyg	3.5
	428409	AW117207	Hs.98523	ESTs	3.5
	431087	H12723	Hs.290791	ESTs	3.5
65	426920	AA393351	Hs.132121	ESTs	3.5
	427687	AW003867	Hs.1570	histamine receptor H1	3.5
	437583	AA761190	Hs.244627	ESTs	3.5
	421599	AA293655	Hs.97293	ESTs	3.5
	433687	AA743991		gb:ny57g01.s1 NCL_CGAP_Pr18 Homo sapiens	3.5
70	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	3.5
	430499	AW969408	Hs.231991	ESTs	3.5
	451531	AA018311	Hs.114762	ESTs	3.5
	457620	AA602711	Hs.336753	EST	3.5
	410658	AW105231	Hs.192036	ESTs	3.5
75	427865	AA416931	Hs.126065	ESTs	3.5
	453390	AA862496	Hs.28482	ESTs	3.5
	419983	V55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	3.5
	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	3.5
	427718	AI798690	Hs.25933	ESTs	3.5
80	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	3.5
	420381	D50640	Hs.337616	phosphodiesterase 3B, cGMP-inhibited	3.5
	410908	AA121686	Hs.10592	ESTs	3.5
	442080	AW444761	Hs.44565	ESTs	3.5
	406685	M18728		gb:Human nonspecific crossreacting anti	3.5

	404200			3.5	
	417976	BE565892	Hs.83077	interleukin 18 (interferon-gamma-inducin	3.5
	433285	AW975944	Hs.237395	ESTs	3.5
	432858	AW974093	Hs.292775	ESTs	3.5
5	433492	AW605849		gb:MR0-HT0241-200100-006-g02 HT0241 Homo	3.5
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	3.4
	428804	AK000713	Hs.193736	hypothetical protein FLJ10706	3.4
	428775	AA434579	Hs.143691	ESTs	3.4
	410004	AI298027	Hs.5057	carboxypeptidase D	3.4
10	422093	AF151852	Hs.111449	CGI-94 protein	3.4
	441736	AW292779	Hs.169799	ESTs	3.4
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	3.4
	405970				3.4
	431954	AK001974	Hs.272242	hypothetical protein FLJ11112	3.4
15	459482	AA625339	Hs.237052	EST, Weakly similar to I38022 hypothetic	3.4
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	3.4
	410804	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar	3.4
	402230				3.4
	436120	AI248193	Hs.119860	ESTs	3.4
20	405336				3.4
	434374	AA631439		gb:np85d02.s1 NCI_CGAP_Thy1 Homo sapiens	3.4
	428911	Z43846	Hs.194478	Homo sapiens mRNA; cDNA DKFZp434O1572 (f	3.4
	437783	AI683150	Hs.201550	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.4
	416057	AI927382	Hs.29857	ESTs	3.4
25	435496	AW840171	Hs.265398	ESTs, Weakly similar to transformation-r	3.4
	436088	AA704687	Hs.191294	ESTs	3.4
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	3.4
	454076	AW204712	Hs.61957	ESTs	3.4
	431733	AW298410	Hs.21475	ESTs	3.4
30	432974	BE348793	Hs.233331	ESTs	3.4
	412576	AA447718	Hs.107057	ESTs	3.4
	446142	AI754693	Hs.145968	ESTs	3.4
	447432	AW958473	Hs.301957	nudix (nucleoside diphosphate linked mol	3.4
35	433384	AI021992	Hs.124244	ESTs	3.4
	413621	AI808648	Hs.184156	ESTs	3.4
	419546	AA244199		gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens	3.4
	436111	AI803082	Hs.157212	ESTs	3.4
	421236	AI287622	Hs.151956	ESTs	3.4
40	433917	AI809325	Hs.122814	Human DNA sequence from clone RP5-1028D1	3.4
	403515				3.4
	429657	D13626	Hs.2465	KIAA0001 gene product; putative G-protein	3.4
	453375	AI990114	Hs.240091	ESTs	3.4
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT	3.4
45	412209	AW901456		gb:RCD-NN1012-270300-031-c07 NN1012 Homo	3.4
	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapl	3.4
	409642	AW450809	Hs.257347	ESTs	3.4
	420092	AA814043	Hs.88045	ESTs	3.4
	453365	AA035211	Hs.17404	ESTs	3.3
50	437007	AA741300	Hs.202599	ESTs, Weakly similar to I38022 hypotheti	3.3
	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	3.3
	439024	R96696	Hs.35598	ESTs	3.3
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	3.3
	417991	AA731452	Hs.190008	ESTs	3.3
	403356				3.3
55	433650	AA603472	Hs.28456	ESTs	3.3
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retroviri	3.3
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	3.3
	413714	AI560944	Hs.71428	ESTs	3.3
	430887	N66801	Hs.260287	KIAA1841 protein	3.3
60	413618	BE154078		gb:PM0-HT0339-200400-010-F04 HT0339 Homo	3.3
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	3.3
	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
	405692				3.3
65	432809	AA565509	Hs.131703	ESTs	3.3
	433805	AA706910	Hs.112742	ESTs	3.3
	436192	W93847	Hs.24139	Homo sapiens cDNA: FLJ23137 fis, clone L	3.3
	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-hergeulin	3.3
	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro	3.3
	448404	BE089973		gb:RC6-BT0709-310300-021-G07 BT0709 Homo	3.3
70	410434	AF051152	Hs.63668	toll-like receptor 2	3.3
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.3
	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	3.3
	444301	AK000136	Hs.10760	aspartin (LRR class 1)	3.3
	428795	R45503	Hs.97469	ESTs, Highly similar to A39769 N-acetyl	3.3
75	458924	BE242158	Hs.24427	DKFZP566O1646 protein	3.3
	435934	R19382	Hs.117869	ESTs	3.3
	400269				3.3
	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	3.3
80	412903	BE007967	Hs.155795	ESTs	3.3
	400889				3.3
	449585	AI655321	Hs.197693	ESTs	3.3
	408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	3.3
	418557	BE140602	Hs.246645	ESTs	3.3

5	453204	R10799	Hs.191990	ESTs	3.3
	450696	AI654223	Hs.16026	hypothetical protein FLJ23191	3.3
	427374	AI150033	Hs.143686	ESTs	3.3
	443367	AW071349	Hs.215937	ESTs	3.3
	446645	AI336596	Hs.156294	ESTs	3.3
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	3.3
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	3.3
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	3.3
10	403895				3.2
	414899	AW975433	Hs.36288	ESTs	3.2
	409044	AI129586	Hs.33033	hypothetical protein FLJ14623	3.2
	447233	AW246333	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,	3.2
	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.2
	427119	AW880562	Hs.114574	ESTs	3.2
15	437073	AI885608	Hs.94122	ESTs	3.2
	443830	AI142095	Hs.143273	ESTs	3.2
	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	433644	AW342028		gb:hb75d03.x1 NCI_CGAP_Ut2 Homo sapiens	3.2
20	417561	AW974345		gb:EST386449 MAGE resequences, MAGM Homo	3.2
	446063	AI720140	Hs.151079	ESTs	3.2
	423609	AA328348	Hs.218289	ESTs	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.2
	435808	AA702866	Hs.113150	ESTs	3.2
25	424001	W67883	Hs.137476	paternally expressed 10	3.2
	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	3.2
	418946	AI798841	Hs.164526	ESTs	3.2
	431750	AA514986	Hs.283705	ESTs	3.2
	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	3.2
30	428268	AA424957	Hs.294132	ESTs	3.2
	418878	W20090	Hs.6616	ESTs	3.2
	416565	AW000960	Hs.44970	endoplasmic reticulum resident protein 5	3.2
	454288	BE222648	Hs.279458	ESTs, Highly similar to c380A1.1b [H.sap	3.2
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.2
35	404588				3.2
	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
	444910	AI201849		gb:qs76g04.x1 NCI_CGAP_Pr28 Homo sapiens	3.2
	407339	AA777542	Hs.132670	ESTs	3.2
40	414093	BE544867	Hs.283077	centrosomal P4.1-associated protein; unc	3.2
	438458	AW975186		gb:EST387294 MAGE resequences, MAGN Homo	3.2
	419340	AA236590	Hs.87530	ESTs	3.2
	423448	AK000776	Hs.128753	Homo sapiens cDNA FLJ20769 fis, clone CO	3.2
	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	3.2
	421187	NM_014721	Hs.102471	KIAA0680 gene product	3.2
45	419929	U90268	Hs.93810	cerebral cavernous malformations 1	3.2
	429276	AF056085	Hs.198612	G protein-coupled receptor 51	3.2
	423841	AW753867		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	3.2
	438839	AW297945	Hs.128490	ESTs	3.2
50	410085	AA428482	Hs.58589	glycogenin 2	3.2
	427961	AW293165	Hs.143134	ESTs	3.2
	429228	AI553633	Hs.337139	ESTs	3.2
	431548	AI834273	Hs.9711	novel protein	3.1
	441839	AW975512	Hs.29160	ESTs	3.1
55	410389	AW954049	Hs.8177	ESTs, Weakly similar to PIHUB6 salivary	3.1
	441274	AW593781	Hs.131357	ESTs	3.1
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
	438154	AA764950	Hs.119898	ESTs	3.1
	406752	AI285598		gb:qu49f06.x1 NCI_CGAP_Lym6 Homo sapiens	3.1
60	450689	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	3.1
	434164	AW207019	Hs.148135	serine/threonine kinase 33	3.1
	436739	BE208022	Hs.127685	KIAA1627 protein	3.1
	451674	AA019104	Hs.175483	Homo sapiens cDNA: FLJ22016 fis, clone H	3.1
	421166	AA305407	Hs.102308	potassium inwardly-rectifying channel, s	3.1
65	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.1
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.1
	426457	AW894867	Hs.169965	chimerin (chimaerin) 1	3.1
	424780	U39576	Hs.153058	butyrophilin, subfamily 1, member A1	3.1
70	456551	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	3.1
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	3.1
	431814	BE256242	Hs.270847	delta-tubulin	3.1
	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.1
	436401	AI087958	Hs.29088	ESTs	3.1
75	437439	H29796	Hs.269622	ESTs	3.1
	403277				3.1
	408547	AA574291	Hs.57837	ESTs	3.1
	424131	AA335714	Hs.199665	ESTs	3.1
	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN A	3.1
80	434636	AA083764	Hs.6101	hypothetical protein MGC3178	3.1
	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.1
	407905	AW103655	Hs.252905	ESTs	3.1
	452311	AW304029	Hs.252744	ESTs	3.1

	434849	AW292765	Hs.8053	ESTs	3.1
	445770	AV660309	Hs.154986	ESTs, Weakly similar to PLLP_HUMAN PLASM	3.1
	424238	AA337401	Hs.137635	ESTs	3.1
	411643	AI924519	Hs.192570	hypothetical protein FLJ22028	3.1
5	447829	AI433029	Hs.164104	ESTs	3.1
	406506				3.1
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypothe	3.1
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	3.1
10	451229	AW967707	Hs.48473	ESTs	3.1
	401103				3.1
	433589	AA886530	Hs.185912	ESTs	3.1
	459370	AA889982	Hs.271826	ESTs, Weakly similar to I38022 hypothe	3.1
	438533	AI440266	Hs.170673	ESTs, Weakly similar to T24832 hypothe	3.1
	404288				3.1
15	406195				3.1
	438202	AW169287	Hs.22588	ESTs	3.1
	425516	BE000707	Hs.29567	ESTs	3.1
	426572	AB037783	Hs.170523	hypothetical protein FLJ11183	3.1
20	422692	AA332376	Hs.24135	transmembrane protein vezatin; hypothe	3.1
	435414	AW270550	Hs.116957	ESTs	3.1
	418950	T78517	Hs.13941	ESTs	3.1
	426890	AA393167	Hs.41294	ESTs	3.1
	457447	X78261	Hs.272177	H.sapiens mRNA for TRE17 5' extremity an	3.1
25	443773	AV646452	Hs.30941	calcium channel, voltage-dependent, beta	3.1
	459371	R20991		gb:yg06h01.r1 Soares infant brain 1NIB H	3.1
	421823	N40850	Hs.28625	ESTs	3.1
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	3.1
	452896	AA831508	Hs.32553	ESTs	3.1
30	425895	AI269484	Hs.161427	zinc finger protein 215	3.1
	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	3.1
	407340	AA810168	Hs.284289	villig-associated protein VIT-1	3.1
	401862				3.1
	444325	AW152618	Hs.16757	ESTs	3.1
35	408171	AA301228	Hs.43299	hypothetical protein FLJ12890	3.1
	423949	AI014546	Hs.130912	ESTs	3.1
	419519	AI198719	Hs.175376	ESTs	3.0
	434683	AW298724	Hs.202639	ESTs	3.0
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
40	415086	AI597963	Hs.118726	ESTs	3.0
	419220	AA811938	Hs.291759	ESTs	3.0
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	3.0
	443634	H73972	Hs.134460	ESTs	3.0
	429682	NM_006306	Hs.211602	SMC1 (structural maintenance of chromoso	3.0
45	405090				3.0
	432267	AK000872	Hs.274227	Homo sapiens cDNA FLJ10010 fis, clone HE	3.0
	443253	AI041212	Hs.132117	ESTs	3.0
	444974	AI203500	Hs.151612	ESTs	3.0
	445717	AW664658	Hs.149332	ESTs	3.0
50	449347	AV649748	Hs.295901	KIAA0493 protein	3.0
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.0
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.0
	424406	D54120	Hs.146409	cell division cycle 42 (GTP-binding prot	3.0
	410371	AA084482	Hs.115850	ESTs	3.0
	426384	AI472078	Hs.303662	ESTs	3.0
55	418200	AW629751	Hs.206654	ESTs, Weakly similar to alternatively sp	3.0
	427050	AA397789	Hs.161803	ESTs	3.0
	449579	AW207260	Hs.134014	ESTs, Weakly similar to T46425 hypothe	3.0
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo	3.0
60	454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	3.0
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	3.0
	447482	AB033059	Hs.18705	KIAA1233 protein	3.0
	439416	W58294	Hs.56254	ESTs	3.0
	436635	AW104325	Hs.272093	ESTs, Weakly similar to I78885 serine/th	3.0
65	419086	NM_000216	Hs.89591	Kallmann syndrome 1 sequence	3.0
	412566	AW962574		gb:EST374647 MAGE resequences, MAGG Homo	3.0
	415452	F09134	Hs.12839	ESTs	3.0
	427874	AA732367	Hs.98198	ESTs	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
70	454193	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo	3.0
	454678	AW813089		gb:RC3-ST0186-240400-111-b05 ST0186 Homo	3.0
	415122	D60708	Hs.22245	ESTs	3.0
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.0
	400227				3.0
75	411905	BE265067		gb:601193893F1 NIH_MGC_7 Homo sapiens cD	3.0
	419503	AA243642	Hs.137422	ESTs	3.0
	445563	BE326588	Hs.141454	ESTs	3.0
	457285	AI038958	Hs.130522	Kv channel-interacting protein 1	3.0
	434998	AW975157	Hs.26037	ESTs	3.0
80	436203	BE384982	Hs.5076	Homo sapiens cDNA: FLJ22128 fis, clone H	3.0
	424539	L02911	Hs.150402	activin A receptor, type I	3.0
	449856	AA203155	Hs.18200	ESTs	3.0
	427698	AW972594	Hs.294140	ESTs	3.0
	451494	AI799444	Hs.247095	ESTs, Moderately similar to ALU7_HUMAN A	3.0

5	442994	AI026718	Hs.16954	ESTs	3.0
	408165	AL137573	Hs.43143	Homo sapiens mRNA; cDNA DKFZp564A2463 (f	3.0
	421072	AI215069	Hs.89113	ESTs	3.0
	456273	AF154846	Hs.1148	zinc finger protein	3.0
	404548				3.0
10	428201	AA424158	Hs.206461	ESTs	3.0
	441519	AA972740	Hs.127092	ESTs	3.0
	445413	AA151342	Hs.12677	CGI-147 protein	3.0
	418717	AI334430	Hs.86984	ESTs	3.0
	428839	AJ767756	Hs.82302	Homo sapiens cDNA FLJ14814 fts, clone NT	3.0
15	407758	D50915	Hs.38365	KIAA0125 gene product	3.0
	431906	AW328038	Hs.37486	ESTs	3.0
	424968	AA349086	Hs.259746	ESTs, Weakly similar to A46010 X-linked	3.0
	431023	AI283133	Hs.297420	ESTs	3.0
	432596	AJ224741	Hs.278461	matriin 3	3.0
20	452412	AA029608	Hs.61373	ESTs	3.0
	421309	AI222086	Hs.270449	ESTs, Moderately similar to ALU1_HUMAN A	2.9
	438128	AA904430	Hs.122049	ESTs, Weakly similar to T2D4_HUMAN TRANS	2.9
	408321	AW405882	Hs.44205	coristatin	2.9
	439236	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	2.9
25	400880				2.9
	417014	AA251720	Hs.104347	ESTs, Weakly similar to ALUC_HUMAN !!!!	2.9
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	2.9
	406603				2.9
	425573	AB006423	Hs.158308	serine (or cysteine) proteinase inhibito	2.9
30	427878	C05766	Hs.181022	CGI-07 protein	2.9
	451700	AI470262	Hs.29553	ESTs	2.9
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	2.9
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	2.9
	422634	NM_016010	Hs.118821	CGI-62 protein	2.9
35	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.9
	408690	AW864542		gb:PM4-SN0016-120500-003-h02 SN0016 Homo	2.9
	408525	AW206972	Hs.253595	ESTs	2.9
	412248	BE176480		gb:RC3-HT0585-160300-022-c02 HT0585 Homo	2.9
	432507	BE391093	Hs.324667	ESTs	2.9
40	447290	AI476732	Hs.263912	ESTs	2.9
	424188	AW954552	Hs.142634	zinc finger protein	2.9
	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	2.9
	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
45	423119	AA322201	Hs.131976	ESTs	2.9
	423717	AA330036	Hs.152003	ESTs	2.9
	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
	431980	AA523695	Hs.324507	hypothetical protein FLJ20986	2.9
	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	2.9
50	444339	T96555	Hs.31562	ESTs	2.9
	446745	AW118189	Hs.156400	ESTs	2.9
	459201	AW391177		gb:MR3-ST0203-221299-023-d05 ST0203 Homo	2.9
	430573	AA744550	Hs.136345	ESTs	2.9
	451073	AI758905	Hs.206063	ESTs	2.9
55	440575	AA889870	Hs.126006	ESTs	2.9
	402046				2.9
	426882	AA393108	Hs.97365	ESTs	2.9
	435738	AA699633	Hs.269543	ESTs, Weakly similar to A56194 thromboxa	2.9
	420656	AA279098	Hs.187636	ESTs	2.9
60	438323	AI985394	Hs.123369	ESTs	2.9
	453123	AI953718	Hs.221849	ESTs	2.9
	418343	AA216372	Hs.159501	ESTs	2.9
	431595	AA508196		gb:nh60f07.s1 NCI_CGAP_Pr8 Homo sapiens	2.9
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fts, clone HE	2.9
65	459440	BE048054		gb:tz46c03.y1 NCI_CGAP_Bm52 Homo sapien	2.9
	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fts, clone PL	2.9
	408434	AW195317	Hs.107716	hypothetical protein FLJ22344	2.9
	456034	AW450979		gb:UI-H-BI3-ata-a-12-O-UI.s1 NCI_CGAP_Su	2.9
	442118	AA976718	Hs.202242	ESTs	2.9
70	420727	H75701	Hs.99886	complement component 4-binding protein,	2.9
	433849	BE465884	Hs.280728	ESTs	2.9
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.9
	429826	N93266	Hs.40747	ESTs	2.9
	437913	AI140825	Hs.121623	ESTs	2.9
75	441330	AI692884	Hs.129354	ESTs	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fts, clone L	2.9
	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	2.9
	444631	AW995395	Hs.84520	ESTs, Weakly similar to TRHY_HUMAN TRICH	2.9
80	458186	AA904244	Hs.153205	ESTs	2.9
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fts, clone MA	2.9
	415757	AA830854	Hs.187810	ESTs	2.9
	449299	AA299919	Hs.84561	ESTs	2.9
	457003	S78234	Hs.172405	cell division cycle 27	2.9
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	2.9
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	2.9
	426174	AA547959	Hs.115838	ESTs	2.9

	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	2.9
	429950	AW081608	Hs.105053	ESTs	2.9
	412733	AA984472	Hs.74554	KIAA0080 protein	2.9
5	423637	AL137279	Hs.130187	Homo sapiens mRNA: cDNA DKFZp434O1214 (f	2.9
	442655	AW027457	Hs.30323	ESTs, Weakly similar to B34087 hypothe	2.9
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	2.9
	430447	W17064	Hs.332848	SW/SNF related, matrix associated, acti	2.9
	416871	H98716		gb:yx13d08.s1 Soares melanocyte 2NbHM Ho	2.9
10	439737	AJ751438	Hs.41271	Homo sapiens mRNA full length insert cDN	2.9
	406815	AA833930	Hs.288036	tRNA Isopentenylpyrophosphate transferas	2.9
	401094				2.9
	401526				2.9
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	2.9
	417320	AA195667	Hs.86022	ESTs	2.9
15	418282	AA215535	Hs.98133	ESTs	2.9
	442927	AJ024347	Hs.131519	ESTs	2.9
	450006	AJ241555	Hs.60171	ESTs	2.9
	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypothe	2.8
	416623	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone C	2.8
20	403329				2.8
	414696	AF002020	Hs.76918	Niemann-Pick disease, type C1	2.8
	419038	AW134924	Hs.190325	ESTs	2.8
	440106	AA864968	Hs.127699	KIAA1603 protein	2.8
25	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.8
	431745	AW972448	Hs.163425	ESTs	2.8
	421426	AA291101	Hs.33020	Homo sapiens, clone IMAGE:3939163, mRNA,	2.8
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.8
	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	2.8
30	441790	AW294909	Hs.132208	ESTs	2.8
	404443				2.8
	428129	AJ244311	Hs.26912	ESTs	2.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	2.8
	423948	AW392342	Hs.283077	centrosomal P4.1-associated protein; unc	2.8
35	449327	AJ638743	Hs.224672	ESTs	2.8
	400983				2.8
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	2.8
	411213	AA676939	Hs.69285	neuropilin 1	2.8
	420896	AW149342	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	2.8
40	409994	D86864	Hs.57735	acetyl LDL receptor, SREC	2.8
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.8
	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.8
	455092	BE152428		gb:CMO-HT0323-151299-126-b04 HT0323 Homo	2.8
	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
45	440192	AA872282	Hs.190596	ESTs	2.8
	448466	AJ522109	Hs.171066	ESTs	2.8
	414869	AA157291	Hs.21479	ubiquitin 1	2.8
	440351	AF030933	Hs.71179	RAD1 (S. pombe) homolog	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
50	439235	N45513	Hs.46608	ESTs	2.8
	417061	AJ675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	2.8
	434812	AA649860	Hs.189496	ESTs	2.8
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	2.8
	455512	AW983608		gb:RC3-HN0001-240400-012-c01 HN0001 Homo	2.8
55	408380	AF123050	Hs.44532	diubiquitin	2.8
	435990	AJ015862	Hs.131793	ESTs	2.8
	410672	AW794600		gb:RC6-UM0014-170300-022-C05 UM0014 Homo	2.8
	432798	AA565309	Hs.194015	ESTs	2.8
	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHst Homo	2.8
60	438886	AA827728	Hs.128705	ESTs, Weakly similar to AF149422 2 unkno	2.8
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.8
	416940	N75620	Hs.43157	ESTs	2.8
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	2.8
	438398	AA805526	Hs.130277	ESTs	2.8
65	435313	AJ769400	Hs.189729	ESTs	2.8
	414605	BE390440		gb:501283601F1 NIH_MGC_44 Homo sapiens c	2.8
	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstr	2.8
	413195	AA127382	Hs.22404	protease, serine, 12 (neutrophysin, moto	2.8
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	2.8
70	401323				2.8
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	2.8
	428532	AF157326	Hs.184786	TBP-interacting protein	2.8
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	2.8
	436027	AJ864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	2.8
	406970	M29694		gb:Human alpha-I spectrin gene, exon 12.	2.8
75	426172	AA371307	Hs.125056	ESTs	2.8
	452114	N22687	Hs.8236	ESTs	2.8
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	430660	R11884	Hs.100826	ESTs	2.8
80	434138	AA625804		gb:zu86h01.s1 Soares_testis_NHT Homo sap	2.8
	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	2.8
	429881	T80112	Hs.192245	ESTs	2.8
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.8

	409435	AI810721	Hs.95424	ESTs	2.8
	442191	W95186	Hs.8136	endothelial PAS domain protein 1	2.8
	407305	AA715284		gb:uv35f03.r1 NCI_CGAP_Br5 Homo sapiens	2.8
5	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.8
	412189	R60982	Hs.22581	ESTs	2.8
	420976	AI924940	Hs.108082	ESTs, Weakly similar to T31636 hypotheti	2.8
	448330	AL036449	Hs.207163	ESTs	2.8
	418912	NM_000685	Hs.89472	angiotensin receptor 1	2.8
10	422505	AL120852	Hs.124165	ESTs	2.8
	427752	AA470687	Hs.104772	ESTs	2.8
	433513	AI566356	Hs.171437	ESTs	2.8
	433703	AA210863	Hs.3532	nemo-like kinase	2.8
	448912	D83781	Hs.22559	KIAA0197 protein	2.8
	405621				2.8
15	430687	BE274217	Hs.249247	heterogeneous nuclear protein similar to	2.8
	450400	AI694722	Hs.279744	ESTs	2.8
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.8
	418342	BE002723	Hs.226627	leptin receptor	2.8
20	420756	AA411800	Hs.189900	ESTs	2.8
	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	440320	AA879294		gb:mv86e09.s1 NCI_CGAP_Pr12 Homo sapiens	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
	439831	AW136488	Hs.25545	ESTs	2.8
25	425661	AL133627	Hs.158923	Homo sapiens mRNA; cDNA DKFZp434K0722 (f	2.8
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	2.8
	418658	AW874263	Hs.32468	ESTs	2.8
	409978	D31897	Hs.57714	double C2-like domains, alpha	2.8
	421340	F07783	Hs.1369	decay accelerating factor for complement	2.8
30	449071	NM_005872	Hs.22960	breast carcinoma amplified sequence 2	2.8
	409241	AF070802	Hs.51649	Homo sapiens clone 24504 mRNA sequence	2.8
	448219	AA228092	Hs.42556	KIAA1681 protein	2.8
	408936	AL138043	Hs.293549	ESTs	2.8
	410784	AW803201		gb:IL2-UM0077-070500-080-E06 UM0077 Homo	2.8
35	426471	M22440	Hs.170009	transforming growth factor, alpha	2.8
	454455	AW752710		gb:IL3-CT0219-281099-024-A03 CT0219 Homo	2.8
	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
	401335				2.7
	436577	W84774	Hs.17643	ESTs	2.7
40	409519	AA075368		gb:zm86h10.r1 Stratagene ovarian cancer	2.7
	421003	T72080	Hs.95657	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	2.7
	436007	AI247716	Hs.232168	ESTs	2.7
45	408874	AW818091	Hs.252730	ESTs	2.7
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	2.7
	435625	H50654	Hs.113999	ESTs	2.7
	435766	R11673	Hs.186498	ESTs	2.7
	410327	T33130	Hs.301746	RAP2A, member of RAS oncogene family	2.7
50	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
	417177	NM_004458	Hs.81452	fatty acid-Coenzyme A ligase, long-chain	2.7
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.7
	427134	AA398409	Hs.173561	EST	2.7
	428137	AA421792	Hs.170999	ESTs	2.7
55	429710	AI337113	Hs.146025	hypothetical protein FLJ23594	2.7
	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.7
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.7
	441928	AI370188	Hs.211454	ESTs	2.7
	409721	AW887732	Hs.257861	ESTs	2.7
60	427112	Z32887	Hs.290951	ESTs	2.7
	403776				2.7
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.7
	427839	AA608823	Hs.98244	ESTs	2.7
	432837	AA310693	Hs.87329	HSPC072 protein	2.7
65	438782	AA828380	Hs.126733	ESTs	2.7
	449396	BE169100	Hs.195029	ESTs	2.7
	458043	AW979009	Hs.326108	ESTs	2.7
	438171	AW976507	Hs.293515	ESTs	2.7
	452959	AI933416	Hs.189674	ESTs	2.7
70	439556	AI623752	Hs.163603	ESTs	2.7
	446152	AI292036	Hs.150028	ESTs	2.7
	434803	AW974640	Hs.303413	ESTs	2.7
	407771	AL138272	Hs.62713	ESTs	2.7
	411069	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	2.7
75	417543	AA203620	Hs.110153	ESTs	2.7
	401517				2.7
	403677				2.7
	416337	H48713		gb:yq78d02.r1 Soares fetal liver spleen	2.7
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.7
80	446800	AI341635	Hs.156485	ESTs	2.7
	457906	AW975939	Hs.153290	Homo sapiens cDNA FLJ14318 fis, clone PL	2.7
	452277	AL049013	Hs.28783	KIAA1223 protein	2.7
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.7
	416370	N90470	Hs.203697	ESTs, Weakly similar to t38022 hypotheti	2.7

	408715	AA768873	Hs.112250	hypothetical protein FLJ23518	2.7
	410743	AA089474	Hs.272153	ESTs	2.7
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.7
5	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.7
	427565	AI287280	Hs.97933	ESTs, Weakly similar to T46370 hypotheti	2.7
	406092				2.7
	410008	AA079552		gb:zm20h12.s1 Stratagene pancreas (93720	2.7
	438504	AW665281	Hs.224625	ESTs	2.7
10	414783	AW069569	Hs.278270	inactive progesterone receptor, 23 kD	2.7
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	2.7
	418686	Z36830	Hs.87268	annexin A8	2.7
	413795	AL040178	Hs.142003	ESTs	2.7
	457528	AW973791	Hs.292784	ESTs	2.7
15	444230	H95537	Hs.146067	ESTs	2.7
	403760				2.7
	416624	H69044		gb:yr77h05.s1 Soares fetal liver spleen	2.7
	428904	AI312526	Hs.46640	ESTs	2.7
	446311	AW007294	Hs.149795	ESTs, Moderately similar to ALU1_HUMAN A	2.7
20	458638	N78553	Hs.282204	nucleosomal binding protein 1	2.7
	459267	AJ003631		gb:AJ003631 Selected chromosome 21 cDNA	2.7
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	2.7
	433906	AI67816	Hs.43355	ESTs	2.7
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	2.7
25	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked mol	2.7
	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	2.7
	421585	U95626	Hs.302043	chemokine (C-C motif) receptor-like 2	2.7
	445158	AI992108	Hs.127206	ESTs	2.7
	421175	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transe	2.7
30	401793				2.7
	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	427038	NM_014633	Hs.173268	KIAA0155 gene product	2.7
	451343	AW975057	Hs.293353	ESTs	2.7
	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
35	438475	W03856	Hs.13188	ESTs, Highly similar to Gene product wil	2.7
	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	2.7
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	2.7
	407930	AA045847	Hs.188351	Homo sapiens cDNA FLJ12807 fis, clone NT	2.7
	453891	AB037751	Hs.36353	Homo sapiens mRNA full length insert cDN	2.7
40	451487	AA018072		gb:ze51g02.r1 Soares retina N2b4HR Homo	2.7
	418269	AA806113	Hs.189025	ESTs	2.7
	419196	AF110908	Hs.297660	TNF receptor-associated factor 3	2.7
	459160	AI904723		gb:CM-BT066-120299-092 BT066 Homo sapien	2.7
	441963	AI733307	Hs.128002	ESTs	2.7
45	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.7
	426902	AI125334	Hs.97408	ESTs	2.7
	414271	AK000275	Hs.75871	protein kinase C binding protein 1	2.7
	453313	BE005771	Hs.153746	hypothetical protein FLJ22490	2.7
	445265	AI218295	Hs.144942	ESTs	2.7
50	422988	AW673847	Hs.97321	ESTs	2.7
	428613	AB037749	Hs.186928	KIAA1328 protein	2.7
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A45010 X-fin	2.7
	457300	AW297436	Hs.158849	Homo sapiens cDNA: FLJ21663 fis, clone C	2.7
	402800				2.7
55	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.7
	414729	BE466928	Hs.281901	ESTs	2.7
	453716	AA037675	Hs.152675	ESTs	2.7
	452693	T79153	Hs.48589	zinc finger protein 228	2.7
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	2.7
60	443305	AI050693	Hs.133318	ESTs	2.7
	416709	R99369	Hs.283108	hemoglobin, gamma G	2.7
	419077	AA233885	Hs.164526	ESTs	2.7
	453878	AW964440	Hs.19025	DC32	2.7
	445660	AI702668	Hs.201955	ESTs	2.7
65	446817	AI700684	Hs.134166	ESTs	2.7
	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	2.6
	410406	AI969703	Hs.1466	glycerol kinase	2.6
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	2.6
	407830	NM_001086	Hs.587	arylacetamide deacetylase (esterase)	2.6
70	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	2.6
	407055	X89211		gb:Hsapiens DNA for endogenous retrovir	2.6
	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 integrin	2.6
	440310	AA878939	Hs.125406	ESTs	2.6
	425659	AK000590	Hs.158836	hypothetical protein FLJ20583	2.6
75	418217	AI910647	Hs.13442	ESTs	2.6
	428667	AI375550	Hs.74407	nucleolar protein p40; homolog of yeast	2.6
	414573	AI821846	Hs.71999	ESTs	2.6
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	2.6
	452821	AW471181	Hs.160874	ESTs	2.6
80	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	2.6
	428483	AI908539	Hs.321444	KIAA0344 gene product	2.6
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	2.6
	405059				2.6
	425178	H16097	Hs.161027	ESTs	2.6

	442952	AI743261	Hs.131860	ESTs	2.6
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	2.6
	456179	H75490	Hs.271930	ESTs	2.6
5	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	2.6
	459456	AA486036	Hs.190124	ESTs	2.6
	425527	AL162032	Hs.158258	Homo sapiens mRNA; cDNA DKFZp434B1272 (I	2.6
	424711	NM_005795	Hs.152175	calcitonin receptor-like	2.6
	417956	AA210704	Hs.190465	ESTs	2.6
10	420621	AA278608		gb:zs79c09.r1 NCI_CGAP_GC81 Homo sapiens	2.6
	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
	438295	AI394151	Hs.37932	ESTs	2.6
	445550	AI242754	Hs.137306	ESTs	2.6
	450469	AI955049	Hs.281326	ESTs	2.6
15	458804	AL157625		gb:DKFZp761L2016_r1 761 (synonym: hamy2)	2.6
	443657	R14973		gb:yf42f10.s1 Soares fetal liver spleen	2.6
	429250	H56585	Hs.198308	tryptophan rich basic protein	2.6
	437906	AA771704	Hs.194626	ESTs	2.6
	426775	AA384564	Hs.108829	ESTs	2.6
20	443372	AI792557	Hs.133107	ESTs	2.6
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.6
	425465	L18964	Hs.1904	protein kinase C, iota	2.6
	422746	NM_004484	Hs.119551	glypican 3	2.6
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	2.6
25	424527	AW138558	Hs.267158	ESTs, Weakly similar to I54374 gene NF2	2.6
	414180	AI863304	Hs.120905	Homo sapiens cDNA FLJ11448 fis, clone HE	2.6
	411402	BE297855	Hs.69855	NRAS-related gene	2.6
	445264	AI218263	Hs.323472	EST	2.6
	458861	AI630223		gb:ad06g08.r1 Proliferating Erythroid Ce	2.6
30	415227	AW821113	Hs.72402	ESTs	2.6
	435429	AW592035	Hs.254414	ESTs, Weakly similar to 18051958 RNA-bin	2.6
	434445	AI349306	Hs.11782	ESTs	2.6
	448570	AI923944	Hs.30913	ESTs	2.6
	452381	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
35	422879	AI241409	Hs.188092	ESTs	2.6
	409026	AL137554	Hs.49927	protein kinase NYD-SP15	2.6
	425717	X07282	Hs.171495	retinoic acid receptor, beta	2.6
	429127	AA749382	Hs.118797	ubiquitin-conjugating enzyme E2D 3 (homo	2.6
	438298	H23542	Hs.181788	ESTs	2.6
40	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.6
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.6
	444517	AI939339	Hs.146683	ESTs	2.6
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.6
45	452453	AI902519		gb:QV-BT009-101198-051 BT009 Homo sapien	2.6
	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6
	437939	AW298600	Hs.141840	ESTs, Weakly similar to S59501 interfero	2.6
	430719	AA488988	Hs.293796	ESTs	2.6
	452864	AA033714	Hs.287629	hypothetical protein FLJ14260	2.6
	432095	AW022273	Hs.105769	ESTs	2.6
50	431088	AI829692	Hs.211561	ESTs	2.6
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	2.6
	423952	AW877787	Hs.136102	KIAA0853 protein	2.6
	453403	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	2.6
	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.6
55	430933	AW863635		gb:MR3-SN0010-270300-103-h02 SN0010 Homo	2.6
	420691	AA829433	Hs.275343	ESTs	2.6
	429761	AI276780	Hs.135173	ESTs	2.6
	437958	BE139550	Hs.121668	ESTs, Moderately similar to PC4259 ferri	2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
60	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.6
	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	2.6
	438647	AA813118	Hs.163230	ESTs	2.6
	438192	AI859065	Hs.337620	Homo sapiens AFG3L1 isoform 1 mRNA, part	2.6
65	417218	AA005247	Hs.285754	met proto-oncogene (hepatocyte growth fa	2.6
	440460	H92571	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	414612	BE274552	Hs.76578	protein inhibitor of activated STAT3	2.6
	428170	H05530	Hs.12585	ESTs	2.6
	457343	NM_013936	Hs.247852	olfactory receptor, family 12, subfamily	2.6
70	424020	R76946	Hs.39738	ESTs	2.6
	455226	AW902103		gb:QV0-NN1022-120500-220-c07 NN1022 Homo	2.6
	411965	BE467339	Hs.280115	ESTs	2.6
	432656	NM_000246	Hs.3076	MHC class II transactivator	2.6
	455488	AA102322		gb:zd90f03.r1 Stratagene colon (937204)	2.6
75	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.6
	404285				2.6
	418744	AI887288	Hs.196379	ESTs, Weakly similar to putative p150 [H	2.6
	454714	AW815098		gb:QV4-ST0212-091199-023-f10 ST0212 Homo	2.6
	429828	AB019494	Hs.225767	IDN3 protein	2.6
80	436387	AA714760	Hs.240075	Homo sapiens cDNA FLJ13234 fis, clone OV	2.6
	448587	AI539652	Hs.28338	KIAA1546 protein	2.6
	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	2.6
	440479	AA886461	Hs.208161	ESTs	2.6
	443160	AA467915	Hs.36053	ESTs	2.6

	428978	AA442784	Hs.125445	ESTs	2.5
	444570	H58373	Hs.332938	hypothetical protein MGC5370	2.5
	453459	BE047032	Hs.257789	ESTs	2.5
5	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	2.5
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.5
	414373	AW162907	Hs.75969	proline-rich protein with nuclear target	2.5
	458760	AA98631	Hs.111334	ferritin, light polypeptide	2.5
	434131	AI858275	Hs.143659	ESTs	2.5
10	441805	AA285136	Hs.301914	neuronal specific transcription factor D	2.5
	457292	AI921270	Hs.334882	hypothetical protein FLJ14251	2.5
	417351	T90278	Hs.15049	ESTs	2.5
	409695	AA296961		gb:EST112514 Adrenal gland tumor Homo sa	2.5
	432824	AK001783	Hs.279012	hypothetical protein FLJ10921	2.5
15	438038	AI732629	Hs.194161	ESTs, Weakly similar to TA2R HUMAN, BETA	2.5
	454836	AW833711		gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
	453919	AW959912	Hs.7076	KIAA1705 protein	2.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	2.5
	408727	AL137259	Hs.47115	hypothetical protein DKFZp434D0513	2.5
20	427491	R43279	Hs.22574	ESTs, Weakly similar to t38022 hypothei	2.5
	435102	AW899053	Hs.76917	F-box only protein 8	2.5
	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	2.5
	455866	BE149024		gb:CM0-HT0249-291099-084-c04 HT0249 Homo	2.5
	432887	AI926047	Hs.162859	ESTs	2.5
25	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5
	401078				2.5
	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	2.5
	425201	AA352111		gb:EST60061 Activated T-cells XX Homo sa	2.5
30	457112	AW772449	Hs.268081	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.5
	455252	AW876627		gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
	444542	AJ161293	Hs.280380	aminopeptidase	2.5
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	2.5
	428497	BE010877	Hs.98584	ESTs	2.5
	457336	AW969657	Hs.291029	ESTs	2.5
35	427621	BE621182	Hs.179882	hypothetical protein FLJ12443	2.5
	423782	AJ472209	Hs.323117	ESTs	2.5
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	2.5
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	2.5
	408562	AA436323	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	2.5
40	417137	U46265	Hs.81281	mitochondrial ribosomal protein S21	2.5
	436787	AA908554	Hs.192756	ESTs	2.5
	440331	AL046412	Hs.202151	ESTs	2.5
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.5
	417169	R13550	Hs.246773	ESTs	2.5
45	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	2.5
	455286	BE144384		gb:MR0-HT0166-191199-004-c11 HT0166 Homo	2.5
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5
	400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	2.5
	415747	AA381209		gb:EST94257 Activated T-cells I Homo sap	2.5
50	446346	AI290205	Hs.309940	ESTs	2.5
	450209	AW008921	Hs.13138	Homo sapiens, clone IMAGE:3448343, mRNA,	2.5
	453202	AW085781	Hs.26270	hypothetical protein FLJ11588	2.5
	425523	AB007948	Hs.158244	KIAA0479 protein	2.5
	433124	U51712	Hs.13775	hypothetical protein SMAP31	2.5
55	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.5
	425657	T89839	Hs.119471	ESTs	2.5
	401254				2.5
	426604	H53354	Hs.97141	ESTs, Weakly similar to hypothetical pro	2.5
	449535	W15267	Hs.23672	low density lipoprotein receptor-related	2.5
60	433138	AB029496	Hs.59729	semaphorin sem2	2.5
	425804	BE501698	Hs.258189	ESTs	2.5
	429515	AL031228	Hs.204370	DNA segment on chromosome 6 (unique, pse	2.5
	437267	AW511443	Hs.258110	ESTs	2.5
	454305	BE062633	Hs.28338	KIAA1546 protein	2.5
65	455631	BE063031		gb:MR0-BT0265-231199-002-e09 BT0265 Homo	2.5
	401878				2.5
	450350	T97817	Hs.174880	ESTs	2.5
	436532	AA721522		gb:nv54h12r1 NCL_CGAP_Ew1 Homo sapiens	2.5
	457450	AI143312	Hs.129206	casein kinase 1, gamma 3	2.5
70	427304	AA761526	Hs.163853	ESTs	2.5
	419721	NM_001650	Hs.288650	aquaporin 4	2.5
	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	2.5
	446252	AI283125	Hs.150099	ESTs	2.5
	421229	AI056590	Hs.7086	hypothetical protein MGC12435	2.5
75	434273	AA913143	Hs.26303	ESTs	2.5
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	2.5
	434353	AA630863	Hs.131375	ESTs, Moderately similar to ALUB_HUMAN !	2.5
	436198	AK001125	Hs.300922	Homo sapiens cDNA FLJ10263 fis, clone HE	2.5
	452232	AW020603	Hs.158423	radial spoke protein 3	2.5
80	433764	AW753676	Hs.39982	ESTs	2.5
	412050	H96503	Hs.109087	Homo sapiens cDNA: FLJ22845 fis, clone K	2.5
	422342	AA309272		gb:EST180209 Liver, hepatocellular carci	2.5
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	2.5
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.5

	408813	AI580090	Hs.48295	RNA helicase family	2.5
	414109	BE250744		gb:600943376F1 NIH_MGC_17 Homo sapiens c	2.5
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.5
	419985	H66373	Hs.15973	ESTs, Highly similar to bA393J16.3 [H.sa	2.5
5	417859	T26453		gb:AB214F6R Infant brain, LNL array of	2.5
	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	2.5
	448015	AI458065	Hs.23196	ESTs	2.5
	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
10	445865	AI262584	Hs.145575	ESTs	2.5
	451800	AW977435	Hs.323867	ESTs	2.5
	456987	AI557290	Hs.173536	ESTs	2.5
	403568				2.5
	435209	AW027809	Hs.187698	Homo sapiens cytomegalovirus partial fus	2.5
	430371	D87466	Hs.240112	KIAA0276 protein	2.5
15	418033	W68180	Hs.259855	elongation factor-2 kinase	2.5
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.5
	453519	H87648	Hs.33922	Homo sapiens, clone MGC:9084, mRNA, comp	2.5
	431071	AA491379		gb:aa65f05.r1 NCI_CGAP_GCB1 Homo sapiens	2.5
20	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	2.5
	409045	AA635062	Hs.50094	Homo sapiens mRNA; cDNA DKFZp43400515 (f	2.5
	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	2.4
	417318	AW953937	Hs.12891	ESTs	2.4
25	413382	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.4
	406748	AW339106	Hs.217493	annexin A2	2.4
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	2.4
	441817	AW969706	Hs.293332	ESTs	2.4
	450551	AI010046	Hs.25155	neuroepithelial cell transforming gene 1	2.4
30	457940	AL360159	Hs.306517	Homo sapiens TRIPartite motif protein ps	2.4
	446135	AW130288	Hs.170318	hypothetical protein FLJ10147	2.4
	436907	AA737171	Hs.131809	ESTs	2.4
	429399	AA452244	Hs.16727	ESTs	2.4
	448782	AL050295	Hs.22039	KIAA0758 protein	2.4
35	434404	AW445034	Hs.256578	ESTs	2.4
	428571	NM_006531	Hs.2291	Probe hTg737 (polycystic kidney disease,	2.4
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	2.4
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	2.4
	450705	U90304	Hs.25351	iroquois homeobox protein 5	2.4
40	425506	NM_003666	Hs.158205	basic leucine zipper nuclear factor 1 (J	2.4
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fascilin	2.4
	458986	AI802772	Hs.208655	ESTs	2.4
	443861	AW449462	Hs.134743	ESTs	2.4
	412879	BE092219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo	2.4
45	415250	F02614	Hs.27319	ESTs	2.4
	434627	AI221894	Hs.39311	ESTs	2.4
	443919	AI091284	Hs.135224	ESTs, Weakly similar to A47582 B-cell gr	2.4
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypotheli	2.4
	400385	NM_020389	Hs.283104	putative capacitative calcium channel	2.4
50	411322	AW887330	Hs.172405	cell division cycle 27	2.4
	434638	H50758		gb:ryp86e06.r1 Soares fetal liver spleen	2.4
	435559	AF209198	Hs.42636	zinc finger protein 277	2.4
	447849	AI538147	Hs.164277	ESTs	2.4
	448005	AW207437	Hs.170378	ESTs	2.4
55	454201	AB023191	Hs.44131	KIAA0974 protein	2.4
	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.4
	449486	AI652715	Hs.270811	ESTs	2.4
	421516	AI362418	Hs.105379	FT005 protein	2.4
	412167	AW897230		gb:CM0-NN0057-150400-335-a11 NN0057 Homo	2.4
60	426910	AA470023	Hs.190089	ESTs, Moderately similar to ALU1_HUMAN A	2.4
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	2.4
	400641				2.4
	430576	AA767125	Hs.293574	ESTs	2.4
	434423	NM_006769	Hs.3844	LIM domain only 4	2.4
65	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	2.4
	441499	AW298235	Hs.101689	ESTs	2.4
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.4
	417819	AI253112	Hs.133540	ESTs	2.4
	431728	NM_007351	Hs.268107	multimerin	2.4
70	425025	AW953168	Hs.12407	ESTs	2.4
	421168	AF182277	Hs.330780	cytochrome P450, subfamily IIB (phenobar	2.4
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.4
	408867	AA437199	Hs.656	cell division cycle 25C	2.4
	439446	AI927629	Hs.57873	ESTs	2.4
	445038	AI635444	Hs.143917	dJ467N11.1 protein	2.4
75	450682	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	2.4
	455107	BE154113		gb:PM1-HT0340-151299-003-a08 HT0340 Homo	2.4
	458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	2.4
	428784	Y12851	Hs.193470	purinergic receptor P2X, ligand-gated io	2.4
80	453864	AW021407	Hs.21068	hypothetical protein	2.4
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	2.4
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.4
	426603	AA382291		gb:EST95683 Testis I Homo sapiens cDNA 5	2.4

	447357	AJ375922	Hs.159367	ESTs	2.4
	452631	AJ188658	Hs.87496	ESTs	2.4
	405041				2.4
	405472				2.4
5	409744	AW675258	Hs.56265	Homo sapiens mRNA; cDNA DKFZp586P2321 (f	2.4
	433868	AA612960	Hs.337300	ESTs	2.4
	437119	AJ379921	Hs.177043	ESTs	2.4
	455114	AW857121		gb:RC1-CT0302-040400-017-a12 CT0302 Homo	2.4
	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.4
10	434936	AI285970	Hs.183817	ESTs	2.4
	408918	BE218603	Hs.279708	ESTs	2.4
	444106	AI123922	Hs.138215	Homo sapiens cDNA FLJ11400 fts, clone HE	2.4
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	2.4
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	2.4
15	446659	AJ335361	Hs.226376	ESTs	2.4
	418636	AW749855		gb:QV4-BT0534-281299-053-c05 BT0534 Homo	2.4
	434995	AW974895		gb:EST387100 MAGE resequences, MAGN Homo	2.4
	438005	BE151746		gb:PM1-HT0305-061299-003-a06 HT0305 Homo	2.4
	444755	AA431791	Hs.113823	CtpX (caseinolytic protease X, E. coli)	2.4
20	427131	AA448460	Hs.112017	GE36 gene	2.4
	442039	AW276240	Hs.128352	ESTs	2.4
	448595	AB014544	Hs.21572	KJAA0644 gene product	2.4
	432949	AA570749	Hs.298866	ESTs	2.4
25	444314	AJ140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	2.4
	417420	T85150	Hs.268814	ESTs	2.4
	427551	T96203		gb:ye48b07.r1 Soares fetal liver spleen	2.4
	420057	AA806899	Hs.184387	ESTs	2.4
	434950	AW974892		gb:EST386997 MAGE resequences, MAGN Homo	2.4
30	425497	AA524596		gb:nh34b02.s1 NCI_CGAP_Pr3 Homo sapiens	2.4
	438214	H06076	Hs.26320	TRABID protein	2.4
	416100	H18700	Hs.268799	ESTs	2.4
	419637	W27493		gb:31h10 Human retina cDNA randomly prim	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
35	454403	BE065985		gb:RC3-BT0319-120200-014-a09 BT0319 Homo	2.4
	419179	AW275281	Hs.113009	hypothetical protein FLJ22527	2.4
	436391	AJ227892	Hs.146274	ESTs	2.4
	449511	AI436187	Hs.296261	guanine nucleotide binding protein (G pr	2.4
	447499	AW262580	Hs.147674	protocadherin beta 16	2.4
40	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.4
	412877	BE011168		gb:PM3-BN0218-100500-003-d08 BN0218 Homo	2.4
	435985	AA703154	Hs.191934	ESTs	2.4
	440674	BE561546		gb:601347208F1 NIH_MGC_8 Homo sapiens cD	2.4
	446476	AW294072	Hs.141376	ESTs	2.4
45	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.4
	435731	AA699581	Hs.186811	ESTs	2.4
	437105	AA744554	Hs.222127	ESTs	2.4
	406091				2.4
	457024	AA397546	Hs.119151	ESTs	2.4
50	404249				2.4
	419556	U29615	Hs.91093	chitinase 1 (chitinobiosidase)	2.4
	424943	AU077260	Hs.153924	death-associated protein kinase 1	2.4
	444229	AV648613	Hs.282397	ESTs	2.4
	404860				2.4
55	432223	AA333283	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	2.4
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.4
	420843	H96982	Hs.42321	ESTs	2.4
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.4
	413642	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo	2.4
60	436998	AA745625	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	441235	AI884586	Hs.135570	Homo sapiens cDNA: FLJ21268 fts, clone C	2.4
	445748	U80766	Hs.13252	Human EST clone 22453 mariner transposon	2.4
	451018	AW965599	Hs.247324	mitochondrial ribosomal protein S14	2.4
	409073	AA063458		gb:zf71a07.s1 Soares_pineal_gland_N3HPG	2.3
65	418782	AJ792648	Hs.14665	ESTs	2.3
	447870	BE139479	Hs.161492	ESTs	2.3
	437370	AL359567	Hs.161962	Homo sapiens mRNA; cDNA DKFZp547D023 (fr	2.3
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	2.3
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypothei	2.3
	424049	AB014524	Hs.138380	KIAA0624 protein	2.3
70	425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	2.3
	430702	U56979	Hs.250651	H factor 1 (complement)	2.3
	409620	AA076278	Hs.13277	hypothetical protein FLJ22054	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
	430884	AF053748	Hs.243114	glial cell derived neurotrophic factor	2.3
75	445523	Z30118	Hs.293788	ESTs, Moderately similar to unnamed prot	2.3
	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	2.3
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	2.3
	417583	AA668782	Hs.191284	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
80	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fts, clone H	2.3
	404513				2.3
	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo	2.3
	448506	AJ524673	Hs.38170	ESTs	2.3
	434811	AW971205	Hs.114280	ESTs	2.3

	457065	AI476318	Hs.192480	ESTs	2.3
	407945	X59208	Hs.606	ATPase, Cu ⁺⁺ transporting, alpha polypep	2.3
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	2.3
	423596	AA328195	Hs.234101	ESTs, Weakly similar to CTL1 protein [H]	2.3
5	455807	BE141140		gb:MR0-HT0075-021299-006-d07 HT0075 Homo	2.3
	435867	AA954229	Hs.114052	ESTs	2.3
	440196	N72847	Hs.125221	ESTs	2.3
	401213				2.3
	407291	AA001464		gb:ze45b01.r1 Soares retina NZb4HR Homo	2.3
10	442490	AW965078	Hs.30212	thyroid receptor interacting protein 15	2.3
	452943	BE247449	Hs.31082	hypothetical protein FLJ10525	2.3
	438138	R98299	Hs.177502	ESTs	2.3
	440283	AI732892	Hs.190489	ESTs	2.3
	447039	AV661798	Hs.282915	ESTs	2.3
15	412777	AI335773	Hs.270123	ESTs	2.3
	421424	AW452690	Hs.258775	ESTs	2.3
	406673	M34996	Hs.198253	major histocompatibility complex, class	2.3
	440555	D31292	Hs.6853	hypothetical protein FLJ22167	2.3
	451516	AI800515	Hs.12024	ESTs	2.3
20	424890	BE538356	Hs.151777	eukaryotic translation initiation factor	2.3
	421046	AA810854	Hs.89081	ESTs	2.3
	423604	AA486585	Hs.258901	ESTs	2.3
	409029	BE087807		gb:QV1-BT0681-290400-181-g02 BT0681 Homo	2.3
	444206	AW301017	Hs.146492	ESTs	2.3
25	451836	T63673	Hs.173220	ESTs	2.3
	454784	AW820626		gb:RC0-ST0299-190100-012-e10 ST0299 Homo	2.3
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.3
	436671	AW137159	Hs.146151	ESTs	2.3
	434988	AI418055	Hs.161160	ESTs	2.3
30	452862	AW378065	Hs.8687	ESTs	2.3
	439480	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	2.3
	410606	AW418779	Hs.114889	ESTs	2.3
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	2.3
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	2.3
35	430217	N47863	Hs.336901	ribosomal protein S24	2.3
	417479	AI057052	Hs.133554	ESTs, Weakly similar to Z195_HUMAN ZINC	2.3
	421253	AI188102	Hs.31028	ESTs	2.3
	438180	AA808189	Hs.272151	ESTs	2.3
	439715	AA524504	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
40	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypothe	2.3
	443055	AV653742	Hs.15536	hypothetical protein DKFZp761J139	2.3
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	2.3
	448831	AL080123	Hs.22182	zinc finger protein Z3 (KOK 16)	2.3
	412953	Z45794	Hs.238809	ESTs	2.3
45	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78865 serine/th	2.3
	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.3
	423003	AL120077	Hs.122967	kelch (Drosophila)-like 2 (Mayven)	2.3
	428595	AB037795	Hs.186547	KIAA1374 protein	2.3
	437887	AA811524	Hs.29263	hypothetical protein FLJ11896	2.3
50	447720	AL038765	Hs.161304	ESTs	2.3
	452355	N54926	Hs.29202	G protein-coupled receptor 34	2.3
	408374	AW025430	Hs.155591	forkhead box F1	2.3
	440381	AA917808	Hs.190495	ESTs	2.3
	425478	AB007953	Hs.268840	ESTs	2.3
55	432231	AA339977	Hs.274127	CLST 11240 protein	2.3
	431757	AA196930	Hs.268526	Homo sapiens chromosome 21q22.1 anonymou	2.3
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	2.3
	452837	AL121053	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	2.3
	417426	NM_002291	Hs.82124	laminin, beta 1	2.3
60	423739	AA398155	Hs.97600	ESTs	2.3
	416847	L43821	Hs.80261	enhancer of filamentation 1 (cas-like do	2.3
	425876	AW005887	Hs.234058	ESTs	2.3
	457411	AW085961	Hs.130093	ESTs	2.3
	413136	BE066941		gb:PM0-BT0340-091299-002-e11 BT0340 Homo	2.3
65	420313	AB023230	Hs.96427	KIAA1013 protein	2.3
	421751	AW813731	Hs.159153	ESTs, Moderately similar to S65657 alpha	2.3
	424827	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fis, clone L	2.3
	436331	AI239495	Hs.120189	ESTs	2.3
	439275	AF086093	Hs.141566	ESTs	2.3
70	449272	AW137656	Hs.197645	ESTs	2.3
	454352	AW389668		gb:RC2-ST0168-071299-013-06 ST0168 Homo	2.3
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	2.3
	407242	M18728		gb:Human nonspecific crossreacting anti	2.3
	445326	AI220072	Hs.165893	ESTs	2.3
75	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.3
	452607	AI160029	Hs.61438	ESTs	2.3
	423161	AI049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (I	2.3
	418851	AI417828	Hs.192435	ESTs	2.3
	458332	AI000341	Hs.220491	ESTs	2.3
80	432565	AA553477	Hs.152428	ESTs	2.3
	437511	AI807500	Hs.125247	ESTs	2.3
	430957	AI937072	Hs.55043	Homo sapiens cDNA FLJ13277 fis, clone OV	2.3
	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	2.3

5	448225	AI476429	Hs.19238	ESTs	2.3
	408955	BE315170	Hs.8087	NAG-5 protein	2.3
	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
	419699	AA248998	Hs.173044	ESTs, Weakly similar to 138022 hypothetical	2.3
	428976	AL037824	Hs.194695	ras homolog gene family, member I	2.3
10	458925	R15891	Hs.281587	Human (clone CTG-AA) mRNA sequence	2.3
	440348	AW015802	Hs.47023	ESTs	2.3
	436340	R42246	Hs.21606	ESTs	2.3
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	2.3
	438462	AI624122	Hs.89578	general transcription factor IIH, polype	2.3
15	411124	AW196937	Hs.53929	ESTs, Weakly similar to ALUB_HUMAN III	2.3
	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	2.3
	412505	AA974491	Hs.21734	ESTs	2.3
	418236	AW994005	Hs.337534	ESTs	2.3
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	2.3
20	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.3
	418565	AK001529	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.3
	433404	T32982	Hs.102720	ESTs	2.3
	409517	X90780	Hs.120036	troponin I, cardiac	2.3
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	2.3
25	445641	AI245987	Hs.149442	ESTs	2.3
	449276	AW241510	Hs.252713	ESTs	2.3
	436547	AJ297351	Hs.30824	leucine zipper transcription factor-like	2.3
	437770	AA767881	Hs.122897	ESTs	2.3
	409064	AA062954	Hs.141883	ESTs	2.3
30	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.3
	449869	W57990	Hs.60059	Homo sapiens cDNA FLJ11478 fis, clone HE	2.3
	422108	AA297914	Hs.111749	postmeiotic segregation increased (S. ce	2.3
	418251	AA832123	Hs.177723	ESTs	2.3
	432005	AA524190	Hs.120777	ESTs, Weakly similar to ELL2_HUMAN RNA P	2.3
35	413638	H71252		gb:ys12h12.s1 Soares fetal liver spleen	2.3
	415980	R52414		gb:yg80b05.r1 Soares infant brain 1N1B H	2.3
	449232	AW192780	Hs.196080	ESTs	2.3
	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	2.3
	454389	AW752571		gb:IL3-CT0213-170100-055-F02 CT0213 Homo	2.3
40	438089	W05391	Hs.83623	nuclear receptor subfamily 1, group I, m	2.3
	400238				2.3
	404488				2.3
	407809	AW082279	Hs.244106	ESTs	2.3
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.3
45	420478	AA521259	Hs.193796	ESTs	2.3
	422711	D60641	Hs.21739	Homo sapiens mRNA; cDNA DKFZp586i1518 (f	2.3
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kD (con	2.3
	426567	AA381579	Hs.182962	ESTs	2.3
	435708	AI362949	Hs.75169	ESTs	2.3
50	441417	AI733297	Hs.144474	ESTs	2.3
	445117	AI208754	Hs.147369	ESTs	2.3
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.2
	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	2.2
	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	2.2
55	445280	AW055063	Hs.306088	v-crk avian sarcoma virus CT10 oncogene	2.2
	420653	AI224532	Hs.88550	ESTs	2.2
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	2.2
	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	2.2
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	2.2
60	411893	R82845	Hs.273789	ESTs	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
	437637	AJ003029	Hs.65792	syntrophin, gamma 2	2.2
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
65	446164	AW273539	Hs.288750	hypothetical protein FLJ23577	2.2
	450232	BE300815	Hs.201326	ESTs	2.2
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	2.2
	402745				2.2
	434008	AA740878	Hs.112982	ESTs	2.2
70	439492	AF086310	Hs.103159	ESTs	2.2
	436853	BE328074	Hs.148661	ESTs	2.2
	417648	R06552		gb:yf09e12.r1 Soares fetal liver spleen	2.2
	427690	AI253134	Hs.283410	ESTs	2.2
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.2
75	450229	R18717	Hs.8929	hypothetical protein FLJ11362	2.2
	400756				2.2
	408447	AK002089	Hs.45080	Homo sapiens cDNA FLJ11227 fis, clone PL	2.2
	403388				2.2
	433643	AI821787	Hs.179586	ESTs	2.2
80	442078	AW268583	Hs.262629	ESTs	2.2
	455585	BE066976		gb:PM0-BT0340-211299-003-c12 BT0340 Homo	2.2
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.2
	439920	H05430	Hs.286433	neurotrophin	2.2
	432436	AW300248	Hs.181693	ESTs	2.2
	429493	AL134708	Hs.145998	ESTs	2.2
	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	2.2
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	2.2

	442757	AI739528	Hs.28345	ESTs	2.2
	430212	AA469153		gb:nc67f04.s1 NCL_CGAP_Pr1 Homo sapiens	2.2
	437146	AA730977		gb:mv55f05.s1 NCL_CGAP_Ew1 Homo sapiens	2.2
5	432101	AI918950	Hs.123642	EphA3	2.2
	459644				2.2
	453887	BE564037	Hs.36237	hypothetical protein	2.2
	431170	AW971246	Hs.291022	ESTs	2.2
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	2.2
10	443582	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	2.2
	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	2.2
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.2
	425810	AI923627	Hs.31903	ESTs	2.2
	433037	NM_014158	Hs.279938	HSPC067 protein	2.2
15	407162	N53855	Hs.142634	zinc finger protein	2.2
	441826	AW503603	Hs.129915	phosphotriesterase related	2.2
	446901	AI347274		gb:tc05d02.x1 NCL_CGAP_Co16 Homo sapiens	2.2
	454766	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	414221	AW450979		gb:U1-H-BI3-afa-a-12-0-UI.s1 NCL_CGAP_Su	2.2
20	459608	AL119471		gb:DKFZp761M141_r1 761 (synonym: hanny2)	2.2
	406639				2.2
	406149				2.2
	424027	AW337575	Hs.201591	ESTs	2.2
	427531	AA405097	Hs.97957	ESTs	2.2
25	448353	BE407125	Hs.231510	ESTs	2.2
	417669	T99898		gb:ye68g01.r1 Soares fetal liver spleen	2.2
	449650	AF055575	Hs.23838	calcium channel, voltage-dependent, L ty	2.2
	452335	AW188944	Hs.61272	ESTs	2.2
	419216	AI076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.2
30	447748	AI422023	Hs.161338	ESTs	2.2
	403534				2.2
	410594	AW770778	Hs.281238	ESTs	2.2
	438550	AW976002	Hs.258402	ESTs	2.2
	439626	N22415	Hs.189080	ESTs	2.2
	444540	AI693927	Hs.265165	ESTs	2.2
35	450024	AA005129		gb:zh90h08.r1 Soares fetal liver spleen	2.2
	450221	AA328102	Hs.24641	cytoskeleton associated protein 2	2.2
	439443	AF086261	Hs.127892	ESTs	2.2
	418824	AW751661	Hs.53542	choreoacanthocytosis gene; KIAA0986 prot	2.2
40	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.2
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.2
	432702	AW973953	Hs.293744	ESTs	2.2
	414195	BE263293	Hs.89605	cholinergic receptor, nicotinic, alpha p	2.2
	425570	AA359558		gb:EST68590 Fetal lung II Homo sapiens c	2.2
	414935	C15671		gb:C15671 Clontech human aorta polyA+ mR	2.2
45	453153	N53893	Hs.24360	ESTs	2.2
	430832	AI073913	Hs.100686	ESTs, Weakly similar to JE0350 Anterior	2.2
	439867	AA847510	Hs.161292	ESTs	2.2
	419780	AA713522	Hs.87752	ESTs	2.2
50	433420	AI674093	Hs.293961	ESTs, Moderately similar to putative DNA	2.2
	434690	AI867679	Hs.148410	ESTs	2.2
	436572	AA723274	Hs.279596	ESTs	2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	431688	AA513906		gb:ng67c08.s1 NCL_CGAP_Ulp2 Homo sapiens	2.2
	403133				2.2
55	414885	AA157531	Hs.269276	ESTs, Moderately similar to S65657 alpha	2.2
	432111	AW972777		gb:EST384871 MAGE resequences, MAGL Homo	2.2
	410073	AW408163	Hs.58488	catenin (cadherin-associated protein), a	2.2
	448869	AI792798	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.2
60	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	2.2
	446565	D13757	Hs.311	phosphoribosyl pyrophosphate amidotransf	2.2
	422386	AF105374	Hs.115830	heparan sulfate (glucosamine) 3-O-sulfat	2.2
	406687	M31126	Hs.272620	pregnancy specific beta-1-glycoprotein 9	2.2
	403378				2.2
65	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (2.2
	438580	AA811262	Hs.299202	ESTs	2.2
	409191	AW818390	Hs.175613	homolog of Xenopus Claspin	2.2
	412282	BE160188		gb:QV1-HT0413-010200-059-g05 HT0413 Homo	2.2
	411966	AA099113	Hs.118609	ESTs	2.2
70	443915	Z40763	Hs.135292	ESTs	2.2
	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.2
	446094	AK001760	Hs.13801	KIAA1685 protein	2.2
	436486	AA742221	Hs.120633	ESTs	2.2
	411139	AW819461		gb:RC5-ST0293-061299-031-C03 ST0293 Homo	2.2
	409070	AA063003	Hs.224560	ESTs	2.2
75	432713	AL118623	Hs.29494	PRO1912 protein	2.2
	419384	AA490866	Hs.39429	ESTs	2.2
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	2.2
	408444	AW661839	Hs.253204	ESTs	2.2
80	432128	AA127221	Hs.117037	ESTs	2.2
	418027	AB037807	Hs.83293	hypothetical protein	2.2
	446060	Z42061	Hs.27004	ESTs	2.2
	436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fs, clone HE	2.2
	411987	AA375975	Hs.183380	ESTs, Moderately similar to ALU8_HUMAN A	2.2

	443401	AI394067	Hs.160159	ESTs	2.2
	424665	AW368576	Hs.139851	caveolin 2	2.2
	416143	AI955650	Hs.79033	glutaminyl-peptide cyclotransferase (glu	2.2
5	426261	AW242243	Hs.168670	peroxisomal fatty acylated protein	2.2
	414564	AA164803	Hs.71994	ESTs, Weakly similar to I38022 hypothe	2.2
	427897	NM_017413	Hs.303084	apelin, peptide ligand for APJ receptor	2.2
	419160	AA911342	Hs.35524	KIAA1559 protein	2.2
	420111	AA255652		gbzs21h11.1 r1 NC1_CGAP_GCB1 Homo sapiens	2.2
10	442879	AF032922	Hs.8813	synixin binding protein 3	2.2
	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	2.2
	453823	AL137957		gb:DKFZp76102315_r1 761 (synonym: hamy2)	2.2
	432074	AA525248	Hs.149723	ESTs	2.2
	431848	AI378857	Hs.126758	ESTs, Highly similar to AF175283 1 zinc	2.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	2.2
15	409723	AW885757	Hs.257862	ESTs	2.2
	425627	AF019612	Hs.297007	membrane-bound transcription factor prot	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	449369	AA001256	Hs.27260	ESTs	2.2
20	425514	AF112345	Hs.158237	integrin, alpha 10	2.2
	455821	BE143341		gb:MR0-HT0162-191099-002-d04 HT0162 Homo	2.2
	427224	AL135554	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.2
	432284	AA532807	Hs.105822	ESTs	2.2
	403467				2.2
25	436032	AA150797	Hs.109276	latexin protein	2.2
	404356				2.2
	434205	AF119861	Hs.283032	hypothetical protein PRO2015	2.2
	405257				2.2
	402103				2.2
30	456649	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	2.2
	432985	T92363	Hs.178703	ESTs	2.2
	417649	AW239285	Hs.82359	tumor necrosis factor receptor superfam	2.2
	431277	AA501805	Hs.249965	ESTs	2.2
	454056	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypothe	2.2
	401694				2.2
35	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	431364	AW971382	Hs.294016	ESTs, Moderately similar to B34087 hypot	2.2
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	448390	AL035414	Hs.21068	hypothetical protein	2.2
	449939	T86420	Hs.272139	ESTs	2.2
40	455678	BE066007		gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.2
	404555				2.2
	418186	BE541042	Hs.23240	Homo sapiens cDNA: FLJ21848 fts, clone H	2.2
	419981	AA897581	Hs.128773	ESTs	2.2
	449581	AI989517	Hs.181605	ESTs	2.2
45	419229	AI827237	Hs.282884	ESTs	2.2
	403691				2.2
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	2.2
	443479	AF027219	Hs.9443	zinc finger protein 202	2.2
50	425329	AI961644	Hs.145444	Homo sapiens cDNA FLJ11494 fts, clone HE	2.2
	453345	AA302862	Hs.90063	neurocalcin delta	2.2
	424335	AW021508	Hs.28170	ESTs	2.2
	451072	AA013451	Hs.117929	ESTs	2.2
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	2.2
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.2
55	438035	AA938198	Hs.146123	poly(A) polymerase gamma	2.2
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fts, clone PL	2.2
	400241				2.2
	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
60	409564	AA045857	Hs.54943	fracture callus 1 (rat) homolog	2.2
	411151	AW866497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	446009	AI989885	Hs.231926	ESTs	2.1
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	2.1
	416441	BE407197		gb:601301552F1 NIH_MGC_21 Homo sapiens c	2.1
65	414891	R27124	Hs.268754	Homo sapiens cDNA FLJ11949 fts, clone HE	2.1
	430172	AA468591	Hs.161889	ESTs	2.1
	422109	S73265	Hs.1473	gastrin-releasing peptide	2.1
	422985	AU076411	Hs.1602	dihydropyrimidine dehydrogenase	2.1
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	2.1
70	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fts, clone L	2.1
	450726	AW204600	Hs.250505	retinoic acid receptor, alpha	2.1
	438379	N23018	Hs.171391	C-terminal binding protein 2	2.1
	412608	AA247995	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.1
	451270	AW341392	Hs.235795	ESTs	2.1
75	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	2.1
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	2.1
	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.1
	437132	AL049353	Hs.297268	ESTs	2.1
	415304	T66079	Hs.12799	ESTs	2.1
80	450152	AI138635	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	2.1
	421147	AW592167	Hs.293299	ESTs	2.1
	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protei	2.1
	451750	AA280851	Hs.226930	ESTs	2.1
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	2.1

	406945	K01383	Hs.173451	metallothionein 1A (functional)	2.1
	452449	AW068658	Hs.20943	ESTs	2.1
	436009	H57130	Hs.120925	ESTs	2.1
	418637	T86737	Hs.193536	ESTs	2.1
5	420495	A1338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	2.1
	449203	A1634578	Hs.282121	ESTs	2.1
	437751	AA767373	Hs.35669	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	428412	AA428240	Hs.126083	ESTs	2.1
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.1
10	441967	AA972742	Hs.209786	ESTs	2.1
	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
	406018				2.1
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	2.1
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	2.1
15	431229	AA496479	Hs.259929	ESTs	2.1
	435148	A1918049	Hs.124961	ESTs	2.1
	436349	A1445255	Hs.115315	ESTs	2.1
	446895	AA166655	Hs.282803	ESTs	2.1
	448582	A1538880	Hs.94812	ESTs	2.1
20	442762	AF035119	Hs.8700	deleted in liver cancer 1	2.1
	442738	AW002370	Hs.131055	ESTs, Weakly similar to NPM_HUMAN NUCLEO	2.1
	451874	AW963137	Hs.194233	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	448076	AJ133123	Hs.20196	adenylate cyclase 9	2.1
	443484	A1091458	Hs.134559	ESTs	2.1
25	430686	NM_001942	Hs.2633	desmoglein 1	2.1
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	2.1
	407624	AW157431	Hs.248941	ESTs	2.1
	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.1
	428923	BE047698	Hs.188785	ESTs	2.1
30	422496	AA311301	Hs.278827	ESTs	2.1
	413385	M34455	Hs.840	indoleamine-pyrrole 2,3 dioxygenase	2.1
	408418	AW963897	Hs.44743	KIAA1435 protein	2.1
	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	2.1
	427434	BE538374	Hs.301732	hypothetical protein MGCS306	2.1
35	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
	459325	AW088369	Hs.282184	ESTs	2.1
	416996	W91892	Hs.59609	ESTs	2.1
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	2.1
	408000	L11690	Hs.620	bulbous pemphigoid antigen 1 (230/240kD)	2.1
40	418894	W73921	Hs.50743	ESTs	2.1
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.1
	437378	A1198823	Hs.160473	ESTs	2.1
	454100	A1693231	Hs.126043	chromosome 21 open reading frame 51	2.1
45	452786	R61362	Hs.106542	ESTs, Weakly similar to T09052 hypotheti	2.1
	437311	AA370041	Hs.9456	SWI/SNF related, matrix associated, acti	2.1
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.1
	440028	AW473675	Hs.125843	ESTs, Weakly similar to T17227 hypotheti	2.1
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	2.1
50	424103	NM_001918	Hs.139410	dihydroliipoamide branched chain transacy	2.1
	407995	A1094748	Hs.100134	hypothetical protein FLJ12787	2.1
	449911	A1262106	Hs.12653	ESTs	2.1
	449509	AA001615	Hs.84561	ESTs	2.1
	452762	AW501435	Hs.278582	v-akt murine thymoma viral oncogene homo	2.1
55	422839	A1674784	Hs.298908	ESTs	2.1
	435040	A1932350	Hs.152825	ESTs	2.1
	401200				2.1
	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	2.1
	442262	BE170651	Hs.8700	deleted in liver cancer 1	2.1
60	449754	H00820	Hs.30977	ESTs, Weakly similar to B34087 hypotheti	2.1
	453908	AW613920	Hs.282178	ESTs	2.1
	446965	BE242873	Hs.16677	WD repeat domain 15	2.1
	412798	AW998657	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
	416085	H18072	Hs.92576	ESTs	2.1
65	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.1
	455995	BE179408		gb:IL3-HT0618-060500-125-B07 HT0618 Homo	2.1
	422411	AW749443	Hs.22511	ESTs	2.1
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo	2.1
	446893	A1610818	Hs.7110	ESTs	2.1
70	442992	A1914699	Hs.13297	ESTs	2.1
	407021	U52077		gb:Human mariner1 transposase gene, comp	2.1
	436938	AW139680	Hs.161393	ESTs	2.1
	433194	AB040883	Hs.83243	KIAA1450 protein	2.1
	454790	AW820852		gb:RC2-ST0301-120200-011-f12 ST0301 Homo	2.1
75	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	2.1
	434739	AA804487	Hs.144130	ESTs	2.1
	406468				2.1
	457023	AA001732	Hs.173233	hypothetical protein FLJ10970	2.1
	416226	N55342	Hs.34372	ESTs	2.1
80	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	2.1
	432810	AA863400	Hs.23054	ESTs	2.1
	412894	R09778	Hs.186510	ESTs	2.1
	430502	D13752	Hs.184927	cytochrome P450, subfamily X1B (steroid	2.1
	436981	AA740891	Hs.293316	ESTs	2.1

	452501	AB037791	Hs.29716	hypothetical protein FLJ10980	2.1
	449838	AB020653	Hs.24024	KIAA0846 protein	2.1
	447160	AA330310	Hs.24181	ESTs	2.1
	422156	N34524		gb:yy56d10.s1 Soares_multiple_sclerosis_	2.1
5	440137	AA866199	Hs.171397	ESTs	2.1
	423998	H29138	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	2.1
	436471	AA719813	Hs.117662	ESTs	2.1
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	2.1
	426782	R14614	Hs.191254	ESTs	2.1
10	430027	AB023197	Hs.227743	KIAA0980 protein	2.1
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.1
	413252	BE074910		gb:RCS-BT0580-170300-021-F12 BT0580 Homo	2.1
	427115	AW972853	Hs.112237	ESTs	2.1
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.1
15	400451				2.1
	435255	W87434	Hs.106015	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	2.1
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	2.1
	442835	AI021989	Hs.131903	ESTs	2.1
20	400196				2.1
	415734	NM_014747	Hs.78748	KIAA0237 gene product	2.1
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	2.1
	438940	AF075045	Hs.271609	ESTs	2.1
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	2.1
25	448515	H68441	Hs.13528	hypothetical protein FLJ14054	2.1
	410557	AA085803	Hs.192997	ESTs, Moderately similar to I78885 serin	2.1
	442562	BE379584	Hs.34789	dolichyl-4-diphosphooligosaccharide-protei	2.1
	413488	BE144017		gb:MR0-HT0165-191199-004-d09 HT0165 Homo	2.1
	419088	AI538323	Hs.52620	Integrin, beta 8	2.1
30	447373	AI381922	Hs.158781	ESTs	2.1
	457465	AW301344	Hs.122908	DNA replication factor	2.1
	413918	AW015898	Hs.71245	ESTs	2.1
	402820				2.1
	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
35	428552	AW274560	Hs.129520	ESTs	2.1
	435464	BE548300	Hs.192999	ESTs, Moderately similar to KIAA0961 pro	2.1
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	2.1
	420838	AW118210	Hs.5244	ESTs	2.1
40	428231	U17989	Hs.183105	nuclear autoantigen	2.1
	434933	R91095	Hs.4276	KIAA1701 protein	2.1
	444870	AI200621	Hs.148504	ESTs	2.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	2.1
	429183	AB014604	Hs.197955	KIAA0704 protein	2.1
	439155	H81076	Hs.269001	ESTs	2.1
45	442787	W93048	Hs.250723	hypothetical protein MGC2747	2.1
	429864	AA460039	Hs.286	ribosomal protein L4	2.1
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	2.1
	437140	AA312799	Hs.283689	activator of CREM in testis	2.1
	421991	NM_014918	Hs.110488	KIAA0990 protein	2.1
50	446534	AI307356	Hs.175225	ESTs	2.1
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	2.1
	444838	AV651680	Hs.208558	ESTs	2.1
	402318				2.1
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
55	414494	AA768491	Hs.6783	hypothetical protein FLJ22724	2.1
	421306	AA806207	Hs.125889	ESTs	2.1
	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
	429088	D61542	Hs.227716	KIAA0934 protein	2.1
60	428859	NM_007050	Hs.225952	protein tyrosine phosphatase, receptor t	2.1
	428060	AA420616	Hs.249483	ESTs	2.1
	419953	BE267154	Hs.125752	ESTs	2.1
	443718	AI083580	Hs.221373	ESTs	2.1
	444187	AW138466	Hs.151274	ESTs	2.1
65	428048	AA705745		gb:zf41b11.s1 Soares_fetal_heart_NbHH19W	2.1
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	2.1
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.1
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.1
	430335	D80007	Hs.239499	KIAA0185 protein	2.1
70	414618	AI204600	Hs.96978	hypothetical protein MGC10764	2.1
	434029	AA621763	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	2.1
	410945	AWB11552		gb:QV2-ST0145-071299-017-h10 ST0145 Homo	2.1
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.1
	433374	AI821409	Hs.332789	EST	2.1
75	445644	R77766	Hs.271593	ESTs, Moderately similar to A47582 B-cel	2.1
	450271	AI693900	Hs.200920	ESTs	2.1
	448084	AI467800	Hs.271000	ESTs, Weakly similar to I38022 hypotheti	2.1
	407864	AF069291	Hs.40539	chromosome 8 open reading frame 1	2.1
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	2.1
80	435542	AA687376	Hs.269533	ESTs	2.1
	443544	AI076315	Hs.16359	ESTs	2.1
	421103	AI625835	Hs.27104	Homo sapiens mRNA; cDNA DKFZp667D226 (tr	2.1
	405759				2.1
	446242	N66336	Hs.7360	ESTs	2.1

	457938	AI373638	Hs.133900	ESTs	2.1
	433017	Y15057	Hs.279914	zinc finger protein 232	2.1
	436729	BE621807	Hs.3337	transmembrane 4 superfamily member 1	2.1
5	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	2.1
	439224	AW471088	Hs.145950	ESTs, Highly similar to T08692 hypotheti	2.1
	410976	R36207	Hs.25092	hypothetical protein MGC10744	2.1
	454574	AW809109		gb:MR4-ST0117-070100-027-a04 ST0117 Homo	2.1
	411020	NM_006770	Hs.67726	macrophage receptor with collagenous str	2.1
10	452279	AA286844	Hs.61260	hypothetical protein FLJ13164	2.1
	446891	AL036877	Hs.282878	ESTs	2.1
	434294	AJ271379	Hs.76194	ribosomal protein S5	2.1
	449057	A8037784	Hs.22941	KIAA1363 protein	2.1
	432769	AA620814	Hs.144959	ESTs	2.1
15	441224	AU076964	Hs.7753	calumenin	2.1
	407891	AA486620	Hs.41135	endomucin-2	2.1
	429017	AA463605	Hs.66295	multi-PDZ-domain-containing protein	2.1
	406817	AI936028		gb:wo47a09.x1 NCI_CGAP_Gas4 Homo sapiens	2.1
	430566	AA481282	Hs.190149	ESTs	2.1
20	449208	AW263635	Hs.48643	ESTs	2.1
	451397	AA017432	Hs.84529	ESTs, Weakly similar to Z202_HUMAN ZINC	2.1
	452042	H38857	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE	2.1
	444779	AI192105	Hs.147170	ESTs	2.0
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	2.0
25	415954	AA171850	Hs.42251	ESTs	2.0
	420273	AI652864	Hs.197257	ESTs	2.0
	411354	AW992424	Hs.288141	hypothetical protein MGC3156	2.0
	422389	AF240635	Hs.115897	protocadherin 12	2.0
	446994	AV650435	Hs.16755	MBIP protein	2.0
30	417793	AW405434	Hs.82575	small nuclear ribonucleoprotein polypept	2.0
	422654	AA314316	Hs.163725	ESTs	2.0
	425999	AW513051	Hs.332981	ESTs, Weakly similar to I38022 hypotheti	2.0
	405634				2.0
	451562	H04150	Hs.107708	ESTs	2.0
35	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	2.0
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	2.0
	442010	AI032680	Hs.132213	ESTs	2.0
	442891	BE281238	Hs.8886	hypothetical protein FLJ20424	2.0
	425312	AA354940	Hs.145958	ESTs	2.0
40	415191	AA190381	Hs.120810	ESTs	2.0
	416406	D86961	Hs.79299	lipoma HMGIC fusion partner-like 2	2.0
	425316	AA354977	Hs.191565	ESTs, Moderately similar to T14342 NSD1	2.0
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	2.0
	452241	AL050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (f	2.0
45	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	2.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	2.0
	409190	AU076536	Hs.50984	sarcoma amplified sequence	2.0
	413783	AA314337	Hs.301547	ribosomal protein S7	2.0
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo saplen	2.0
50	429418	AI381028	Hs.118769	ESTs	2.0
	445829	AI452457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
	425704	U79293	Hs.159264	Human clone Z3948 mRNA sequence	2.0
	446593	W79572	Hs.13277	hypothetical protein FLJ22054	2.0
	400462				2.0
55	422003	AA361760	Hs.296326	ESTs	2.0
	444585	AW170015	Hs.6594	ESTs	2.0
	444898	AI201548	Hs.308338	ESTs	2.0
	403525				2.0
60	443031	AW134696	Hs.49418	ESTs	2.0
	430818	AI311928		gb:qo89h04.x1 NCI_CGAP_Kid5 Homo sapiens	2.0
	423690	AA329548	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	2.0
	440941	BE268362	Hs.7535	COBW-like protein	2.0
	409627	AW997628	Hs.313637	ESTs	2.0
65	433258	AI805626	Hs.207300	ESTs, Weakly similar to ALUB_HUMAN IIII	2.0
	412853	AA121673	Hs.59757	zinc finger protein 281	2.0
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.0
	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	2.0
	417280	AW173116	Hs.262206	ESTs	2.0
	423528	AB011137	Hs.300938	KIAA0565 gene product	2.0
70	424800	AL035588	Hs.153203	MyoD family inhibitor	2.0
	446019	AI362520	Hs.279789	histone deacetylase 3	2.0
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	2.0
	424882	AI379451	Hs.153636	far upstream element (FUSE) binding prot	2.0
75	430473	AW130690	Hs.59962	ESTs	2.0
	431363	M86528	Hs.266902	neurotrophin 5 (neurotrophin 4/5)	2.0
	438118	AW753311	Hs.259415	ESTs	2.0
	400859				2.0
	405829				2.0
80	415258	AW752247	Hs.293853	ESTs	2.0
	420314	H81671	Hs.320921	ESTs, Weakly similar to T22688 hypotheti	2.0
	437733	AI792574	Hs.122876	ESTs	2.0
	452019	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	2.0
	453118	AW195849	Hs.252757	ESTs	2.0

5	430706	NM_003540	Hs.247816	H4 histone family, member C	2.0
	420668	F09247	Hs.247735	protocadherin alpha 10	2.0
	452759	AW590773	Hs.258996	ESTs	2.0
	408496	AI683802	Hs.136182	ESTs	2.0
	420674	NM_000055	Hs.1327	butyrylcholinesterase	2.0
	410358	AW975168	Hs.13337	ESTs, Weakly similar to unnamed protein	2.0
	450086	AWD16343	Hs.233301	ESTs	2.0
	410853	H04588	Hs.30469	ESTs	2.0
10	438607	AW080237	Hs.252884	ESTs	2.0
	422232	D43945	Hs.113274	transcription factor EC	2.0
	432801	NM_016260	Hs.278963	zinc finger DNA binding protein Helios	2.0
	402490				2.0
	446551	AI308176	Hs.65636	ESTs	2.0
15	438315	R56795	Hs.82419	ESTs	2.0
	445261	T79759	Hs.282939	ESTs, Weakly similar to I38022 hypotheti	2.0
	401986				2.0
	420335	AA258771	Hs.43616	Homo sapiens mRNA for FLJ00029 protein,	2.0
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	2.0
20	435413	AI267476	Hs.46669	ESTs	2.0
	458175	AW296024	Hs.150434	ESTs	2.0
	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.0
	417494	AI369494	Hs.222137	ESTs	2.0
	416045	H15990	Hs.31403	ESTs	2.0
25	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	2.0
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-4	2.0
	411578	AW238524		gb:xp27c05.x1 NCI_CGAP_HN10 Homo sapiens	2.0
	453116	AI276680	Hs.146086	ESTs	2.0
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.0
30	435608	AW183971	Hs.250896	ESTs	2.0
	402102				2.0
	458308	AI828155	Hs.211055	ESTs	2.0
	438177	BE327015	Hs.281391	ESTs	2.0
	415205	H71616	Hs.135233	ESTs	2.0
35	427244	AA402400	Hs.178045	ESTs	2.0
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	2.0
	438979	AW976218	Hs.32565	ESTs	2.0
	400285				2.0
	405966				2.0
40	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
	427739	AW196755	Hs.98105	NYD-SP14 protein	2.0
	433584	AW295399		gb:U1-H-BI2-ahv-h-03-0-ULs1 NCI_CGAP_Su	2.0
	448956	AK001674	Hs.22630	cofactor required for Sp1 transcriptiona	2.0
	439474	AI824060	Hs.211501	ESTs	2.0
45	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.0
	454566	AW807605		gb:MR4-STD098-120100-001-b06 STD098 Homo	2.0
	418836	AI655499	Hs.161712	ESTs	2.0
	453108	AI311457	Hs.99472	ESTs	2.0
	447101	N72185	Hs.44189	ESTs	2.0
50	408873	ALD46017	Hs.182278	calmodulin 2 (phosphorylase kinase, delt	2.0
	426226	AA769045		gb:aa80h07.s1 NCI_CGAP_GCB1 Homo sapiens	2.0
	401157				2.0
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	2.0
	425646	AW157044	Hs.158512	cyclin-dependent kinase-like 2 (CDC2-rel	2.0
55	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	2.0
	418839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	2.0
	402855				2.0
	443644	AI080491	Hs.93270	ESTs, Moderately similar to S65657 alpha	2.0
	445672	AI907438	Hs.282862	ESTs	2.0
60	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.0
	411941	AW876909	Hs.25201	ESTs, Weakly similar to FAT DROME CADHER	2.0
	430664	AW969834	Hs.303303	ESTs	2.0
	402812				2.0
	457434	AW628192	Hs.18851	hypothetical protein FLJ10875	2.0
65	448133	AA723157	Hs.73769	folate receptor 1 (adult)	2.0
	402048				2.0
	423347	AI660412	Hs.234557	ESTs	2.0
	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	2.0
	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
70	437373	H67505	Hs.191979	KIAA1733 protein	2.0
	439217	AF086041	Hs.42975	ESTs	2.0
	446609	BE395090	Hs.15535	Homo sapiens clone 24582 mRNA sequence	2.0

75 TABLE 3B: List of accession numbers for primekeys lacking unigeneID's for Table 3A. For such probeset is listed a gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

80 Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT number Accession

5	408690	107490_1	AW864542 AA056567 AW882724
	409029	1095422_1	BE087807 AW301579
	409073	109651_1	AA063458 AA063018 AA444822
	409519	113722_1	AA075368 AA075369
	409695	114876_1	AA296951 AA296889 AA076945 AA077528 AA077497
	410008	116812_1	AA079552 BE142525 BE142527
	410615	1212203_1	AW772721 AW873372 H89212
	410672	1214882_1	AW794600 AW794730
10	410784	1221005_1	AW803201 BE079700 BE062940
	410785	1221055_1	AW803341 AW803265 AW803403 AW803466 AW803402 AW803413 AW803268 AW803396 AW803334 AW803355
	410888	1225955_1	AW861207 AW809508
	410901	1226077_1	AW810001 AW810092 AW810170 AW809884 AW809664 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786
			AW810006 AW809572 AW809694 AW810552 AW810345 AW810432 AW809950
15	410934	1227240_1	AW811114 AW811095 AW811087 AW811124 AW811054 AW811094 AW811157
	410945	1227561_1	AW811552 AW811470 AW811523 AW811482 AW811514 AW811456 AW811525
	410999	1228809_1	AW813004 AW812962 AW812951
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	411018	1229132_1	AW813428 AW813444 AW813367 AW813368 AW813429 AW813424
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	411151	1234022_1	AW866497 AW819775 AW819868 AW866602 AW866561
	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069
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25	411514	1248638_1	AW850178 AW850233 AW850445 AW850446
	411578	125013_1	AW238524 AA094059 R59022
	411745	1256160_1	AW667826 AW859896
	411880	1263110_1	AW872477 BE088101 T05990
	411905	1265181_1	BE265087 BE264978 AW875420
	412167	1280605_1	AW897230 AW897252 AW897244 AW897231 AW897263
30	412209	1283610_1	AW901456 AW901450 AW901441
	412248	1285000_1	BE176480 AW903298 AW903313
	412282	1287679_1	BE160188 AW935785 BE160401 BE160319 BE160313 BE160395
	412303	1288130_1	AW936336 AW936339
	412566	1305469_1	AW962574 BE073261
35	412877	1333953_1	BE011168 BE006371 BE011172 BE0111313 BE011166
	412879	1334272_1	BE092219 BE092361 BE006789
	413087	1348720_1	BE064655 BE153953
	413136	1350379_1	BE066941 BE066911 BE066979 BE066929 BE066925
	413252	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
40	413382	1355954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686
	413488	1373234_1	BE144017 BE185527 BE144023
	413499	1373910_1	BE144884 H97942
	413618	1380384_1	BE154078 BE154006 BE153891 BE153523 BE153983
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45	413642	1381386_1	BE154837 BE154879 BE154850 BE154877 BE154835 BE154849 BE154902 BE154905 BE154867 BE154901 BE154904 BE154899
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	414109	1417307_1	BE250744 BE294770
	414221	142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368
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50	414605	1465790_1	BE390440
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	415236	1531080_1	R41400 H06659 Z38537 F02023 T16516
	415635	1540853_1	F13168 R21289 T77628
	415747	155189_1	AA381209 AA381245 AA167683
55	415980	1564218_1	R52414 R61681 H12009 T74429
	416288	1585983_1	H51299 H44619 H46391 R86024 H51892 T72744
	416337	1589299_1	H48713 H83057 H48694 H65247
	416441	159480_1	BE407197 AA182474 AA180369 BE275628 BE276131
	416548	1600181_1	H62953 N76608 N72413
60	416624	1604694_1	H69044 T47567 H75691 T50292
	416871	1626761_1	H58716 N90792 N24283
	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	416972	163668_1	BE019670 AA191284 AA191255
	417561	168747_2	AW974345 BE145400 T97088 AA639076
65	417648	1691070_1	R06552 T98985 R08656
	417669	1692157_1	T99898 T92080 T91447 R07806 R07779
	417859	1703724_1	T26453 Z44226 R20425
	418378	174656_1	AW962081 AA218925 AA354237
	418636	177402_1	AW749855 AA225995 AW750208 AW750206
70	419546	185766_1	AA244199 AA244272 H57440
	419637	186639_1	W27493 AA248063 AA249685 AA429679
	419807	188252_1	R77402 AA262462 AA250988 R06794
	420111	190755_1	AA255652 AA280911 AW967920 AA262684
	420621	195113_1	AA278808 BE082076 BE081812 BE081581
75	420637	195241_1	AW976153 AA278945 AA747691
	421065	198936_1	AA329711 AA287435 AA283148
	422063	210852_1	BE156476 BE156473 BE156474 BE156475 AA302839
	422156	212379_1	N34524 AA305071 AW954803 AA502335 AJ433430 AJ203597 AW026670 AW265323 AW850787 AA317554 AW93643 AW835572 AW385512
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	422429	216469_1	AA309272 AA309312 AW961837
	422977	223410_1	AA310527 AW962295 Z44865 H06641
			AA631498 AJ017191 AA491211 AA761823 AA714555 AA768099 AA808286 AJ934069 AA570223 AA574389 AA582438 AJ745346 AW964510
			AA319542 AW853758 H56414
	423121	225175_1	AW864848 AA322213 AA322209 AW961624

	423377	22769_1	AL049377 AL079930 AL047223 AW885968 AA385235
	423532	229362_1	BE090503 BE090490 BE090483 BE090501 BE090500 BE090365 BE090505 BE090509 BE090499 BE090502 BE090504 BE090497 AA327285
	423735	231498_1	AA330259 AA661806 AA502431 AW974633 AA649496
5	423841	232507_1	AW753957 AA370795 AA331630 AW962550
	423867	232732_1	AA331886 AW962659 AW962655 T89841
	424872	244505_1	AA347923 AA347928 AW961769
	425201	247933_1	AA352111 AW962247 AA429695
	425497	252499_1	AA524596 AA358494 AA513507
10	425570	253248_1	AA359558 AA359819 AW963122
	426226	262918_1	AA769045 AA372590 AW963633
	426497	268121_1	AA379913 AA379981 AW963523
	426603	269825_1	AA382291 AA994657
	427551	280163_1	T96203 AA05343 T96121
	428048	286394_1	AA705745 AA420850 AA420433
15	428679	294049_1	AA431765 AA432015
	430212	314437_1	AA469153 A1718503 AA469225
	430818	324239_1	A1311928 AA936030 T51931 AA609816 AA487195 AA664207
	430844	324570_1	T94960 AA487679 T95013
20	430933	325757_1	AW863635 BE179901 BE179402 AW863789 AA489179 BE010747 BE010748
	431071	327550_1	AA491379 H86020 AW969148
	431169	328799_1	AW971240 AA493843 AA493723
	431322	331543_1	AW970622 AA503009 AA502998 AA502989 AA502805 T92188
	431595	335512_1	AA508196 BE142920 A1280311 A1205616 D61709
25	431688	336609_1	AA513906 AA847734 A1357044
	432111	341618_1	AW972777 AA526795 AA526305
	432189	342819_1	AA527941 A1810608 A1620190 AA635266
	432222	343347_1	A1204995 AW827539 AW969908 AW440776 AA528756
	432779	354024_1	AW979241 AA565006 AA847102
30	432803	354267_1	AA565398 AW894072 H97930
	432869	355475_1	AW974094 AA569074 AA602574
	433347	36388_1	AF023130 AF181250 AA984703 AA694303 AA351792
	433492	367934_1	AW605849 AW262898 N41060 AA594852
	433584	370400_1	AW295399 AW207772 AW300641 AW070290 BE348854 AW170383 AA600968 AA778832
35	433644	371919_1	AW342028 AA641080 AA603282
	433687	373061_1	AA743991 AA604852 AW272737
	434138	380572_1	AA625804 AW418787 AW074833 A1675642 A1393368
	434374	384889_1	AA631439 A1086355 A1082577
	434613	389550_1	A1821826 AA640657 AA658836 AA650055 A1821079
40	434638	38990_1	H50758 AF147434 H50666
	434950	396061_1	AW974892 AA654375
	434995	397210_1	AW974995 A1821880 A1821932 A1791196 AA659617 A1821137 AA658925
	435079	399783_1	AA664192 H60250 T71388
	435463	406582_1	AA682507 AW851124
45	435634	409239_1	T82384 R05307 AA693714
	435532	421802_1	AA721522 AW975443 T93070
	437146	43371_1	AA730977 A1261584 AA334473 Z43283 AW875861 AW938044 BE150701 AW936262 AA306862 BE565575 BE567380 AA728920 AA167612
			A1239729 A1251752 AA485791 BE568425 AW962958
50	438005	447553_1	BE151746 BE336853 D63271 T94955 AA774994
	438458	457837_1	AW975186 AA807807 D29548
	438909	46684_1	AF085839 R69137 AW188788 R69254
	438993	467651_1	AA828995 AA834879 A1926361
	440320	491930_1	AA879294 N67538 A1474541
	440674	49997_1	BE561546 Z25124 A1307139 Z28800
55	443613	575391_1	A1079356 W23287
	443657	576685_1	R14973 R14967 A1081006
	444314	600667_1	A1140497 AW749625 AW749626 AW749644
	444810	612257_1	A1174783 R83569 R12271
	444910	624951_1	A1201849 BE069007 AW946544
60	446096	661959_1	A1276454 A1633717 A1275116
	446901	697809_1	A1347274 AW844024
	447197	711623_1	R36075 A1366546 R36167
	448404	761515_1	BE089973 A1498612 AW805032
	449540	80945_2	AA001713 H63836
65	450024	82296_1	AA005129 AA679084 AA694399
	450458	83586_1	AA009926 BE149301
	450522	837264_1	A1698839 A1909260 A1909259
	451024	85585_1	AA442176 AA259181
	451487	87131_1	AA018072 N46370 R84847
	452453	918300_1	A1902519 A1902518 A1902516
70	452542	921410_1	AW812256 AW812257 A1906423 A1906422
	453823	982526_1	AL137967 BE064160 BE064186
	453901	986414_1	BE065902 AW749032 AW003637
	454190	1049996_1	AW177821 AW177896 AW177867
75	454193	1050256_1	BE141183 AW178167 AW178162 AW178166 AW178172 AW845893 AW178159 AW178222 AW178213 AW178215 AW178090 AW178091
			AW178161 AW178207 AW178210 AW178214 AW178212 BE140918 BE140917 AW178135 AW178205 AW178209 AW178223 AW178220
			AW178206 AW178203 AW178165 AW178168 AW178160 AW178136 AW845878 AW178131 AW178138 AW178105 AW845894 AW178129
			AW845810 AW845828 AW178216 AW178112 AW178211 AW178224 BE140915 AW178221 AW178130 AW178134 AW178096 AW178108
			AW178133 AW178164 AW178218 AW178171 AW178157 AW178158 AW178103 BE141189 AW178170 AW845816 BE141586 AW178156
			AW178104 AW178163 AW178093 AW178208 AW178137 AW178140 AW178219 BE141592 AW845901 BE141580 AW178155 BE141598 BE140957
80	454352	1129667_1	AW389668 AW389657 AW609198 AW389649
	454359	1130674_1	N71277 AW390764
	454389	115682_1	AW752571 AW847602 AA077979
	454403	1170435_1	BE065985 BE065944 BE066008 BE066083 BE066093

5	454455	1206965_1	AW752710 BE180336 BE180186
	454566	1224432_1	AW807605 AW807690 AW807839 AW807752 AW807673 AW807667 AW807955 AW807760 AW807615 AW807898 AW807849 AW807821 AW807832 AW807842 AW807827 AW807822 AW807829 AW807830 AW807825 AW807603 AW807612 AW807908 AW807595 AW807617 AW807678 AW807687 AW807918 AW807921 AW807596 AW807602 AW807688 AW807609 AW807684 AW807770 AW807593 AW807754 AW807679 AW807957 AW807683 AW807763 AW807902 AW807840 AW807819 AW807836 AW807769 AW807685 AW807847 AW807674 AW807685 AW807670 AW807917 AW807677 AW807680 AW807900 AW807669 AW807952 AW807907 AW807846 AW807756 AW807835 AW807608 AW807753 AW807601 AW807956 AW809109 AW809112 AW809122 AW809126 AW809128 AW809133 AW809131 AW809113 AW809111 AW809132 AW810001 AW810092 AW810170 AW809884 AW809864 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786 AW810006 AW809672 AW809694 AW810552 AW810345 AW810432 AW809960 AW813089 W28102 AW813428 AW813444 AW813367 AW813368 AW813429 AW813424 AW815098 BE154843 BE154831 AW866497 AW819775 AW819868 AW866502 AW866561 AW820626 AW820621 AW820608 AW820852 AW820773 AW821088 AW833711 AW833620 AW833699 AW847645 AW847791 AW854083 AW853945 AW852530 AW852527 AW852526 BE152428 AW855572 AW855607 BE160198 AW935898 T11520 AW935930 AW856073 AW861034 BE154113 AW856797 AW856847 AW861128 AW856817 AW857121 AW857123 AW861238 AW860972 AW862598 AW862599 AW860988 AW860983 AW860898 AW860925 AW860922 AW860986 AW860984 AW860989 AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878 AW902103 AW869012 AW869139 AW876627 AW876630 AW876631 AW876625 BE144384 AW887474 AW887403 BE144386 AW893961 AW893998 AW894034 AW894019 AW938484 BE001245 BE001190 AA102322 BE144762 AW979091 AW983608 AW983628 AW983610 AW983688 AW983601 AW983645 AW983607 AW983640 AW983625 AW983612 AW983642 AW983687 AW983602 AW983624 AW983634 AW983637 AW983632 AW983617 AW983635 AW983630 AW983636 AW983639 AW983616 AW983689 AW983641 AW983621 AW983603 AW983609 AW983623 AW983644 AW983618 AW983615 AW983611 AW983604 AW983686 AW983622 AW983619 AW983633 AW983589 AW983605 AW983626 AW983643 AW983631 AW983627 AW983613 AW983614 AW983685 AW983593 AW983590 AW983594 AW983620 AW983638 AW983592 AW983588 BE003714 BE003721 BE003720 BE003716 BE063031 BE063002 BE063008 BE063024 BE063040 BE063006 BE063072 BE066007 BE066017 BE066074 BE066976 BE066928 BE066927 BE141140 BE141139 BE141105 BE141143 BE141127 BE141202 BE141108 BE143341 BE143344 BE143378 BE143358 BE149024 BE149056 BE152826 BE149025 BE149057 BE152819 BE149030 BE149062 BE149023 BE149055 BE179015 BE178965 BE179010 BE179002 BE178961 BE179005 BE178964 BE179012 BE179011 BE178963 BE178997 BE179408 BE179798 BE179880 AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367 BE011368 BE011362 BE011215 BE011365 BE011363 AL157625 N72696 BE622492 AI630223 AI630470 AI904723 AI904725 AI904729 AI904722 AI904758 AI904736 AW391177 W45021 AJ003631 AJ003650 AJ003651
10	454574	1225636_1	
	454600	1226077_1	
15	454678	1228915_1	
	454693	1229132_1	
	454714	1230493_1	
	454766	1234022_1	
	454784	1234630_1	
	454790	1234752_1	
	454836	1236509_1	
	454962	1246750_1	
20	455047	1250536_1	
	455092	1252971_1	
	455100	1253334_1	
	455107	1253874_1	
	455114	1254106_1	
25	455170	1256906_1	
	455201	1259748_1	
	455226	1262534_1	
	455252	1266222_1	
	455286	1273576_1	
30	455310	1278158_1	
	455431	1289854_1	
	455488	1293772_1	
	455511	1321229_1	
	455512	1321443_1	
35			
40	455571	1331885_1	
	455631	1347545_1	
	455678	1349716_1	
	455685	1350393_1	
	455807	1370914_1	
	455821	1372714_1	
	455866	1377119_1	
45	455992	1398552_1	
	455995	1398903_1	
	456034	142696_1	
50	458804	75803_1	
	458861	798085_1	
	459160	920051_1	
	459201	925883_1	
	459267	966605_1	
55			

TABLE 29C

60	Pkey:	Unique number corresponding to an Eos probe set	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.	
	Strand:	Indicates DNA strand from which exons were predicted.	
	Nt_position:	Indicates nucleotide positions of predicted exons.	
65	Pkey	Ref	Nt_position
	400451	8113550	Minus 82189-82320
	400462	9929659	Minus 197610-197785
70	400608	9887666	Minus 96756-97558
	400639	9887597	Plus 23150-23580
	400641	8117693	Plus 4786-4992
	400756	8119084	Minus 38734-38857
	400859	9757499	Minus 91888-92018,98131-98294,99474-99570
75	400880	9931121	Plus 29235-29336,36363-36580
	400889	9958234	Minus 169782-170036
	400983	8081198	Plus 107903-108832
	401045	8117619	Plus 90044-90184,91111-91345
	401049	7232177	Plus 149157-150692
80	401078	3687273	Plus 105052-105171
	401094	9965511	Plus 137130-137302,139283-139506
	401103	8568122	Minus 98330-98449
	401157	9438289	Minus 114133-114247,114567-114645
	401189	9690246	Minus 90815-90929

	401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
	401213	9858408	Plus	98243-98380,98489-98619
	401254	9796309	Plus	152209-152383
5	401323	9212516	Plus	213509-214450
	401335	9884881	Plus	15736-16352
	401497	7381770	Plus	92607-92813
	401517	7677912	Plus	29278-29770
	401526	7770561	Plus	91570-93177
10	401575	7229804	Minus	76253-76364
	401694	3540172	Minus	64056-64168
	401793	7263888	Minus	102945-103083
	401862	7770606	Minus	55839-55993,59145-59293
	401878	8099802	Minus	162268-162474,163089-163195
15	401985	4406829	Minus	31137-31293
	402046	8072415	Plus	165394-166556,168167-168395
	402048	8072512	Plus	43936-44078
	402102	8117771	Minus	174566-174740
	402103	7249203	Plus	14453-15414
20	402230	9966312	Minus	29782-29932
	402318	7582559	Minus	12843-13403
	402490	9797648	Plus	149982-150929
	402745	9212200	Minus	76516-76690
	402800	6010175	Plus	43921-44049,46181-46273
25	402812	6010110	Plus	25026-25091,25844-25920
	402820	6456853	Minus	82274-82443
	402855	9662953	Minus	59763-59909
	403133	7331427	Plus	38314-38634
	403271	7230852	Plus	134283-134485
30	403277	8072597	Minus	27494-27642
	403310	8139936	Minus	183883-184026
	403329	8516120	Plus	98450-96598
	403356	8569930	Plus	92839-93036
	403378	9438244	Minus	44264-44443
35	403388	9438331	Plus	112733-113001,114599-114735
	403467	9929556	Minus	73431-73602
	403515	7658757	Minus	173358-179553
	403525	7960440	Plus	152431-153243
	403534	8076917	Minus	46652-47332
40	403568	8101145	Minus	85509-85658
	403574	8101156	Plus	5542-6176
	403637	8671936	Minus	142647-142771,145531-145762
	403677	7331517	Minus	55008-55083,62860-63051
	403691	7387384	Minus	88280-88463
45	403760	7712202	Minus	45910-46260,47563-47824
	403776	7770611	Minus	1414-1513,1624-1756
	403895	7381715	Minus	3502-4002,4070-4308
	403937	7711761	Minus	12609-12773
	404043	9558573	Plus	28042-29135,46597-46699
	404097	7770701	Plus	55512-55781
50	404200	6010176	Minus	7066-7210
	404249	8655533	Plus	64270-64633
	404274	9885189	Plus	104127-104318
	404285	2326514	Plus	32282-32416
55	404288	2769644	Plus	3512-3691
	404356	7630858	Minus	126433-126623
	404443	7579073	Minus	87198-87441
	404476	8080699	Plus	101841-102043
	404488	8113286	Minus	64835-64994
60	404513	8151941	Minus	112837-113339
	404548	8570305	Minus	83896-84162
	404555	7243881	Minus	63963-64157
	404561	9795980	Minus	69039-70100
	404588	6456726	Minus	40059-40210
65	404593	9944086	Minus	74922-75788
	404599	8705107	Plus	110443-110733
	404860	8979555	Plus	65852-66081
	404916	7341826	Plus	91057-91188
	404957	7407927	Plus	147512-148011
70	405041	7547195	Plus	121230-121714
	405059	7656683	Plus	349-822
	405090	8072525	Minus	38552-39202
	405257	7329310	Plus	73121-73273
	405336	6094635	Plus	33267-33563
75	405472	8439781	Plus	106297-106447,108462-108596
	405494	8050952	Minus	70284-70518
	405547	1054740	Plus	124361-124520,124914-125050
	405621	5523811	Plus	59362-59607
	405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
80	405654	4895155	Minus	53624-53759
	405692	4314424	Plus	61379-62562
	405759	3288022	Minus	18283-18399
	405829	7109593	Minus	15628-16127
	405848	7651809	Minus	28135-28244

5	405966	8247788	Minus	51762-51978
	405970	8247789	Minus	45795-46295
	406018	6758904	Minus	37795-38168
	406091	9123919	Minus	197370-197935
	406092	9123919	Plus	251370-251797,252168-252882
	406149	7144791	Minus	44464-45164
	406195	7289992	Minus	36293-36827
	406333	9213235	Plus	64689-64798
10	406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880
	406506	7711374	Minus	6843-8077
	406554	7711566	Plus	106956-107121
	406603	8272659	Minus	39506-39694

15

TABLE 30A: ABOUT 1840 GENES UP-REGULATED IN IDIOPATHIC PULMONARY FIBROSIS (IPF) COMPARED TO HYPERSENSITIVITY PNEUMONITIS (HP)

20 Table 30A lists about 1840 genes that are up regulated in idiopathic pulmonary fibrosis (IPF) samples as compared with hypersensitivity pneumonitis (HP) samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 Gene Chip array such that the ratio of "average" idiopathic pulmonary fibrosis sample expression level to "average" hypersensitivity pneumonitis sample expression was greater than or equal to about 2.0. The "average" idiopathic pulmonary fibrosis level was set to the 90th percentile amongst idiopathic pulmonary fibrosis samples. The "average" hypersensitivity pneumonitis level was set to the 90th percentile amongst hypersensitivity pneumonitis samples.

25 Pkey: Unique Eos probe set identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of IPF (idiopathic pulmonary fibrosis) to HP (hypersensitivity pneumonitis)

30	Pkey	ExAccn	Unigene ID	Unigene Title	R1
	450478	AW451709	Hs.271200	ESTs	20.2
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244	11.9
	405654				11.8
	440209	H05049	Hs.22269	neurexin 3	10.8
35	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagonist	10.4
	439606	W79123	Hs.58561	G protein-coupled receptor 87	10.3
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	10.2
	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	9.5
	416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.3
40	420481	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	9.2
	403574				9.1
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	8.8
	419519	AI198719	Hs.176376	ESTs	8.2
	435256	AF193766	Hs.13872	cytokine-like protein C17	8.1
45	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	8.1
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	8.0
	405443				7.8
	428766	AA477989	Hs.98800	ESTs	7.7
	441802	AA968636	Hs.127877	ESTs	7.6
50	453649	Y07494	Hs.34114	ATPase, Na+/K+ transporting, alpha 2 (+)	7.5
	447410	AI470236	Hs.172698	EST	7.2
	442353	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	7.2
	405494				6.9
	442377	AA993807	Hs.167367	ESTs	6.9
55	409928	AL137163	Hs.57549	hypothetical protein dJ47384	6.8
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	6.8
	415236	R41400		gb:Y94b12.s1 Soares infant brain 1N1B H	6.8
	451562	H04150	Hs.107708	ESTs	6.8
	403310				6.7
60	445189	AI936450	Hs.147482	ESTs	6.7
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	6.7
	439780	AL109688		gb:Homo sapiens mRNA full length insert	6.6
	402076				6.6
	415025	AW207091	Hs.72307	ESTs	6.5
65	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	6.5
	438557	AW364104	Hs.143509	hypothetical protein FLJ21924	6.5
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	6.4
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	6.4
	409545	BE296182	Hs.19002	hypothetical protein MGC4575	6.4
70	445619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.4
	411956	AA099113	Hs.118609	ESTs	6.4
	440274	R24595	Hs.7122	scrapie responsive protein 1	6.3
	442879	AF032922	Hs.8813	syntaxin binding protein 3	6.3
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	6.3
75	420185	AL044056	Hs.158047	ESTs	6.3
	415672	N53097	Hs.193579	ESTs	6.2
	455488	AA102322		gb:Z190103.1 Stratagene colon (937204)	6.2
	420026	AI831190	Hs.166676	ESTs	6.1
80	446888	AV660737	Hs.135100	ESTs	6.1
	431622	AW979271	Hs.293184	ESTs	6.1
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	6.1
	421300	AW297398	Hs.96617	ESTs	6.0
	416045	H15990	Hs.31403	ESTs	6.0

5	414175	AJ308876	Hs.103849	hypothetical protein DKFZp761D112	6.0
	424693	BE169810	Hs.47557	ESTs	6.0
	436397	AA715013	Hs.169835	ESTs	6.0
	440504	AJ948966	Hs.130017	ESTs, Weakly similar to JN0908 H+-transp	6.0
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	6.0
10	403625				6.0
	418986	AJ123555	Hs.81796	ESTs	5.9
	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	5.9
	400292	AA250737	Hs.72472	ESTs	5.9
	442849	R10099	Hs.269805	ESTs	5.9
15	440887	AJ799488	Hs.135905	ESTs	5.8
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	5.7
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	5.7
	431374	BE258532	Hs.251871	CTP synthase	5.7
	444963	AJ916973	Hs.213603	ESTs	5.7
20	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	5.6
	444992	R37658	Hs.21375	ESTs	5.6
	416575	W02414	Hs.38383	ESTs	5.5
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	5.5
	451830	H18433	Hs.21542	KJAA1035 protein	5.5
25	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	5.5
	404043				5.5
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	5.5
	455540	BE080231		gb:RC4-BT0629-120200-012-f11 BT0629 Homo	5.5
	434683	AW298724	Hs.202639	ESTs	5.5
30	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence	5.5
	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	5.5
	428895	AA437124	Hs.187247	ESTs	5.4
	450018	AA421642	Hs.24309	hypothetical protein FLJ11106	5.4
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	5.4
35	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	5.4
	454039	AW079064	Hs.245540	ESTs	5.3
	403637				5.3
	414725	AA769791	Hs.125300	ring finger protein 21, interferon-respo	5.3
	409073	AA063458		gb:z71a07.s1 Soares_pineal_gland_N3HPG	5.3
40	403329				5.3
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	5.3
	459664				5.3
	401497				5.3
	410797	AW857191		gb:RC2-CT0304-080100-011-b12 CT0304 Homo	5.2
45	411402	BE297855	Hs.69855	NRAS-related gene	5.2
	448844	AJ581519	Hs.177164	ESTs	5.2
	435202	AJ971313	Hs.170204	KIAA0551 protein	5.1
	439418	AJ282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	5.1
	443584	AJ807036	Hs.267245	hypothetical protein FLJ14803	5.1
50	434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
	430838	N46664	Hs.169395	hypothetical protein FLJ12015	5.1
	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	5.1
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.0
	437636	AA764781	Hs.291844	ESTs	5.0
55	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.0
	455464	AW983901		gb:RC1-HN0003-220300-011-f10 HN0003 Homo	5.0
	418771	AA807881	Hs.25329	ESTs	5.0
	434820	AJ821863		gb:ns90f05.x5 NCI_CGAP_Pr3 Homo sapiens	5.0
	440615	AJ733055	Hs.130806	ESTs	5.0
60	454482	BE147919		gb:RC3-HT0230-160200-016-a08 HT0230 Homo	4.9
	400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	4.9
	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	4.9
	423607	AA328329	Hs.6591	ESTs	4.9
	407415	AF073328		gb:Homo sapiens tetracycline transporter-	4.9
65	401878				4.9
	443162	T49951	Hs.9029	DKFZP434G032 protein	4.9
	451325	AA021283	Hs.59788	ESTs	4.9
	440515	AJ131245	Hs.7239	SEC24 (S. cerevisiae) related gene famil	4.9
	406333				4.9
70	409105	AW467539	Hs.255877	ESTs	4.8
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	4.8
	421482	AL135462	Hs.104715	inversin	4.8
	442757	AJ739528	Hs.28345	ESTs	4.8
	459717				4.8
75	436637	AJ783629	Hs.26766	ESTs	4.8
	412222	AA528283	Hs.292737	ESTs	4.8
	450101	AV649989	Hs.24385	Human hbc647 mRNA sequence	4.8
	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
	426217	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	4.8
80	441640	AJ733345	Hs.144104	ESTs	4.8
	422977	AA631498		gb:np83h04.s1 NCI_CGAP_Thy1 Homo sapiens	4.8
	425361	AA355933	Hs.132221	hypothetical protein FLJ12401	4.8
	414955	C15506		gb:C15506 Clontech human aorta polyA+ mR	4.8
	411965	BE467339	Hs.280115	ESTs	4.7
80	403341				4.7
	411726	AW858612		gb:CM3-CT0341-190400-152-h12 CT0341 Homo	4.7
	443271	BE568568	Hs.195704	ESTs	4.7

	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	426097	BE327369	Hs.112238	ESTs	4.7
	439199	R40373	Hs.26299	ESTs	4.7
5	440728	AW086077	Hs.153272	Homo sapiens cDNA: FLJ22715 fis, clone H	4.6
	434381	AA631834		gb:np77h05.s1 NCL_CGAP_Pr2 Homo sapiens	4.6
	417428	N87579		gb:LL2030F Human fetal heart, Lambda ZAP	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	431242	AA987742	Hs.251278	KIAA1201 protein	4.6
10	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
	442360	AI374621	Hs.29055	ESTs	4.6
	452171	AI863302	Hs.211930	EST	4.6
	440801	AA906366	Hs.190535	ESTs	4.5
	411738	AW859353		gb:MR1-CT0353-150300-102-a12 CT0353 Homo	4.5
15	431447	AA505138	Hs.291341	ESTs	4.5
	433485	AA93076	Hs.201967	aldo-keto reductase family 1, member C2	4.5
	401365				4.5
	408281	BE141183		gb:MR0-HT0071-191199-001-b04 HT0071 Homo	4.5
	411657	AW855583		gb:CM4-CT0278-221099-027-407 CT0278 Homo	4.5
20	423065	R96158	Hs.267130	Homo sapiens, clone MGC:5406, mRNA, comp	4.5
	428528	AI004034	Hs.98638	ESTs	4.5
	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.5
	417252	AA195014	Hs.85971	ESTs	4.5
	417135	AA422067	Hs.50547	ESTs	4.5
	403089				4.4
25	420691	AA829433	Hs.275343	ESTs	4.4
	412147	AW895984		gb:QV4-NN0039-040500-197-e08 NN0039 Homo	4.4
	425578	U65652	Hs.158313	chromosome 17 open reading frame 1A	4.4
	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	4.4
30	454438	AA224053	Hs.172405	cell division cycle 27	4.4
	435434	AA680387	Hs.187850	ESTs	4.4
	420828	AA280778	Hs.186878	ESTs	4.3
	435586	AI279137	Hs.151498	ESTs	4.3
	452393	H87398	Hs.99858	ribosomal protein L7a	4.3
35	416170	H42454	Hs.220645	ESTs	4.3
	408691	AW250525		gb:2821626.5prime NIH_MGC_7 Homo sapiens	4.3
	428912	AW103117	Hs.98949	ESTs, Weakly similar to MEA6 [H.sapiens]	4.3
	455511	BE144762		gb:CM0-HT0180-041099-065-b04 HT0180 Homo	4.3
	413849	BE173561	Hs.15384	AP1 gamma subunit binding protein 1	4.3
40	401189				4.3
	425733	F13287	Hs.159388	Homo sapiens clone 23578 mRNA sequence	4.3
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3
	422654	AA314316	Hs.163725	ESTs	4.3
	435463	AA682507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	4.3
45	417919	AI928203	Hs.86379	ESTs	4.3
	405784				4.3
	431853	AA521034	Hs.70834	ESTs	4.3
	409529	AW449589	Hs.279724	ESTs	4.2
	403281				4.2
50	427173	BE255017	Hs.97540	ESTs	4.2
	433717	AF063536		gb:AF063536 Homo sapiens library (Yu Y)	4.2
	406777	T23625	Hs.150580	putative translation initiation factor	4.2
	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	4.2
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.2
55	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	4.2
	449762	N93057	Hs.54888	ESTs	4.2
	421106	AA877124	Hs.172844	ESTs	4.2
	439382	BE247684	Hs.103070	ESTs	4.1
	404957				4.1
60	436332	AL049679	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	4.1
	446393	AW014174	Hs.301956	zinc finger protein	4.1
	452728	AI915676	Hs.239708	ESTs	4.1
	456386	W28481		gb:47e1 Human retina cDNA randomly prime	4.1
	406288	AW068311	Hs.311054	Homo sapiens mRNA full length insert cDN	4.1
65	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	4.1
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.1
	403344				4.1
	438993	AA828995		gb:od77b08.s1 NCL_CGAP_Ov2 Homo sapiens	4.1
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.1
70	401596	AA172106	Hs.110950	Rag C protein	4.1
	418693	AI750878	Hs.87409	thrombospondin 1	4.1
	414299	AA142989	Hs.71730	ESTs	4.1
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.0
	458552	AW136139	Hs.245856	ESTs	4.0
75	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
	441201	AW118822	Hs.128757	ESTs	4.0
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	4.0
	440472	AA886169	Hs.169071	ESTs	4.0
80	418379	AA218940	Hs.137516	fidgetin-like 1	4.0
	435878	RD8330	Hs.20152	ESTs	4.0
	437263	AA747822		gb:bx97a04.s1 NCL_CGAP_GCB1 Homo sapiens	4.0
	444087	AV647899	Hs.282375	ESTs	4.0
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0

	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	4.0
	405521				4.0
	411597	AW852925		gb:PMO-CT0248-131099-001-110 CT0248 Homo	4.0
5	415655	W05433	Hs.49890	ESTs	4.0
	404822				4.0
	441107	AA917075	Hs.190520	ESTs	4.0
	404834				4.0
	412768	AW996044	Hs.25239	Human DNA sequence from clone RP11-438B2	4.0
10	428102	AA968441	Hs.126866	ESTs	4.0
	436511	AA721252	Hs.291502	ESTs	4.0
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieli	4.0
	453098	Z25935	Hs.86379	ESTs	3.9
	410811	AW805687	Hs.300648	ESTs	3.9
15	425048	H05468	Hs.164502	ESTs	3.9
	431071	AA491379		gb:ae65f05.r1 NCI_CGAP_GC81 Homo sapiens	3.9
	436298	AW293496	Hs.180138	ESTs	3.9
	440356	AI933184	Hs.127922	ESTs, Moderately similar to S65657 alpha	3.9
	452768	AW069459	Hs.61539	ESTs	3.9
20	455241	AW876249		gb:PM4-PT0019-131299-006-B05 PT0019 Homo	3.9
	409070	AA063003	Hs.224560	ESTs	3.9
	409044	AI129586	Hs.33033	hypothetical protein FLJ14623	3.9
	419091	T85332	Hs.178294	ESTs	3.9
	422591	L07648	Hs.118630	MAX-interacting protein 1	3.9
	403188				3.9
25	418857	D10216	Hs.89394	POU domain, class 1, transcription facto	3.9
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	3.9
	436149	AI754308	Hs.159452	ESTs	3.9
	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.9
30	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.9
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length Insert cDN	3.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.9
	451221	AI949701	Hs.210589	ESTs	3.9
	455475	AW948126		gb:RCO-MT0013-280300-031-a12 MT0013 Homo	3.9
35	433197	AB040889	Hs.281022	KIAA1456 protein	3.9
	429881	T80112	Hs.192245	ESTs	3.9
	415598	AI433165	Hs.9856	ESTs	3.9
	431220	N52937	Hs.102679	ESTs	3.9
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.9
40	424029	AB014594	Hs.137579	KIAA0694 gene product	3.9
	404443				3.9
	407340	AA810168	Hs.284289	vifilgo-associated protein VIT-1	3.9
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retroviru	3.9
	412400	AW948066		gb:RCO-MT0012-290300-031-h10 MT0012 Homo	3.9
45	427167	AI239607	Hs.99196	hypothetical protein MGC11324	3.9
	438090	AA777534	Hs.191992	ESTs	3.8
	407938	AA905097	Hs.85060	phospholamban	3.8
	440454	AI733037	Hs.129990	ESTs	3.8
	417706	T90797	Hs.268623	ESTs	3.8
50	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	3.8
	407762	AW235638	Hs.29475	ESTs	3.8
	420727	H75701	Hs.99886	complement component 4-binding protein,	3.8
	417508	BE163512	Hs.180877	H3 histone, family 3B (H3.3B)	3.8
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	3.8
	425798	AA364002		gb:EST74529 Pineal gland II Homo sapiens	3.8
55	459429	AA278779	Hs.335696	EST	3.8
	430205	AB025904	Hs.235168	carbonic anhydrase XIV	3.8
	437458	AL390131	Hs.128751	Homo sapiens cDNA FLJ12235 fis, clone MA	3.8
	451073	AI758905	Hs.206063	ESTs	3.8
60	452786	R61362	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	3.8
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.8
	444414	AW293214	Hs.8752	transmembrane protein 4	3.8
	402615				3.7
	410585	AW770523	Hs.337501	ESTs	3.7
65	425168	R96366		gb:yrq37c04.s1 Soares fetal liver spleen	3.7
	449729	R72032	Hs.29235	ESTs	3.7
	459359	N99545		gb:za40a05.r1 Soares fetal liver spleen	3.7
	456443	AW967500	Hs.133543	ESTs	3.7
	439001	AF075068		gb:Homo sapiens full length insert cDNA	3.7
70	443657	R14973		gb:yr42f10.s1 Soares fetal liver spleen	3.7
	404193				3.7
	416379	N38857	Hs.203933	ESTs	3.7
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	3.7
	426603	AA382291		gb:EST95683 Testis I Homo sapiens cDNA 5	3.7
75	412589	R28660	Hs.24305	ESTs	3.7
	421037	AI684808	Hs.197653	ESTs	3.7
	427088	AA398085	Hs.142390	ESTs	3.7
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	3.7
	453375	AI990114	Hs.240091	ESTs	3.7
80	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-hergulin	3.7
	451882	AI821324	Hs.100445	ESTs	3.7
	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	3.7
	405001	U58196	Hs.296281	Interleukin enhancer binding factor 1	3.7
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	3.7

	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	3.7
	432781	NM_014133	Hs.278940	PRO0618 protein	3.7
	443773	AV846452	Hs.30941	calcium channel, voltage-dependent, beta	3.7
5	406964	M21305		gb:Human alpha satellite and satellite 3	3.7
	430682	AW971949	Hs.291252	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.7
	449804	AJ535663	Hs.39379	ESTs	3.7
	411505	AF155659	Hs.70565	molybdenum cofactor synthesis 2	3.7
	430503	AA533574	Hs.152274	ESTs	3.7
10	443305	AJ060693	Hs.133318	ESTs	3.7
	415076	NM_000857	Hs.77890	guanylate cyclase 1, soluble, beta 3	3.7
	452280	AJ911410	Hs.167224	ESTs	3.6
	432189	AA527941		gb:nh30c04.s1 NCL CGAP_Pt3 Homo sapiens	3.6
	406992	S82472		gb:beta -pol=DNA polymerase beta (exon a	3.6
15	441416	AJ990139	Hs.148609	ESTs	3.6
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	3.6
	413998	AW103807	Hs.243933	ESTs	3.6
	440385	AA884283	Hs.192136	ESTs	3.6
	431673	AW971302	Hs.293233	ESTs	3.6
20	401887				3.6
	404793				3.6
	422054	AA322506		gb:EST25146 Cerebellum II Homo sapiens c	3.6
	432030	AJ908400	Hs.143789	ESTs	3.6
	449645	AJ961092	Hs.196155	ESTs	3.6
25	404476				3.6
	449336	AL119995	Hs.15260	ESTs, Highly similar to AC007228.2 BC372	3.6
	401200				3.6
	403937				3.6
	437918	AJ761449	Hs.121629	ESTs	3.6
30	443394	AJ055865	Hs.133485	ESTs	3.6
	439107	AL046134	Hs.13944	adrenergic, beta, receptor kinase 2	3.6
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.6
	425403	AL023753	Hs.156405	Human DNA sequence from clone 1199H6 on	3.6
	436269	AA707472	Hs.190760	ESTs	3.6
35	453823	AL137957		gb:DKFZp761D2315_r1 761 (synonym: hamy2)	3.6
	416394	H64111		gb:yr57f03.r1 Soares fetal liver spleen	3.6
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	3.6
	439326	W07140	Hs.54721	ESTs	3.6
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
40	435766	R11673	Hs.185498	ESTs	3.6
	448067	R68568	Hs.183373	src homology 3 domain-containing protein	3.6
	441605	AA984647	Hs.128801	ESTs	3.5
	414400	X06948	Hs.897	Fc fragment of IgE, high affinity L rec	3.5
	418405	AJ868282	Hs.11898	ESTs, Highly similar to KIAA1370 protein	3.5
45	437642	AL079309		gb:Homo sapiens mRNA full length insert	3.5
	450350	T97817	Hs.174880	ESTs	3.5
	451704	AJ755209	Hs.205616	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	459037	AW439497	Hs.290656	EST	3.5
	419247	S65791	Hs.89764	fragile X mental retardation 1	3.5
50	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	426724	AA383623	Hs.293616	ESTs	3.5
	434273	AA913143	Hs.26303	ESTs	3.5
	438042	AW296971	Hs.255593	ESTs	3.5
	410500	R09442		gb:yt26c09.r1 Soares fetal liver spleen	3.5
55	416154	Z46122		gb:HSC0V8031 normalized infant brain cDN	3.5
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	3.5
	454447	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	3.5
	458057	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.5
	444338	AJ937026	Hs.146642	ESTs	3.5
60	427687	AW003867	Hs.1570	histamine receptor H1	3.5
	415929	AA724373	Hs.49344	hypothetical protein FLJ11006	3.5
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.5
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1, I	3.5
	403515				3.5
65	435793	AB037734	Hs.4993	KIAA1313 protein	3.5
	439953	AA918129	Hs.124638	ESTs	3.5
	457620	AA602711	Hs.336753	EST	3.5
	442006	AW975183	Hs.292663	ESTs, Weakly similar to S72482 hypothei	3.5
	453931	AL121278	Hs.25144	ESTs	3.5
70	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	3.5
	413468	BE504766		gb:htz40g01.x1 NCL CGAP_GC6 Homo sapiens	3.5
	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	3.5
	451065	AW295132	Hs.222231	ESTs, Weakly similar to granule cell mar	3.5
	444493	R59410	Hs.282094	ESTs, Moderately similar to I38022 hypol	3.5
75	426447	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha po	3.5
	410908	AA121686	Hs.10592	ESTs	3.5
	440364	AA910460	Hs.128626	ESTs	3.5
	406190				3.5
80	430762	AJ343652	Hs.105657	ESTs	3.5
	451182	D52562	Hs.296317	KIAA1789 protein	3.4
	432437	W07088	Hs.293685	ESTs	3.4
	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	3.4
	405870				3.4
	407676	AW064111	Hs.279823	ESTs	3.4

	413141	BE166323		gb:QV4-HT0492-270100-086-e12 HT0492 Homo	3.4
	431418	X68242	Hs.252722	Hin-1	3.4
	431954	AK001974	Hs.272242	hypothetical protein FLJ11112	3.4
5	459371	R20991		gb:yq06h01.r1 Soares infant brain 1NIB H	3.4
	428062	AA420683	Hs.98321	hypothetical protein FLJ14103	3.4
	423841	AW753957		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	3.4
	420430	AJ703192		gb:wd92h04.x1 NCI_CGAP_Lu24 Homo sapiens	3.4
	443921	AJ091310	Hs.134848	ESTs	3.4
10	444453	AW379394	Hs.145126	ESTs	3.4
	443475	AJ066470	Hs.134482	ESTs	3.4
	414136	AA812434	Hs.119023	SMC2 (structural maintenance of chromoso	3.4
	453263	R91778	Hs.99359	ESTs	3.4
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo	3.4
15	456303	AA224872	Hs.115088	ESTs	3.4
	431474	AL133990	Hs.190642	ESTs	3.4
	439702	AW085525	Hs.134182	ESTs	3.4
	458797	AW001835	Hs.13323	hypothetical protein FLJ22059	3.4
	430140	AW296771	Hs.221999	ESTs	3.4
20	423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	3.4
	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	3.4
	446672	T05514		gb:EST03403 Fetal brain, Stratagene (cat	3.4
	431548	AJ834273	Hs.9711	novel protein	3.4
	416182	NM_004354	Hs.79069	cyclin G2	3.4
25	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.4
	417663	R07483	Hs.180461	ESTs	3.3
	405455				3.3
	426235	AJ631964	Hs.34447	ESTs	3.3
	439567	AJ056618	Hs.134314	ESTs	3.3
30	444848	AW451176	Hs.195954	ESTs	3.3
	451426	AW205003	Hs.208063	ESTs	3.3
	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	3.3
	401626				3.3
	405780				3.3
35	417991	AA731452	Hs.190008	ESTs	3.3
	443212	AW269515	Hs.102500	hypothetical protein FLJ20481	3.3
	403356				3.3
	404518	AJ815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	3.3
40	413581	BE150618		gb:RC3-HT0272-110100-013-d06 HT0272 Homo	3.3
	426701	AJ968103	Hs.209461	Homo sapiens cDNA FLJ12836 fis, clone NT	3.3
	445510	AA946676	Hs.282824	ESTs	3.3
	418663	AK001100	Hs.41690	desmocollin 3	3.3
	447617	AJ400762	Hs.176675	ESTs	3.3
	448150	AJ472167	Hs.302739	ESTs	3.3
45	410140	AL134435	Hs.22269	neurexin 3	3.3
	443283	BE568610		gb:601342622F1 NIH_MGC_53 Homo sapiens c	3.3
	454777	AW820027		gb:QV0-ST0294-240300-173-g04 ST0294 Homo	3.3
	410767	AJ001873	Hs.66185	Homo Sapiens mRNA, partial cDNA sequence	3.3
	433183	AF231338	Hs.222024	transcription factor BMAL2	3.3
50	436168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
	438456	AA913381	Hs.190513	ESTs	3.3
	411186	AW821257		gb:PM3-ST0307-231299-001-b11 ST0307 Homo	3.3
	411880	AW872477		gb:hnm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	3.3
	433567	AF073299	Hs.103132	solute carrier family 9 (sodium/hydrogen	3.3
55	433805	AA706910	Hs.112742	ESTs	3.3
	409434	AF278761	Hs.131581	Homo sapiens testis transcript Y 7 (TTY7	3.3
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	3.3
	456555	AW592167	Hs.293299	ESTs	3.3
	419189	T95862	Hs.112318	6.2 kd protein	3.3
60	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfam	3.3
	407995	AJ094748	Hs.100134	hypothetical protein FLJ12787	3.3
	413200	AA127395	Hs.222414	ESTs	3.3
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.3
	416737	AF154335	Hs.79691	LIM domain protein	3.3
65	428356	AL046991	Hs.10338	ESTs	3.3
	429216	AJ369472	Hs.65407	ESTs	3.3
	432488	AA551010	Hs.216640	ESTs	3.3
	433386	AW360833		gb:PM1-CT0243-201099-004-d08 CT0243 Homo	3.3
	400889				3.3
70	416294	D86980	Hs.79170	KIAA0227 protein	3.3
	446190	AJ279299	Hs.256564	ESTs	3.3
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	3.3
	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	3.3
	418375	NM_003081	Hs.84389	synaptosomal-associated protein, 25kD	3.3
75	443367	AW071349	Hs.215937	ESTs	3.3
	446645	AJ336596	Hs.156294	ESTs	3.3
	434294	AJ271379	Hs.76194	ribosomal protein S5	3.3
	452372	AJ885742	Hs.228474	ESTs	3.3
	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	3.2
80	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	3.2
	430548	AW450575	Hs.163203	ESTs, Weakly similar to B34087 hypotheri	3.2
	427119	AW880562	Hs.114574	ESTs	3.2
	437073	AJ885608	Hs.94122	ESTs	3.2
	437845	AA769578	Hs.90488	ESTs	3.2

5	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	414394	AI904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.2
	417175	R44558	Hs.94002	ESTs	3.2
	456536	AW135986	Hs.257859	ESTs	3.2
10	401132				3.2
	407764	BE008347		gb:CM0-BN0154-080400-325-h04 BN0154 Homo	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	450947	AI745400	Hs.204662	ESTs	3.2
15	456605	AI827786	Hs.259044	ESTs	3.2
	452879	AW905328	Hs.180842	ribosomal protein L13	3.2
	454754	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	3.2
	429479	AA453488	Hs.99333	ESTs	3.2
20	448090	AI608821	Hs.270289	ESTs	3.2
	401324				3.2
	404731				3.2
	419936	AI792788		gb:091d05.y5 NCI_CGAP_Kid5 Homo sapiens	3.2
25	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	3.2
	433990	AA889328	Hs.112950	ESTs	3.2
	415239	R42608	Hs.139270	ESTs	3.2
	418878	W20090	Hs.6616	ESTs	3.2
30	438079	R09664	Hs.191223	ESTs	3.2
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	3.2
	457460	AI143312	Hs.129206	casein kinase 1, gamma 3	3.2
	454145	AA046872	Hs.62798	ESTs	3.2
35	446577	AB040933	Hs.15420	KIAA1500 protein	3.2
	430664	AW969834	Hs.303303	ESTs	3.2
	404588				3.2
	407834	AW084991	Hs.26100	ESTs	3.2
40	413087	BE084655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
	440790	AW593050	Hs.128580	ESTs	3.2
	452081	AW958859	Hs.7514	Homo sapiens cDNA FLJ12141 fis, clone MA	3.2
	421916	R34441	Hs.101007	Homo sapiens cDNA: FLJ23546 fis, clone L	3.2
45	419261	X07876	Hs.89791	wingless-type MMTV integration site faml	3.2
	419340	AA236590	Hs.87530	ESTs	3.2
	444771	AB023201	Hs.11912	KIAA0984 protein	3.2
	445233	AV653034	Hs.297559	ESTs	3.2
50	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	3.2
	408334	AW514652	Hs.321637	ESTs	3.2
	410085	AA428482	Hs.58589	glycogenin 2	3.2
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	3.2
55	403623				3.2
	432223	AA333283	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	3.2
	444050	AW138295	Hs.135024	ESTs	3.2
	421036	AA810560	Hs.303577	ESTs	3.2
60	401459				3.1
	404404				3.1
	450438	AI696071	Hs.253800	ESTs	3.1
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibitor	3.1
65	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypothetical	3.1
	441274	AW593781	Hs.131357	ESTs	3.1
	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	3.1
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
70	400816				3.1
	410307	AF022913	Hs.62187	phosphatidylinositol glycan, class K	3.1
	431906	AW328038	Hs.37486	ESTs	3.1
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
75	450271	AI693900	Hs.200920	ESTs	3.1
	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	3.1
	415273	Z39840	Hs.22229	ESTs	3.1
	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
80	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.1
	446364	AB006624	Hs.14912	KIAA0266 protein	3.1
	436638	AI271945	Hs.134984	ESTs	3.1
	418079	R40058	Hs.6911	ESTs	3.1
85	448466	AI522109	Hs.171066	ESTs	3.1
	448835	BE277929	Hs.11081	UBX domain-containing 2	3.1
	415046	R40018	Hs.56400	ESTs	3.1
	448134	AI470790	Hs.34494	ESTs	3.1
90	456027	BE327387	Hs.13913	KIAA1577 protein	3.1
	458023	AW978161	Hs.268555	5'-3' exonuclease 2	3.1
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.1
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	3.1
95	414884	R54418	Hs.183745	hypothetical protein FLJ13456	3.1
	449138	AW294215	Hs.195631	ESTs	3.1
	455756	BE079307		gb:RC1-BT0623-120200-011-g09 BT0623 Homo	3.1
	428170	H05530	Hs.12565	ESTs	3.1
100	429878	AA460188	Hs.127263	ESTs	3.1
	455000	AW850283	Hs.324429	Homo sapiens cDNA FLJ14015 fis, clone HE	3.1
	438369	T77686	Hs.83428	nuclear factor of kappa light polypeptide	3.1
	415840	R15955	Hs.21758	ESTs	3.1
105	444955	AW002844	Hs.148641	ESTs	3.1
	436020	AA778177	Hs.121724	ESTs	3.1
	453051	AW196690	Hs.224269	ESTs	3.1

	425178	H16097	Hs.161027	ESTs	3.1
	402145				3.1
	410685	AA497117	Hs.129600	ESTs, Moderately similar to ALU1_HUMAN A	3.1
5	449238	AA428229	Hs.331561	muscle-specific RING-finger protein 3	3.1
	456737	BE247203	Hs.124831	CGI-67 protein	3.1
	438214	H05076	Hs.26320	TRABID protein	3.1
	436250	AY004867	Hs.85844	neurotrophic tyrosine kinase, receptor,	3.1
	411622	AJ807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp564B176 (fr	3.0
10	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
	449357	AJ076363	Hs.288806	Homo sapiens cDNA FLJ11778 fis, clone HE	3.0
	418950	T78517	Hs.13941	ESTs	3.0
	431508	NM_012481	Hs.182979	ribosomal protein L12	3.0
	405090				3.0
15	445409	AJ949081	Hs.147862	ESTs	3.0
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.0
	455577	BE006341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	3.0
	408235	AA053381	Hs.75969	proline-rich protein with nuclear target	3.0
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	3.0
20	452073	AA625150	Hs.82098	ESTs	3.0
	427050	AA397789	Hs.161803	ESTs	3.0
	427244	AA402400	Hs.178045	ESTs	3.0
	448405	AW207634	Hs.170849	ESTs	3.0
	433767	AA609245		gb:af13a11.s1 Soares_testis_NHT Homo sap	3.0
25	421376	AA287948	Hs.134110	ESTs	3.0
	441519	AA972740	Hs.127092	ESTs	3.0
	404367				3.0
	453502	AL039786	Hs.21273	transcription factor NYD-sp10	3.0
	421948	L42583	Hs.334309	keratin 6A	3.0
30	438165	AA779344	Hs.138136	ESTs, Weakly similar to 1510254A L1 repe	3.0
	400608				3.0
	404042				3.0
	405229				3.0
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	3.0
35	415452	F09134	Hs.12839	ESTs	3.0
	430371	D87466	Hs.240112	KIAA0276 protein	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
	455851	BE145879		gb:QV4-HT0222-261099-014-c11 HT0222 Homo	3.0
	429014	AI800518	Hs.118158	ESTs	3.0
40	405605				3.0
	400227				3.0
	439037	AF075084		gb:Homo sapiens full length insert cDNA	3.0
	439693	AI741816	Hs.125897	ESTs	3.0
45	427533	R36022	Hs.179566	hypothetical protein FLJ22624	3.0
	418355	L42563	Hs.1165	ATPase, H ⁺ /K ⁺ transporting, nongastric,	3.0
	433536	AI732163	Hs.188909	ESTs, Weakly similar to alternatively sp	3.0
	448446	AI521251	Hs.171030	ESTs	3.0
	449623	C00719	Hs.120440	EST	3.0
	445568	H00918	Hs.268744	KIAA1796 protein	3.0
50	440448	AA885428	Hs.125645	ESTs	3.0
	428201	AA424158	Hs.206461	ESTs	3.0
	444148	AW003204	Hs.151167	ESTs	3.0
	447972	AL137275	Hs.20137	hypothetical protein DKFZp434P0116	3.0
	432584	AA928829	Hs.47099	hypothetical protein FLJ21212	3.0
55	440925	AW511090	Hs.130419	ESTs	3.0
	428398	AJ249368	Hs.98558	ESTs	3.0
	415913	H70302		gb:yr95f07.r1 Soares fetal liver spleen	3.0
	418145	AF121260	Hs.83577	cysteine and glycine-rich protein 3 (car	3.0
	413252	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	3.0
60	400335	Y13187	Hs.248067	Homo sapiens dmd gene, intron 11	3.0
	426132	AA370501		gb:EST82261 Prostate gland I Homo sapien	3.0
	436938	AW139680	Hs.161393	ESTs	3.0
	437980	R50393	Hs.278436	KIAA1474 protein	3.0
	455955	BE162394		gb:PM2-HT0451-170100-004-a08 HT0451 Homo	3.0
65	414899	AW975433	Hs.36288	ESTs	2.9
	403786				2.9
	430187	AJ799909	Hs.158969	ESTs	2.9
	451700	AJ470262	Hs.29553	ESTs	2.9
	455866	BE149024		gb:CM0-HT0249-291099-084-c04 HT0249 Homo	2.9
70	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	2.9
	457041	AA399018	Hs.250835	ESTs	2.9
	415716	N59294	Hs.179662	nucleosome assembly protein 1-like 1	2.9
	422336	AI761322	Hs.115285	dihydrolipoamide S-acetyltransferase (E2	2.9
	451664	AA889081	Hs.153952	5' nucleotidase (CD73)	2.9
75	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.9
	455249	AW876538		gb:RC3-PT0028-190100-012-b06 PT0028 Homo	2.9
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	2.9
	406076	AL390179	Hs.137011	Homo sapiens mRNA; cDNA DKFZp547P134 (fr	2.9
	405302				2.9
80	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	423119	AA322201	Hs.131976	ESTs	2.9
	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
	431980	AA523696	Hs.324507	hypothetical protein FLJ20986	2.9

	425793	AA363946	Hs.20969	ESTs	2.9
	401462				2.9
	458817	AI522129	Hs.173119	ESTs	2.9
5	422163	AF027208	Hs.112360	prominin (mouse)-like 1	2.9
	419875	AA853410	Hs.93557	proenkephalin	2.9
	423047	NM_005323	Hs.123054	H1 histone family, member T (testis-spec	2.9
	425349	AA425234	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	2.9
	401358				2.9
10	418531	R96760	Hs.183758	ESTs	2.9
	447290	AA76732	Hs.263912	ESTs	2.9
	441143	AI027604	Hs.159650	ESTs	2.9
	431292	AA370141	Hs.2281	chromogranin B (secretogranin 1)	2.9
	405783				2.9
15	444459	AI680624	Hs.148676	ESTs	2.9
	402112	R58624	Hs.2186	eukaryotic translation elongation factor	2.9
	425745	U44060	Hs.14427	Homo sapiens cDNA: FLJ21800 fs, clone H	2.9
	444827	R09764	Hs.20416	ESTs	2.9
	451195	U10492	Hs.438	mesenchyme homeo box 1	2.9
20	411417	AW845481		gb:MR1-CT0056-201199-008-b04 CT0056 Homo	2.9
	418343	AA216372	Hs.159501	ESTs	2.9
	431595	AA508196		gb:nh60/07.s1 NCI_CGAP_Pr8 Homo sapiens	2.9
	436187	AK000995	Hs.297221	Homo sapiens cDNA FLJ10136 fs, clone HE	2.9
	455699	BE068121		gb:CM1-BT0368-061299-060-a02 BT0368 Homo	2.9
25	459440	BE048054		gb:tz46c03.y1 NCI_CGAP_Brn52 Homo sapien	2.9
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
	423492	AF020761	Hs.129683	ubiquitin-conjugating enzyme E2D 1 (homo	2.9
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.9
	437913	AI140825	Hs.121623	ESTs	2.9
30	443185	NM_006134	Hs.284142	chromosome 21 open reading frame 4	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
	426803	AA362568	Hs.179747	ecotropic viral integration site 5	2.9
	437183	AI928184	Hs.122011	ESTs	2.9
	420879	N31165	Hs.238837	ESTs, Weakly similar to S43603 RNA bindi	2.9
35	442726	AW136066	Hs.19145	ESTs	2.9
	456189	H91010	Hs.44940	ESTs	2.9
	441115	R69910	Hs.29041	Homo sapiens cDNA FLJ14177 fs, clone NT	2.9
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu	2.9
	415628	F13080		gb:HSC3ID041 normalized infant brain cDN	2.9
40	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (f	2.9
	443246	T75157	Hs.337603	ESTs, Weakly similar to T08680 hypotheti	2.9
	450877	AI799608	Hs.29178	ESTs	2.9
	439063	AF085922	Hs.113968	ESTs	2.9
	401526				2.9
45	408751	N91553	Hs.258343	ESTs	2.9
	417320	AA195667	Hs.86022	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
	444125	AI124882	Hs.118121	ESTs	2.9
	452148	AF007143	Hs.28205	Homo sapiens clone 23738 mRNA sequence	2.9
50	453901	BE065902		gb:RC2-BT0318-150200-011-b09 BT0318 Homo	2.9
	452589	BE159915	Hs.61406	ESTs, Weakly similar to 2004399A chromos	2.8
	403011				2.8
	436154	AA764950	Hs.119898	ESTs	2.8
	408221	AA912183	Hs.47447	ESTs	2.8
55	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.8
	415399	T26994	Hs.177198	ESTs	2.8
	441817	AW969706	Hs.293332	ESTs	2.8
	443556	AA256769	Hs.94949	methylmalonyl-CoA epimerase	2.8
	455092	BE152428		gb:CMD-HT0323-151299-126-b04 HT0323 Homo	2.8
60	439703	AF086538	Hs.196245	ESTs	2.8
	411024	BE062590		gb:QV1-BT0260-281099-023-f05 BT0260 Homo	2.8
	414546	BE379492		gb:601236215F1 NIH_MGC_44 Homo sapiens c	2.8
	434715	BE005346	Hs.116410	ESTs	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
	439235	N45513	Hs.46608	ESTs	2.8
65	453736	AL118674	Hs.34871	zinc finger homeobox 1B	2.8
	404967				2.8
	437783	AI683150	Hs.201550	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
	412687	BE007420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.8
70	426942	AA393551	Hs.97450	ESTs	2.8
	403513				2.8
	419077	AA233885	Hs.164526	ESTs	2.8
	421823	N40850	Hs.28625	ESTs	2.8
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	2.8
75	451007	H38108	Hs.32759	ESTs	2.8
	407803	AW081681	Hs.269064	ESTs, Weakly similar to T42689 hypotheti	2.8
	409642	AW450809	Hs.257347	ESTs	2.8
	439492	AF086310	Hs.103159	ESTs	2.8
	420814	AA721156	Hs.190440	ESTs	2.8
80	449508	AK001566	Hs.23618	hypothetical protein FLJ10704	2.8
	428350	AW873520	Hs.112017	GE36 gene	2.8
	405456				2.8
	442459	AI264628	Hs.125428	ESTs	2.8
	415763	Z42285	Hs.5181	proliferation-associated 2G4, 38kD	2.8

	428532	AF157326	Hs.184786	TBP-interacting protein	2.8
	435720	AW975902		gb:EST388011 MAGE resequences, MAGN Homo	2.8
	449539	W80363	Hs.58446	ESTs	2.8
5	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.8
	408749	H65489	Hs.250659	ESTs	2.8
	404652				2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	424960	BE245380	Hs.153952	5' nucleotidase (CD73)	2.8
10	402131				2.8
	419530	X98330	Hs.90821	ryanodine receptor 2 (cardiac)	2.8
	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	444217	AV648751	Hs.282395	ESTs	2.8
	449579	AW207260	Hs.134014	ESTs, Weakly similar to T46425 hypotheti	2.8
15	412323	AW937143		gb:PM1-DT0041-281299-001-01 DT0041 Homo	2.8
	418912	NM_000685	Hs.89472	angiotensin receptor 1	2.8
	433513	AJ566356	Hs.171437	ESTs	2.8
	448912	D83781	Hs.22559	KIAA0197 protein	2.8
	451496	AW503407		gb:U1-HF-BN0-zkw-d-11-0-U1.r1 NIH_MGC_50	2.8
20	420273	AJ652864	Hs.197257	ESTs	2.8
	451949	U03884	Hs.463	potassium inwardly-rectifying channel, s	2.8
	420756	AA411800	Hs.189900	ESTs	2.8
	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	425012	T77666	Hs.92414	Homo sapiens cDNA: FLJ22030 fis, clone H	2.8
25	441609	AA946764	Hs.133460	ESTs	2.8
	448870	BE181783	Hs.175358	ESTs, Weakly similar to A47582 B-cell gr	2.8
	451206	H86228	Hs.271780	ESTs, Weakly similar to I38022 hypotheti	2.8
	457314	AA479597	Hs.193659	hypothetical protein DKFZp586J1119	2.8
	416192	NM_005036	Hs.998	peroxisome proliferative activated recep	2.8
30	418888	AJ076801	Hs.89436	cadherin 17, LI cadherin (liver-Intestin	2.8
	455310	AW893961		gb:RC4-NN0027-060400-011-d11 NN0027 Homo	2.8
	459450	AA426429	Hs.98463	EST	2.8
	424188	AW954552	Hs.142634	zinc finger protein	2.7
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	2.7
35	427443	AA402713	Hs.97872	ESTs	2.7
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.7
	413091	BE065063		gb:RC1-BT0313-110500-017-e02 BT0313 Homo	2.7
	421003	T72080	Hs.95667	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
40	445611	AW418497	Hs.145583	ESTs	2.7
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	2.7
	408243	Y00787	Hs.624	interleukin 8	2.7
	407308	H67394	Hs.331325	ESTs, Weakly similar to I38022 hypotheti	2.7
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	2.7
45	404587	M99587	Hs.104134	homeo box (H6 family) 1	2.7
	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.7
	416431	AW384459	Hs.172004	titin	2.7
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
	417177	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain	2.7
50	427134	AA398409	Hs.173561	EST	2.7
	428137	AA421792	Hs.170999	ESTs	2.7
	430844	T94960		gb:ye38d07.r1 Stratagene lung (937210) H	2.7
	441218	BE327561	Hs.202345	ESTs	2.7
	440911	AA909536	Hs.143562	ESTs	2.7
55	411131	AW819212		gb:CM1-ST0283-071299-061-c07 ST0283 Homo	2.7
	438602	AJ167149	Hs.123374	ESTs, Weakly similar to mariner transpos	2.7
	441191	AJ693930	Hs.148816	ESTs	2.7
	403776				2.7
	420159	AJ572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.7
60	427839	AA608823	Hs.98244	ESTs	2.7
	429905	AL080128	Hs.225998	DKFZP434C153 protein	2.7
	449396	BE169100	Hs.195029	ESTs	2.7
	450777	AA255646	Hs.60478	ESTs, Moderately similar to S47073 fringe	2.7
	458043	AW979009	Hs.326108	ESTs	2.7
65	405523				2.7
	434849	AW292765	Hs.8053	ESTs	2.7
	452755	AW138937	Hs.213436	ESTs, Weakly similar to A34087 hypotheti	2.7
	438055	AA776655	Hs.270942	ESTs	2.7
	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	2.7
70	405738				2.7
	417806	AJ867277	Hs.183733	ESTs	2.7
	430698	AA492071		gb:ne97b04.s1 NCI_CGAP_Kd1 Homo sapiens	2.7
	441969	AJ733386	Hs.129194	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	446092	N33522	Hs.145894	ESTs	2.7
75	456869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.7
	413617	BE155373	Hs.279518	amyloid beta (A4) precursor-like protein	2.7
	444931	AV652066	Hs.75113	general transcription factor IIIA	2.7
	412236	AW902583		gb:QV3-NN1024-260400-171-f10 NN1024 Homo	2.7
	453264	AA034137	Hs.271955	ESTs	2.7
80	438370	AA843242	Hs.48523	ESTs	2.7
	406092				2.7
	454874	AW836407	Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.7
	455880	BE153208		gb:PM0-HT0335-050400-007-F10 HT0335 Homo	2.7
	459275	AJ808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.7

	411987	AA375975	Hs.183380	ESTs, Moderately similar to ALU8_HUMAN A	2.7
	441884	AW172630	Hs.144884	ESTs	2.7
	416211	R14625		gb:yg45c03.r1 Soares infant brain 1N1B H	2.7
5	433128	AB021923	Hs.23367	EST-YD1 protein	2.7
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	2.7
	453696	AI989482	Hs.146286	kinesin family member 13A	2.7
	456208	AW299698	Hs.334625	Homo sapiens cDNA FLJ14890 fis, clone PL	2.7
	425876	AW005887	Hs.234058	ESTs	2.7
	450458	AA009926		gb:zi07e05.r1 Soares_fetal_liver_spleen_	2.7
10	406603				2.7
	410181	AA68210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	410871	D78367	Hs.66739	keratin 12 (Meesmann corneal dystrophy)	2.7
	412706	R97106	Hs.167546	ESTs	2.7
	422897	AA579784	Hs.4290	ESTs	2.7
15	436329	AI798750	Hs.163960	Homo sapiens heat shock transcription fa	2.7
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	2.7
	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
	452594	AL076405	Hs.29981	solute carrier family 26 (sulfate transp	2.7
	419296	AA236115	Hs.120785	ESTs	2.7
20	454747	AW818535		gb:RC1-ST0278-140300-016-f05 ST0278 Homo	2.7
	455791	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
	411409	AW844803		gb:RC3-CN0056-170300-015-f08 CN0056 Homo	2.7
	426662	AA879474	Hs.122710	ESTs	2.7
	400268				2.7
25	438782	AA828380	Hs.126733	ESTs	2.7
	443764	F23283		gb:HSPD22980 HM3 Homo sapiens cDNA clone	2.7
	412486	AF210650	Hs.150858	NAG19 protein	2.7
	411514	AW850178		gb:IL3-CT0219-271099-022-H12 CT0219 Homo	2.7
	457900	AW976692	Hs.291665	ESTs	2.7
30	417376	AA253314	Hs.154103	LIM protein (similar to rat protein kina	2.7
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.7
	435608	AW183971	Hs.250896	ESTs	2.7
	413627	BE182082	Hs.246973	ESTs	2.7
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	2.7
35	445660	AI702668	Hs.201955	ESTs	2.7
	441396	AW293577	Hs.186890	ESTs	2.6
	452046	AB018345	Hs.27657	KIAA0802 protein	2.6
	454936	AW846082		gb:MR3-CT0176-081099-002-d01 CT0176 Homo	2.6
	454434	AA083558	Hs.261286	ESTs	2.6
40	436888	AI942357	Hs.187870	ESTs	2.6
	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (I	2.6
	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 integrin	2.6
	416690	H84078	Hs.108551	ESTs	2.6
	436471	AA719813	Hs.117662	ESTs	2.6
45	425659	AK000690	Hs.158836	hypothetical protein FLJ20583	2.6
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	2.6
	458257	U48351	Hs.201219	ESTs, Weakly similar to S18946 ultra hig	2.6
	455544	AW993880		gb:RC3-BN0034-240400-017-d09 BN0034 Homo	2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
50	452821	AW471181	Hs.160874	ESTs	2.6
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	2.6
	429864	AA460039	Hs.285	ribosomal protein L4	2.6
	456273	AF154846	Hs.1148	zinc finger protein	2.6
	402603				2.6
55	411162	AW819944		gb:QV0-ST0294-240300-172-e03 ST0294 Homo	2.6
	420621	AA278808		gb:zs79c09.r1 NCL_CGAP_GCB1 Homo sapiens	2.6
	435113	AA665469	Hs.117136	ESTs	2.6
	438188	AA779975	Hs.128859	ESTs	2.6
	438295	AI394151	Hs.37932	ESTs	2.6
60	450181	H05254	Hs.201198	ESTs	2.6
	433764	AW753676	Hs.39982	ESTs	2.6
	433229	AB040925	Hs.91625	KIAA1492 protein	2.6
	443718	AI083580	Hs.221373	ESTs	2.6
	418246	AI472179	Hs.121276	ESTs, Weakly similar to R5HU7A ribosomal	2.6
65	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	2.6
	400365	Y10259	Hs.274501	H.sapiens ACTH receptor mRNA 3'UTR	2.6
	419318	AW969742	Hs.291005	ESTs	2.6
	428527	AI902398	Hs.34492	Cyt19 protein	2.6
	404414				2.6
70	446444	AI743737	Hs.24370	ESTs	2.6
	411354	AW992424	Hs.288141	hypothetical protein MGC3156	2.6
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	2.6
	418310	AA814100	Hs.86693	ESTs	2.6
	454481	AW794878	Hs.314230	ESTs, Highly similar to clock (H.sapiens	2.6
75	441216	BE299830	Hs.192908	ESTs	2.6
	438257	AW474419	Hs.224794	ESTs	2.6
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	419505	AA243660	Hs.143061	ESTs	2.6
	417596	R07343	Hs.226823	ESTs, Moderately similar to I54374 gene	2.6
80	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.6
	444517	AI939339	Hs.146883	ESTs	2.6
	454867	AW835924		gb:PM1-LT0018-250200-002-e09 LT0018 Homo	2.6
	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6

5	457630	AI680803	Hs.112627	ESTs	2.6
	424210	T71397	Hs.222707	KIAA1718 protein	2.6
	447748	AI422023	Hs.161338	ESTs	2.6
	411970	AA099142	Hs.13804	hypothetical protein dJ462023.2	2.6
	441233	AA972955	Hs.135568	ESTs	2.6
10	400705				2.6
	436033	H75391	Hs.255748	ESTs	2.6
	440836	AW370882	Hs.222080	ESTs	2.6
	431086	AI829692	Hs.211561	ESTs	2.6
	455110	BE154505		gb:PM0-HT0343-281299-003-e06 HT0343 Homo	2.6
15	455678	BE066007		gb:RC3-BT0319-120200-014-d09 BT0319 Homo	2.6
	413088	BE064962		gb:RC1-BT0313-130400-016-c02 BT0313 Homo	2.6
	436196	AK001084	Hs.333498	Homo sapiens cDNA FLJ10222 fis, clone HE	2.6
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	2.6
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	2.6
20	442690	AI014727	Hs.160047	ESTs, Weakly similar to B28096 line-1 pr	2.6
	441700	AA233556	Hs.126908	hypothetical protein FLJ12994	2.6
	410286	AI739159	Hs.61898	DKFZP586N2124 protein	2.6
	403271				2.6
	429761	AI276780	Hs.135173	ESTs	2.6
25	437085	AA743935	Hs.202329	ESTs	2.6
	450822	AW771860	Hs.205130	ESTs	2.6
	457506	AF131757	Hs.274533	Homo sapiens clone 24926 mRNA sequence	2.6
	416585	X54162	Hs.79386	leiomodrin 1 (smooth muscle)	2.6
	430357	AW976789	Hs.165607	ESTs	2.6
30	417249	N58198	Hs.182898	ESTs	2.6
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	2.6
	440400	AA994364	Hs.125594	ESTs, Weakly similar to T25472 hypothi	2.6
	440460	H92571	Hs.234478	Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	446302	AI285848	Hs.149757	ESTs	2.6
35	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	2.6
	428944	AA780181	Hs.41182	Homo sapiens DIC47 mRNA, complete cds	2.6
	419647	AA348947	Hs.91816	hypothetical protein	2.6
	455600	AW963582		gb:EST375655 MAGE resequences, MAGH Homo	2.6
	419435	AI200540	Hs.14877	ESTs, Weakly similar to (define not ava	2.6
40	452450	AW854891	Hs.194720	ATP-binding cassette, sub-family G (WHIT	2.6
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	2.6
	436421	AI678031	Hs.122813	ESTs, Weakly similar to ZN22_HUMAN ZINC	2.6
	447505	AL049266	Hs.18724	Homo sapiens mRNA: cDNA DKFZp564F093 (fr	2.6
	419758	U31973	Hs.93173	phosphodiesterase 6C, cGMP-specific, con	2.6
45	426698	AA394104	Hs.97489	ESTs	2.6
	446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	2.6
	423025	AA831267	Hs.12244	hypothetical protein FLJ20097	2.5
	447624	AI640326	Hs.62713	ESTs	2.5
	411736	AW859089		gb:MR1-CT0350-150200-002-d02 CT0350 Homo	2.5
50	416334	H53139	Hs.36271	ESTs	2.5
	446818	AI342668	Hs.279765	ESTs	2.5
	454836	AW833711		gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
	442278	AI733477	Hs.166313	ESTs	2.5
	453393	AW956392	Hs.110376	ESTs	2.5
55	420854	AW296927		gb:U1-H-BW0-ajc-c-07-0-ULs1 NCL_CGAP_Su	2.5
	408729	AA195764	Hs.72639	ESTs	2.5
	455675	BE065984		gb:RC3-BT0319-120200-014-a06 BT0319 Homo	2.5
	411680	AW855718		gb:RC1-CT0279-070100-021-a06 CT0279 Homo	2.5
	455252	AW876627		gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
60	409156	N76186	Hs.173518	M-phase phosphoprotein homolog	2.5
	423175	W27595	Hs.18653	hypothetical protein FLJ14627	2.5
	430291	AV660345	Hs.238126	CGI-49 protein	2.5
	401785				2.5
	402369				2.5
65	439079	AF085937	Hs.38348	ESTs	2.5
	412566	AW962574		gb:EST374647 MAGE resequences, MAGG Homo	2.5
	411463	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	2.5
	413758	BE162391		gb:PM2-HT0451-090100-002-04 HT0451 Homo	2.5
	404988				2.5
70	409446	AI581173	Hs.67688	ESTs	2.5
	412613	AA653507	Hs.285711	hypothetical protein FLJ13089	2.5
	417909	R35614		gb:y966e08.r1 Soares Infant brain 1NIB H	2.5
	454743	AW818456	Hs.79347	KIAA0211 gene product	2.5
	406364				2.5
75	404108				2.5
	411934	AW876538		gb:RC3-PT0028-190100-012-b06 PT0028 Homo	2.5
	415747	AA381209		gb:EST94257 Activated T-cells I Homo sap	2.5
	443526	AW792804	Hs.134002	ESTs	2.5
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	2.5
80	454864	AW835775		gb:QV4-LT0016-240200-110-d04 LT0016 Homo	2.5
	458771	AW295151	Hs.163612	ESTs	2.5
	414349	BE512968		gb:601172296F1 NIH_MGC_15 Homo sapiens c	2.5
	426589	AW954460		gb:EST366530 MAGE resequences, MAGC Homo	2.5
	429515	AL031228	Hs.204370	DNA segment on chromosome 6 (unique, pse	2.5
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	2.5
	411772	BE170301		gb:QV4-HT0536-040500-193-05 HT0536 Homo	2.5
	434784	AA649051	Hs.164007	ESTs	2.5

	429322	D86984	Hs.199243	KIAA0231 protein	2.5
	446252	AI283125	Hs.150009	ESTs	2.5
	453361	AA035197	Hs.107375	ESTs	2.5
5	455275	AW977806		gb:EST389810 MAGE resequences, MAGO Homo	2.5
	449410	AA001356	Hs.18159	ESTs	2.5
	451403	AA885669	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT	2.5
	458861	AI630223		gb:ad05g08.r1 Proliferating Erythroid Ce	2.5
	416944	N22809		gb:yyw41e07.s1 Weizmann Olfactory Epithel	2.5
10	423010	W25436	Hs.90725	ESTs, Moderately similar to I38022 hypot	2.5
	412505	AA974491	Hs.21734	ESTs	2.5
	446399	AI298405	Hs.150080	ESTs	2.5
	412139	BE044976		gb:hn25b10.x1 NCL_CGAP_Thy7 Homo sapiens	2.5
	403691				2.5
15	424025	AI701852	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	2.5
	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	2.5
	422342	AA309272		gb:EST180209 Liver, hepatocellular carci	2.5
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.5
	457770	BE065030	Hs.124179	ESTs	2.5
20	427731	AA411750	Hs.20943	ESTs	2.5
	426920	AA393351	Hs.132121	ESTs	2.5
	427794	AA709186	Hs.282963	ESTs	2.5
	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	2.5
	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
25	414550	BE379808		gb:6011159567T1 NIH_MGC_53 Homo sapiens c	2.5
	436391	AJ227892	Hs.146274	ESTs	2.5
	401989				2.5
	423346	AI267677	Hs.127416	synaptojanin 1	2.5
	444905	AW135863	Hs.209228	ESTs	2.5
30	424539	L02911	Hs.150402	activin A receptor, type I	2.5
	400861				2.5
	458426	AI084514	Hs.249587	ESTs	2.5
	429520	AA160142	Hs.205058	hypothetical protein FLJ20075	2.5
	403568				2.5
35	430592	X80240		gb:H.sapiens endogenous retrovirus HERV-	2.5
	451078	AI927694	Hs.204470	ESTs	2.5
	424560	AA158727	Hs.150555	protein predicted by clone 23733	2.5
	427888	AA417088	Hs.137598	ESTs	2.5
	425541	AA359119		gb:EST68172 Fetal lung II Homo sapiens c	2.5
40	422840	U44059	Hs.121481	thyrotrophic embryonic factor	2.5
	404708				2.5
	405008				2.5
	453772	BE281431	Hs.16323	Homo sapiens, Similar to G antigen 8, cl	2.5
	411036	AA857218	Hs.297007	membrane-bound transcription factor prot	2.5
45	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
	443311	AI657014		gb:tt49a12.x1 NCL_CGAP_GC6 Homo sapiens	2.5
	454277	AW295069	Hs.31743	ESTs, Weakly similar to Z157_HUMAN ZINC	2.5
	454566	AW807605		gb:MR4-ST0098-120100-001-b06 ST0098 Homo	2.5
	454597	AW809648		gb:MR4-ST0124-261099-015-d01 ST0124 Homo	2.5
50	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	2.4
	407851	NM_014496	Hs.40434	ribosomal protein S6 kinase, 90kD, polyp	2.4
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	2.4
	452850	H23230	Hs.22481	ESTs, Moderately similar to A46010 X-in	2.4
	406468				2.4
55	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell e3 93	2.4
	408617	R61736	Hs.124128	ESTs	2.4
	409627	AW997628	Hs.313637	ESTs	2.4
	416665	H72974		gb:yu28a10.s1 Soares fetal liver spleen	2.4
	417404	NM_007350	Hs.82101	pleckstrin homology-like domain, family	2.4
60	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	2.4
	428709	BE268717	Hs.104916	hypothetical protein FLJ21940	2.4
	429654	AI435046	Hs.164318	ESTs	2.4
	432253	AW090822	Hs.274174	transcription elongation factor (SII) e	2.4
	439786	AV652707	Hs.33756	Homo sapiens mRNA full length insert cDN	2.4
65	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	2.4
	453052	R63050	Hs.223813	ESTs	2.4
	454137	AW500340	Hs.313876	ESTs, Weakly similar to I38022 hypoteti	2.4
	459608	AL119471		gb:DKFZp761M141_r1 761 (synonym: hamy2)	2.4
	452843	AI796769	Hs.208320	ESTs	2.4
70	433222	AW514472	Hs.238415	ESTs, Moderately similar to ALU8_HUMAN A	2.4
	449695	AA164569	Hs.34550	ESTs	2.4
	431532	AI537817	Hs.270311	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4
	425967	NM_007159	Hs.4007	Sarcolemmal-associated protein	2.4
	400641				2.4
75	430982	R17432	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	2.4
	432808	NM_015985	Hs.278973	angiopoietin-3	2.4
	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	2.4
	411561	H81164	Hs.285017	hypothetical protein FLJ21799	2.4
	421083	AA283628	Hs.298016	ESTs, Weakly similar to I38022 hypoteti	2.4
80	423513	AF035960	Hs.129719	transglutaminase 5	2.4
	434627	AI221894	Hs.39311	ESTs	2.4
	435663	AI023707	Hs.134273	ESTs	2.4
	455879	BE153275		gb:PM0-HT0335-180400-008-e11 HT0335 Homo	2.4
	451797	AW663858	Hs.333513	small inducible cytokine subfamily E, me	2.4

	409041	AB033025	Hs.50081	KIAA1199 protein	2.4
	423244	AL039379	Hs.209602	ESTs, Weakly similar to ubiquitous TPR m	2.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.4
5	448889	BE140802		gb:L1-HT0028-240699-001-C11 HT0028 Homo	2.4
	439481	AF086294	Hs.125844	ESTs	2.4
	412074	S74683	Hs.73139	ADP-ribosyltransferase 1	2.4
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	2.4
	409298	AA070211		gb:z.m68c04.s1 Stratagene neuroepithelium	2.4
10	411322	AW887330	Hs.172405	cell division cycle 27	2.4
	447640	AI417187		gb:lg75g11.x1 Soares_NhHMPu_S1 Homo sapi	2.4
	447849	AI538147	Hs.164277	ESTs	2.4
	458763	AI693417	Hs.293309	ESTs	2.4
	404638				2.4
15	413885	Z43567		gb:HSC1FC021 normalized infant brain cDN	2.4
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	2.4
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	2.4
	408238	W95901		gb:ze43d11.1.r1 Soares retina N2b4HR Homo	2.4
	436747	AW977192	Hs.291343	ESTs	2.4
	437048	AA743240	Hs.91582	ESTs	2.4
20	413143	BE067232		gb:PM3-BT0347-170200-001-b05 BT0347 Homo	2.4
	404561				2.4
	444009	AI380792	Hs.135104	ESTs	2.4
	400250				2.4
	403891				2.4
25	417002	T79613	Hs.14613	ESTs	2.4
	439446	AI927629	Hs.57873	ESTs	2.4
	441227	AW295407	Hs.128893	ESTs	2.4
	445038	AI635444	Hs.143917	dJ467N11.1 protein	2.4
	455107	BE154113		gb:PM1-HT0340-151299-003-a08 HT0340 Homo	2.4
30	458624	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.4
	459344	AW499533	Hs.257976	ESTs	2.4
	452605	AW968557	Hs.90012	hypothetical protein FLJ23441	2.4
	457652	AF116656	Hs.273809	Homo sapiens PRO1167 mRNA, complete cds	2.4
	450068	AW207212	Hs.280925	ESTs	2.4
35	444750	AW242684	Hs.243623	ESTs	2.4
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	407264	L34727		gb:Homo sapiens T-cell receptor beta (TC	2.4
	443169	AI038687	Hs.133338	ESTs	2.4
40	426536	AI949749	Hs.44441	ESTs	2.4
	449752	AI668626	Hs.61773	Homo sapiens cDNA FLJ11648 fis, clone HE	2.4
	459592	AL037421	Hs.208746	ESTs, Moderately similar to pot. ORF 1 [2.4
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	2.4
	429063	AW363845	Hs.122142	ESTs, Weakly similar to A46010 X-linked	2.4
45	430484	D82880	Hs.241548	RAS p21 protein activator 2	2.4
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	2.4
	447375	AI376660	Hs.257822	ESTs	2.4
	444230	H95537	Hs.146067	ESTs	2.4
	439911	AA854024	Hs.189110	ESTs	2.4
50	421296	NM_002666	Hs.103253	penlipin	2.4
	449385	AI650471	Hs.270370	ESTs	2.4
	430044	AA464510	Hs.152812	ESTs	2.4
	427131	AA448460	Hs.112017	GE36 gene	2.4
	409103	AF251237	Hs.112208	XAGE-1 protein	2.4
55	421354	AA766485	Hs.269664	ESTs	2.4
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	2.4
	440048	AA897461	Hs.328737	ESTs, Weakly similar to envelope protein	2.4
	441359	AW173212	Hs.129041	ESTs	2.4
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	2.4
60	414290	AI568801	Hs.71721	ESTs	2.4
	427342	AL110150	Hs.176680	Homo sapiens mRNA; cDNA DKFZp586D0724 (f	2.4
	459459	AA460445		gb:z.m66h11.1.r1 Soares_tetal_fetus_Nb2HFB_	2.4
	434638	H50758		gb:yp86e06.r1 Soares fetal liver spleen	2.4
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypothe	2.4
65	419537	W27493		gb:31h10 Human retina cDNA randomly prim	2.4
	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
	458734	AI554946	Hs.158794	ESTs	2.4
	449529	AI990559	Hs.232033	ESTs	2.4
70	426088	AF038007	Hs.166196	ATPase, Class I, type 8B, member 1	2.4
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	2.4
	418105	AW937488	Hs.178000	ESTs, Weakly similar to FV1 MOUSE FRIEND	2.4
	430957	AI937072	Hs.55043	Homo sapiens cDNA FLJ13277 fis, clone OV	2.4
	418188	AW139413	Hs.151880	ESTs	2.4
75	424103	NM_001918	Hs.139410	dihydroipoamide branched chain transacy	2.4
	454324	AW608930	Hs.52184	hypothetical protein FLJ20518	2.4
	437369	AA765230	Hs.121742	ESTs	2.4
	453211	W84829		gb:zh53f04.r1 Soares_fetal_liver_spleen_	2.4
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.4
80	400462				2.4
	413697	AA131315	Hs.47144	DKFZP586N0819 protein	2.4
	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.4
	424195	U50536	Hs.142907	Human BRCA2 region, mRNA sequence CG011	2.4
	434163	AW974720	Hs.25206	group XII secreted phospholipase A2	2.4

5	435985	AA703154	Hs.191934	ESTs	2.4
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, Isoenzyme	2.4
	458661	AI299789	Hs.166999	ESTs, Moderately similar to I38344 fin	2.4
	459023	AW968226	Hs.50798	ESTs	2.4
	406005				2.4
10	456561	AI868634	Hs.246358	ESTs, Weakly similar to T32250 hypothei	2.4
	452161	R43077	Hs.221747	ESTs	2.4
	436590	AI393115	Hs.127655	ESTs	2.4
	430151	AW968203		gb:EST380398 MAGE resequences, MAGJ Homo	2.4
	445635	AI769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.4
15	433479	AW511459	Hs.249972	ESTs	2.4
	441676	BE564206	Hs.49889	ESTs	2.4
	407965	W21483	Hs.41707	heat shock 27kD protein 3	2.4
	450682	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	2.4
	452958	AA883929	Hs.40527	ESTs	2.4
20	454032	W31790	Hs.194293	ESTs, Weakly similar to I54374 gene NF2	2.4
	405347				2.4
	440577	AA889945	Hs.326381	EST	2.4
	455780	BE088828		gb:CM2-BT0693-230300-129-g09 BT0693 Homo	2.4
	457024	AA397546	Hs.119151	ESTs	2.4
25	404249				2.4
	437511	AI807500	Hs.125247	ESTs	2.4
	421338	AA287443		gb:zs52c10.r1 NCI_CGAP_GCB1 Homo sapiens	2.4
	425146	AW954627		gb:EST366697 MAGE resequences, MAGC Homo	2.4
	428277	AA425220	Hs.179203	ESTs	2.4
30	444870	AI200621	Hs.148504	ESTs	2.4
	402090				2.4
	458507	AI185703	Hs.206957	ESTs	2.4
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	2.4
	446534	AI307356	Hs.175225	ESTs	2.4
35	453111	AB014598	Hs.31720	hephaestin	2.4
	405230				2.4
	405935				2.4
	413642	BE154837		gb:PM1-HT0345-121199-001-c08 HT0345 Homo	2.4
	420724	AA279694	Hs.191540	ESTs	2.4
40	436998	AA745825	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.4
	445748	U80766	Hs.13252	Human EST clone Z2453 mariner transposon	2.4
	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	2.3
	407404	AF040257		gb:Homo sapiens TNF receptor homolog mRNA	2.3
	440621	AW296024	Hs.150434	ESTs	2.3
45	423417	AP000365	Hs.128342	potassium large conductance calcium-acti	2.3
	424131	AA335714	Hs.199665	ESTs	2.3
	450737	AW007152	Hs.203330	ESTs	2.3
	453687	T55674	Hs.283108	hemoglobin, gamma G	2.3
	442704	AI015463	Hs.130987	ESTs	2.3
50	457756	AA126136	Hs.38125	interferon-induced protein 75, 52kD	2.3
	412732	AW993300		gb:RC2-BN0033-180200-015-g06 BN0033 Homo	2.3
	418998	F13215	Hs.287849	ESTs, Weakly similar to T22074 hypothei	2.3
	419751	AW195581	Hs.93121	KIAA0761 protein	2.3
	429485	AW197086	Hs.99338	ESTs	2.3
55	433377	AI752713	Hs.43845	ESTs	2.3
	434896	AW022054	Hs.136591	ESTs	2.3
	441675	AI914329	Hs.5461	ESTs	2.3
	444711	AI188739	Hs.148488	ESTs	2.3
	445621	AI733818	Hs.145549	ESTs	2.3
60	449182	AW292381	Hs.224150	ESTs	2.3
	430987	Y08564	Hs.248190	UDP-N-acetyl-alpha-D-galactosamine:polyp	2.3
	404058				2.3
	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	2.3
	438315	R56795	Hs.82419	ESTs	2.3
65	423161	AL049227	Hs.124776	Homo sapiens mRNA; cDNA DKFZp564N1116 (f	2.3
	447998	AI768289	Hs.304389	ESTs	2.3
	410150	AW382942	Hs.6774	ESTs	2.3
	432792	AA448114	Hs.278950	protocadherin beta 1.	2.3
	443363	AI792629	Hs.133293	ESTs	2.3
70	440729	AA904739	Hs.128204	ESTs	2.3
	411045	AW854691	Hs.115325	RAB7, member RAS oncogene family-like 1	2.3
	459207	AW138410	Hs.45051	ESTs	2.3
	459124	AW301478	Hs.184592	protein kinase, lysine deficient 1	2.3
	458684	BE281115	Hs.98855	hypothetical protein FLJ20909	2.3
75	427962	AA946582	Hs.8700	deleted in liver cancer 1	2.3
	401899				2.3
	432116	AA902953	Hs.308538	ESTs	2.3
	404196				2.3
	410999	AW813004		gb:RC3-ST0186-230300-019-t02 ST0186 Homo	2.3
80	413308	W28131		gb:427 Human retina cDNA randomly prime	2.3
	430264	AA470519		gb:nc71110.s1 NCI_CGAP_P1 Homo sapiens	2.3
	443482	AW188093	Hs.250385	ESTs	2.3
	453305	R39224	Hs.267997	EHM2 gene	2.3
	451963	AI825440	Hs.224952	ESTs	2.3
80	453043	AW136440	Hs.224277	ESTs	2.3
	435559	AF209198	Hs.42636	zinc finger protein 277	2.3
	440727	AI073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	2.3

	434120	AI436050	Hs.143937	ESTs	2.3
	429768	AA805719	Hs.192154	ESTs	2.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	2.3
5	455841	BE145836		gb:MR0-HT0208-101299-202-b08 HT0208 Homo	2.3
	411093	BE057650		gb:MR4-BT0358-090300-003-e01 BT0358 Homo	2.3
	430706	NM_003540	Hs.247816	H4 histone family, member C	2.3
	428268	AA424957	Hs.294132	ESTs	2.3
	458833	AW236702	Hs.171431	ESTs, Weakly similar to A46010 X-linked	2.3
10	452215	AK002043	Hs.28472	hypothetical protein FLJ111181	2.3
	444109	AI124553	Hs.48965	Homo sapiens cDNA: FLJ21693 fis, clone C	2.3
	428411	AW291464	Hs.10338	ESTs	2.3
	433098	AW190593	Hs.151143	ESTs	2.3
	424882	AI379451	Hs.153636	far upstream element (FUSE) binding prot	2.3
	453178	AA496086	Hs.61648	ESTs	2.3
15	404569				2.3
	413841	M34276	Hs.75576	plasminogen	2.3
	424068	U50531	Hs.138751	Human BRCA2 region, mRNA sequence CG030	2.3
	433532	AW975367		gb:EST387475 MAGE resequences, MAGN Homo	2.3
20	442710	AI015631	Hs.23210	ESTs	2.3
	444206	AW301017	Hs.146492	ESTs	2.3
	451264	AI768235		gb:wg82g08.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.3
	454784	AW820826		gb:RCO-ST0299-190100-012-e10 ST0299 Homo	2.3
	429080	AA446228	Hs.99067	ESTs	2.3
	404166				2.3
25	416327	R99822	Hs.36172	ESTs	2.3
	400631	AF173937	Hs.109494	secreted protein of unknown function	2.3
	438504	AW665281	Hs.224625	ESTs	2.3
	435325	AI038388	Hs.119309	ESTs	2.3
30	421253	AI188102	Hs.31028	ESTs	2.3
	427046	BE246180	Hs.121385	ESTs	2.3
	432711	AA563785	Hs.152465	ESTs, Weakly similar to I38022 hypothe	2.3
	439715	AA524504	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypothe	2.3
35	448458	AW614367	Hs.171054	ESTs	2.3
	452542	AW812256		gb:RCO-ST0174-191099-031-a07 ST0174 Homo	2.3
	417768	R24732	Hs.175139	ESTs	2.3
	427374	AI150033	Hs.143686	ESTs	2.3
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.3
40	423600	AI633559	Hs.310359	ESTs	2.3
	413006	W03857	Hs.34298	ESTs	2.3
	434698	BE044674		gb:hmm46f02.x1 NCI_CGAP_RDF1 Homo sapiens	2.3
	407639	AW205369	Hs.312830	ESTs	2.3
	455121	BE156459		gb:QV0-HT0368-040100-082-f06 HT0368 Homo	2.3
45	448117	H49129	Hs.172982	ESTs	2.3
	443931	H23213	Hs.22657	ESTs	2.3
	450795	AW173371	Hs.60435	ESTs	2.3
	418632	AW118745	Hs.9460	Homo sapiens mRNA; cDNA DKFZp547C244 (fr	2.3
	419441	AW023731	Hs.274368	MSTP032 protein	2.3
50	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	2.3
	418291	BE300369	Hs.289038	hypothetical protein MGC4126	2.3
	455964	BE166924		gb:CM4-HT0501-240300-519-f01 HT0501 Homo	2.3
	445944	H06336	Hs.13480	Homo sapiens clone 24875 mRNA sequence	2.3
	424827	AI057094	Hs.96867	Homo sapiens cDNA: FLJ23155 fis, clone L	2.3
55	449272	AW137656	Hs.197645	ESTs	2.3
	445292	AV653264	Hs.13982	Homo sapiens cDNA FLJ14666 fis, clone NT	2.3
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.3
	444715	AV650947	Hs.282464	ESTs	2.3
	439560	BE565647	Hs.74899	hypothetical protein FLJ12820	2.3
60	444140	AV648089	Hs.282383	ESTs	2.3
	423949	AI014546	Hs.130912	ESTs	2.3
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.3
	445711	T79611	Hs.193691	ESTs	2.3
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	2.3
65	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.3
	429180	AA808287	Hs.58893	ESTs	2.3
	418949	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	2.3
	425523	AB007948	Hs.158244	KJAA0479 protein	2.3
	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
70	419337	AW291112	Hs.209978	ESTs	2.3
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypothe	2.3
	428976	AL037824	Hs.194695	ras homolog gene family, member I	2.3
	436294	AA708310		gb:zg07b07.s1 Soares_pineal_gland_N3HPG	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
75	433939	AL133887	Hs.254122	hypothetical protein	2.3
	450048	AI693269	Hs.202273	ESTs	2.3
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	2.3
	416677	T83470	Hs.334840	ESTs, Moderately similar to I78885 serin	2.3
	405920				2.3
80	405747				2.3
	412105	H07971	Hs.94319	VPS10 domain receptor protein	2.3
	420457	AA482280	Hs.191656	ESTs	2.3
	407726	AA435679	Hs.88594	ESTs	2.3
	423720	AL044191	Hs.23388	hypothetical protein DKFZp434F0318	2.3

	409517	X90780	Hs.120036	troponin I, cardiac	2.3
	435352	AI066599	Hs.120893	ESTs	2.3
	439871	R88518	Hs.46736	hypothetical protein FLJ23476	2.3
5	444098	AV647969	Hs.109694	KIAA1451 protein	2.3
	449276	AW241510	Hs.252713	ESTs	2.3
	417712	AA205569	Hs.194193	ESTs, Moderately similar to ALU1_HUMAN A	2.3
	449015	AL038958	Hs.22668	protein tyrosine phosphatase, non-recept	2.3
	411377	AW841462		gb:RC6-CN0014-080300-012-E09 CN0014 Homo	2.3
10	429276	AF056085	Hs.198612	G protein-coupled receptor 51	2.3
	411816	AW864609		gb:PM3-SN0017-240300-001-h03 SN0017 Homo	2.3
	455280	AW886156		gb:RC5-OT0078-150300-021-E08 OT0078 Homo	2.3
	407809	AW082279	Hs.244106	ESTs	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	424073	U03493	Hs.138959	gap junction protein, alpha 7, 45kd (con	2.3
15	445117	AI208754	Hs.147369	ESTs	2.3
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	2.2
	420230	AL034344	Hs.284186	forkhead box C1	2.2
	411517	AW850267		gb:IL3-CT0219-161199-031-A09 CT0219 Homo	2.2
	403678				2.2
20	457003	S78234	Hs.172405	cell division cycle 27	2.2
	404531	Z25884	Hs.121483	chloride channel 1, skeletal muscle (Th	2.2
	423045	AW967472	Hs.183302	PCTAIRE protein kinase 2	2.2
	409427	AW389668		gb:RC2-ST0168-071299-013-F06 ST0168 Homo	2.2
	434745	AW974445	Hs.185155	ESTs, Weakly similar to T12482 hypotheti	2.2
25	400696				2.2
	407259	L02256		gb:Human Fab fragment binding syncytial	2.2
	411893	R82845	Hs.273789	ESTs	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
30	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
	438018	AK001160	Hs.5999	hypothetical protein FLJ10298	2.2
	458303	AI264628	Hs.125428	ESTs	2.2
	405692				2.2
	403572				2.2
35	415380	F07953	Hs.16085	putative G-protein coupled receptor	2.2
	433014	NM_014711	Hs.279912	KIAA0419 gene product	2.2
	417859	T26453		gb:AB214F6R Infant brain, LLNL array of	2.2
	456472	AK001714	Hs.95744	hypothetical protein similar to ankyrin	2.2
	444106	AI123922	Hs.138215	Homo sapiens cDNA FLJ11400 fis, clone HE	2.2
40	428231	U17989	Hs.183105	nuclear autoantigen	2.2
	454086	AW885909	Hs.6975	PRO1073 protein	2.2
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.2
	416348	H65887	Hs.272163	ESTs	2.2
	403780				2.2
45	414262	AW975616	Hs.291469	ESTs	2.2
	419423	D26488	Hs.90315	KIAA0007 protein	2.2
	442078	AW268583	Hs.262629	ESTs	2.2
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.2
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.2
50	416588	H68558		gb:yu16e04.r1 Soares fetal liver spleen	2.2
	425368	AB014595	Hs.155976	cutlin 4B	2.2
	425686	M73531	Hs.1937	retinal degeneration, slow (retinitis pi	2.2
	441638	AW293202	Hs.133451	ESTs	2.2
	446845	AI343645	Hs.156108	ESTs	2.2
55	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	2.2
	436574	AW293527	Hs.126465	ESTs	2.2
	424584	H10692	Hs.13310	ESTs	2.2
	456347	U00803	Hs.89426	fyn-related kinase	2.2
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	2.2
60	459364	W69284		gb:zd46c03.r1 Soares_fetal_heart_NbHH19W	2.2
	430686	NM_001942	Hs.2633	desmoglein 1	2.2
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	2.2
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.2
	403525				2.2
65	453343	AA905353	Hs.121622	ESTs	2.2
	421574	AJ000152	Hs.105924	defensin, beta 2	2.2
	449327	AI638743	Hs.224672	ESTs	2.2
	454769	AW819848		gb:QV0-ST0294-070300-151-b04 ST0294 Homo	2.2
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/th	2.2
70	401614				2.2
	404767				2.2
	403534				2.2
	410594	AW770778	Hs.281238	ESTs	2.2
	436193	AA706059	Hs.255286	ESTs	2.2
75	439626	N22415	Hs.189080	ESTs	2.2
	456481	AA258033	Hs.108110	DKFZP547E2110 protein	2.2
	441453	AW176106	Hs.285459	ESTs	2.2
	424946	M64572	Hs.153932	protein tyrosine phosphatase, non-recept	2.2
	437332	AA814943		gb:oc07d06.s1 NCI_CGAP_GC81 Homo sapiens	2.2
80	454419	AA082211	Hs.233936	myosin, light polypeptide, regulatory, n	2.2
	416225	AA577730	Hs.188684	ESTs, Weakly similar to PC4259 ferritin	2.2
	450579	AW136774	Hs.48614	ESTs	2.2
	400664				2.2
	447613	AL041057	Hs.33363	DKFZP434N093 protein	2.2

	402689	AK001334	Hs.15470	putative ring zinc finger protein NY-REN	2.2
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor	2.2
	432797	AA565264	Hs.136443	ESTs	2.2
5	405608				2.2
	426365	AA376687	Hs.10283	RNA binding motif protein 8B	2.2
	405634				2.2
	423646	H02364		gb:yrj35d06.r1 Soares placenta Nb2HP Homo	2.2
	434690	AI867679	Hs.148410	ESTs	2.2
10	436572	AA723274	Hs.275596	ESTs	2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	448828	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	2.2
	457802	T78013	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.2
	444585	AW170015	Hs.6594	ESTs	2.2
15	433781	AA609379	Hs.192083	ESTs	2.2
	450587	AI828854	Hs.258538	strafin, calmodulin-binding protein	2.2
	434077	AF116659	Hs.321151	Homo sapiens PRO1412 mRNA, complete cds	2.2
	448756	AI739241	Hs.171480	ESTs	2.2
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.2
20	454471	AW902125		gb:QV0-NN1022-120500-220-h12 NN1022 Homo	2.2
	419107	AW085152	Hs.292987	ESTs	2.2
	455114	AW857121		gb:RC1-CT0302-040400-017-a12 CT0302 Homo	2.2
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	2.2
	454117	BE410100	Hs.40368	adaptor-related protein complex 1, sigma	2.2
25	456056	AA463550	Hs.337532	ESTs, Weakly similar to A47582 B-cell gr	2.2
	409998	M78345	Hs.98265	KIAA1877 protein	2.2
	422352	AA766296	Hs.99200	ESTs	2.2
	409191	AW818390	Hs.175613	homolog of Xenopus Caspin	2.2
	433919	AA746311		gb:aa56d12.r1 NCI_CGAP_GCB1 Homo sapiens	2.2
30	455771	BE084820	Hs.186711	hypothetical protein FLJ20070	2.2
	431632	AK000992	Hs.333144	Homo sapiens cDNA FLJ10130 fis, clone HE	2.2
	454716	AW850584		gb:IL3-CT0219-160200-063-D12 CT0219 Homo	2.2
	413752	BE161807		gb:MR3-HT0446-300300-203-h01 HT0446 Homo	2.2
	458037	AF074982	Hs.226031	ESTs, Highly similar to KIAA0535 protein	2.2
	434239	AF119910	Hs.283047	hypothetical protein PRO2954	2.2
35	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	2.2
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.2
	400697				2.2
	455685	BE066976		gb:PM0-BT0340-211299-003-c12 BT0340 Homo	2.2
40	447039	AV681798	Hs.282915	ESTs	2.2
	404593				2.2
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.2
	421976	AL138443	Hs.23450	mitochondrial ribosomal protein S25	2.2
	401673				2.2
45	425001	U55184	Hs.154145	hypothetical protein FLJ11585	2.2
	447816	NM_007233	Hs.274329	TP53 target gene 1	2.2
	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	2.2
	419118	AA234223	Hs.139204	ESTs	2.2
	426261	AW242243	Hs.168670	peroxisomal farnesylated protein	2.2
50	449808	AA694220	Hs.15403	ESTs, Moderately similar to ALU7_HUMAN A	2.2
	454749	AW818649		gb:RC1-ST0278-040400-018-e02 ST0278 Homo	2.2
	456933	AA363946	Hs.20969	ESTs	2.2
	402942				2.2
	437064	AI023264		gb:ov64h08.s1 Soares_testis_NHT Homo sep	2.2
55	458623	AI305223	Hs.148056	ESTs	2.2
	415257	F03016	Hs.27513	ESTs	2.2
	426269	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	2.2
	442783	AI017586	Hs.131181	ESTs	2.2
	444313	AI140494	Hs.197955	KIAA0704 protein	2.2
60	453444	AL036531		gb:DKFZp564i1162_r1 564 (synonym: hfr2)	2.2
	422757	AI909935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.2
	430013	AA463833	Hs.151275	ESTs, Weakly similar to TRHY_HUMAN TRICH	2.2
	437138	AI935822	Hs.271245	ESTs	2.2
	406298				2.2
65	409723	AW885757	Hs.257862	ESTs	2.2
	414481	AW451956	Hs.8383	bromodomain adjacent to zinc finger doma	2.2
	433266	AI863224	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	457187	AA443927	Hs.144360	EST	2.2
70	445061	AI253094	Hs.145227	ESTs	2.2
	442617	AW340093	Hs.130538	ESTs	2.2
	438298	H23542	Hs.181788	ESTs	2.2
	454916	BE067246		gb:PM1-BT0348-151299-001-d04 BT0348 Homo	2.2
	428017	AA424983	Hs.98312	ESTs	2.2
75	451149	AL047586	Hs.10283	RNA binding motif protein 8B	2.2
	418076	R61388	Hs.6724	ESTs	2.2
	403306	NM_006825	Hs.74358	transmembrane protein (63kD), endoplasmic	2.2
	441811	AI073548	Hs.164597	ESTs	2.2
	434763	AA648618		gb:ms07a11.r1 NCI_CGAP_Ew1 Homo sapiens	2.2
80	447453	AW608645	Hs.18800	hypothetical protein FLJ20281	2.2
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.2
	415424	Z44766		gb:HSC28G081 normalized infant brain cDN	2.2
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	2.2
	421216	AV649282	Hs.102664	vesicle-associated membrane protein 4	2.2

5	429509	AF002246	Hs.210863	cell adhesion molecule with homology to	2.2
	448700	BE614182	Hs.123075	ESTs	2.2
	457741	BE044740		gb:hm55g10.x1 NCI_CGAP_RDF1 Homo sapiens	2.2
	437927	AI039789	Hs.25982	hypothetical protein FLJ21031	2.2
	401694				2.2
10	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	424419	AK001563	Hs.146589	hypothetical protein FLJ10701	2.2
	436640	AA724411	Hs.156065	ESTs	2.2
	438290	AA843719	Hs.122341	ESTs	2.2
	445908	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
15	455735	BE161124		gb:PM0-HT0425-141299-001-A06 HT0425 Homo	2.2
	458455	AV648310	Hs.213488	ESTs	2.2
	430680	AW138724	Hs.168974	ESTs, Highly similar to ALU7_HUMAN ALU S	2.2
	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypotheti	2.2
	424063	NM_002019	Hs.138671	fms-related tyrosine kinase 1 (vascular	2.2
20	441874	AA570389	Hs.128055	ESTs	2.2
	448045	AJ297436	Hs.20166	prostate stem cell antigen	2.2
	433629	R13140	Hs.13359	ESTs	2.2
	415266	AA164199	Hs.270152	ESTs	2.2
	440633	AI140586	Hs.263320	ESTs	2.2
25	442789	AW904361	Hs.131191	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.2
	417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.2
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.2
	401240				2.2
	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
30	411151	AW865497		gb:QV4-SN0024-170400-176-e07 SN0024 Homo	2.2
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	2.2
	436992	AA741074	Hs.120750	ESTs	2.2
	439634	W79377	Hs.167	microtubule-associated protein 2	2.2
	411770	NM_014278	Hs.71992	heat shock protein (hsp 110 family)	2.1
35	400040				2.1
	458762	AW802754		gb:IL2-UM0076-030400-061-H01 UM0076 Homo	2.1
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	2.1
	419953	BE267154	Hs.125752	ESTs	2.1
	410648	AW792909		gb:CM0-UM0001-010300-258-c05 UM0001 Homo	2.1
40	423717	AA330036	Hs.152003	ESTs	2.1
	436683	AW991278	Hs.57787	ESTs	2.1
	445225	AJ216555	Hs.202398	ESTs	2.1
	410991	AW812790		gb:RC3-ST0186-141299-014-g08 ST0186 Homo	2.1
	412639	AW961284	Hs.296235	ESTs	2.1
45	447777	AJ424223		gb:te95a05.x1 NCI_CGAP_Pr28 Homo sapiens	2.1
	451270	AW341392	Hs.235795	ESTs	2.1
	404526	AJ912555	Hs.157195	peptide YY, 2 (seminalplasmin)	2.1
	452492	BE063096		gb:CM4-BT0266-091199-039-e02 BT0266 Homo	2.1
	417154	AJ674701	Hs.21388	ESTs	2.1
50	428152	AA422030		gb:zv26h05.r1 Soares_NhlHMPu_S1 Homo sapi	2.1
	442312	AI820617	Hs.129216	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	456513	AA279143	Hs.88561	ESTs	2.1
	430712	AW044647	Hs.196284	ESTs	2.1
	441445	AJ221959	Hs.187937	ESTs	2.1
55	420288	AW071225	Hs.245556	ESTs	2.1
	412329	AW937445		gb:QV3-DT0043-090200-080-c09 DT0043 Homo	2.1
	447033	AJ357412	Hs.157601	ESTs	2.1
	436853	BE328074	Hs.148661	ESTs	2.1
	455189	AW864176		gb:PM0-SN0014-260400-002-b08 SN0014 Homo	2.1
60	430899	BE018217	Hs.183528	hypothetical protein FLJ14906	2.1
	458356	AI024855	Hs.131575	ESTs	2.1
	457040	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.1
	424480	AA341442	Hs.205299	ESTs	2.1
	403317	U02687	Hs.385	fms-related tyrosine kinase 3	2.1
65	406018				2.1
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	2.1
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein	2.1
	415871	R55995	Hs.283309	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	2.1
70	417725	R25257	Hs.21503	ESTs	2.1
	424856	AA347746	Hs.9521	ESTs, Weakly similar to ZN43_HUMAN ZINC	2.1
	439474	AI824060	Hs.211501	ESTs	2.1
	446895	AA166655	Hs.282803	ESTs	2.1
	448582	AI538880	Hs.94812	ESTs	2.1
75	452783	AA028167	Hs.61486	ESTs	2.1
	442430	R89164	Hs.48320	double ring-finger protein, Dorfin	2.1
	428908	AW303529	Hs.144955	ESTs	2.1
	427335	AA448542	Hs.251677	G antigen 7B	2.1
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.1
80	419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	2.1
	416951	AA190926	Hs.190785	ESTs, Moderately similar to S65657 alpha	2.1
	439950	AW937417	Hs.293561	ESTs	2.1
	458227	Z40670	Hs.181340	ESTs	2.1
	447179	AW015633	Hs.157299	ESTs	2.1
	454950	AW847460		gb:RC3-CT0208-270999-021-e04 CT0208 Homo	2.1
	404453				2.1
	420844	AA595522		gb:nh22c09.s1 NCI_CGAP_Pr1 Homo sapiens	2.1

5	426456	AA580748	Hs.130658	ESTs	2.1
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
	430879	BE149423	Hs.10554	hypothetical protein FLJ12761	2.1
	444584	AI168422		gb:cx30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S	2.1
	446296	AA985662	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT	2.1
10	453853	AL040600	Hs.188083	ESTs	2.1
	414083	AL121282	Hs.257786	ESTs	2.1
	401645				2.1
	435577	W84774	Hs.17643	ESTs	2.1
	427459	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	2.1
15	409168	N94037	Hs.312938	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	410276	AI554545	Hs.68301	ESTs	2.1
	443372	AI792557	Hs.133107	ESTs	2.1
	422093	AF151852	Hs.111449	CGI-94 protein	2.1
	402333				2.1
20	409374	R87083	Hs.19081	ESTs	2.1
	412011	NM_000406	Hs.73064	gonadotropin-releasing hormone receptor	2.1
	412798	AW998557	Hs.119120	E3 ubiquitin ligase SMURF1	2.1
	416085	H18072	Hs.92576	ESTs	2.1
	418378	AW962081		gb:EST374154 MAGE resequences, MAGG Homo	2.1
25	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	2.1
	452374	AL037405	Hs.339639	ESTs	2.1
	450061	AI797034	Hs.201115	ESTs	2.1
	450180	AW449644	Hs.257182	ESTs	2.1
	405120				2.1
30	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.1
	458890	AW865523		gb:PM4-SN0020-010400-009-b05 SN0020 Homo	2.1
	435600	AL047034	Hs.119747	ESTs	2.1
	440964	AI733106	Hs.130218	ESTs	2.1
	417455	AW007066	Hs.18949	ESTs, Weakly similar to CA2B_HUMAN COLLA	2.1
35	435461	AW511956	Hs.293261	ESTs	2.1
	436777	AA731199	Hs.293130	ESTs	2.1
	427521	AW973352	Hs.290585	ESTs	2.1
	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	2.1
	413231	D87461	Hs.75244	BCL2-like 2	2.1
40	423969	AI830571	Hs.331633	hypothetical protein DKFZp566N034	2.1
	411518	AW850246		gb:JL3-CT0219-291099-021-E07 CT0219 Homo	2.1
	443777	AV646510	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	2.1
	416148	H22453	Hs.169187	ESTs	2.1
	402528				2.1
45	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	2.1
	436820	AI684535	Hs.200811	ESTs	2.1
	446209	AI375025	Hs.153368	ESTs	2.1
	453362	H14988	Hs.107375	ESTs	2.1
	417430	AA984546		gb:am88e08.s1 Stratagene schizo brain S1	2.1
50	401069				2.1
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	2.1
	410966	AW812088		gb:RC4-ST0173-191099-032-a07 ST0173 Homo	2.1
	447124	AW976438	Hs.17428	RBP1-like protein	2.1
	449939	T86420	Hs.272139	ESTs	2.1
55	411693	AW852721		gb:CM0-CT0307-210100-158-g09 CT0307 Homo	2.1
	438005	BE151746		gb:PM1-HT0305-061299-003-a06 HT0305 Homo	2.1
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPFZ)	2.1
	407884	BE075316	Hs.95011	syntrophin, beta 1 (dystrophin-associate	2.1
	404694				2.1
60	406668	T62745	Hs.184411	albumin	2.1
	441092	T99289	Hs.126556	EST	2.1
	454643	BE006345		gb:RC2-BN0127-240300-011-d05 BN0127 Homo	2.1
	426646	AA382787	Hs.122713	ESTs	2.1
	431605	AW972407		gb:EST384498 MAGE resequences, MAGL Homo	2.1
65	414452	AA454038	Hs.29032	ESTs	2.1
	401991				2.1
	457176	AA436837		gb:zv57g07.s1 Soares_testis_NHT Homo sap	2.1
	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.1
	428208	AA442327	Hs.104854	ESTs	2.1
70	445049	AV652718		gb:AV652718 GLC Homo sapiens cDNA clone	2.1
	419116	AF292402	Hs.283093	neuromedin U receptor 2	2.1
	427894	AL135709	Hs.28921	zinc finger protein	2.1
	424296	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	2.1
	424323	AA338791	Hs.177788	ESTs	2.1
75	404582				2.1
	418631	AA225921	Hs.115105	ESTs	2.1
	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
	452539	AW105321	Hs.49367	ESTs	2.1
	454658	AW812330	Hs.11123	DKFZP564G092 protein	2.1
80	440310	AA878939	Hs.125406	ESTs	2.1
	433297	AV658581	Hs.282633	ESTs	2.1
	410900	AW810169		gb:MR4-ST0124-040500-007-h07 ST0124 Homo	2.1
	419386	AA236867	Hs.143868	ESTs, Weakly similar to I38022 hypotheti	2.1
	402451				2.1
	447842	AW160804	Hs.247302	twisted gastrulation	2.1
	453880	AI803166	Hs.28462	ESTs, Weakly similar to I38022 hypotheti	2.1
	425189	H16622		gb:ym26c07.r1 Soares infant brain 1N18 H	2.1

	457225	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.1
	400612				2.1
	402318				2.1
5	410534	AW905138		gb:QV0-NN1071-280400-207-g07 NN1071 Homo	2.1
	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
	412029	AW886238		gb:RCS-OT0078-280300-022-F01 OT0078 Homo	2.1
	414494	AA758491	Hs.6783	hypothetical protein FLJ22724	2.1
	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
10	444498	AI151413	Hs.26330	ESTs	2.1
	435191	R15912	Hs.4817	Homo sapiens clone 24461 mRNA sequence	2.1
	425324	M89470	Hs.155644	paired box gene 2	2.1
	430719	AA488988	Hs.293795	ESTs	2.1
	432577	BE208545	Hs.317590	hypothetical protein FLJ14640	2.1
15	407593	AW044083	Hs.237008	ESTs	2.1
	401098				2.1
	440299	AI871778	Hs.250112	ESTs	2.1
	414146	BE549372	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	2.1
	428627	BE002993	Hs.187660	putative Rab5 GDP/GTP exchange factor ho	2.1
20	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphate cyclase	2.1
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	2.1
	439831	AW136488	Hs.25545	ESTs	2.1
	451829	AW964081	Hs.247377	ESTs	2.1
	404595				2.1
25	421498	AA292084	Hs.191575	ESTs, Moderately similar to ALU2_HUMAN A	2.1
	456083	U46922	Hs.77252	fragile histidine triad gene	2.1
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	2.1
	406413				2.1
	439483	T69980	Hs.58323	Homo sapiens cDNA FLJ11613 fis, clone HE	2.1
30	446242	N66336	Hs.7360	ESTs	2.1
	449625	NM_014253	Hs.23796	odt (odd Oz/ten-m, Drosophila) homolog 1	2.1
	457938	AI373638	Hs.133900	ESTs	2.1
	413101	BE066215		gb:RC1-BT0314-310300-015-101 BT0314 Homo	2.1
	406350	AW183350	Hs.250127	ESTs	2.1
35	419812	NM_000562	Hs.93210	complement component 8, alpha polypeptid	2.1
	430881	NM_000809	Hs.248112	gamma-aminobutyric acid (GABA) A recepto	2.1
	429682	NM_008306	Hs.211602	SMC1 (structural maintenance of chromoso	2.1
	409955	U60665	Hs.57692	chromosome 6 open reading frame 10	2.1
	435579	AI332373	Hs.156924	ESTs	2.1
40	436088	AA704687	Hs.191294	ESTs	2.1
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.1
	416100	H18700	Hs.268799	ESTs	2.1
	403218	AL134878	Hs.119500	ribosomal protein, large P2	2.1
	409747	H60964	Hs.331250	ESTs	2.1
45	428764	W21550		gb:zb52112.r1 Soares_fetal_lung_NbHL19W	2.1
	425075	AA506324	Hs.1852	acid phosphatase, prostate	2.1
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.1
	428299	AL038004	Hs.29419	ESTs	2.1
	406817	AI936028		gb:wo47a09.x1 NCI_CGAP_Gas4 Homo sapiens	2.1
50	411940	AW876586		gb:CM4-PT0031-180200-507-e05 PT0031 Homo	2.1
	412446	AI768015	Hs.92127	ESTs	2.1
	414012	AW452334	Hs.128148	ESTs	2.1
	421966	AA904519	Hs.130710	ESTs	2.1
	430566	AA481282	Hs.190149	ESTs	2.1
55	456606	AA292862	Hs.275369	ESTs	2.1
	451604	T65365	Hs.172851	arginase, type II	2.0
	440826	AW196772	Hs.131323	ESTs	2.0
	420687	AA279392	Hs.88605	Homo sapiens cDNA FLJ13427 fis, clone PL	2.0
	459082	BE551721	Hs.282149	ESTs	2.0
60	413241	BE073771	Hs.302414	Homo sapiens clone FLB8945 PRO2411 mRNA,	2.0
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	2.0
	447552	AI394125	Hs.160413	ESTs	2.0
	420905	AA521307	Hs.186651	ESTs	2.0
	428052	AA420477	Hs.26993	ESTs	2.0
65	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.0
	432527	AW975028	Hs.102754	ESTs	2.0
	430202	T85775		gb:yd60g02.r1 Soares fetal liver spleen	2.0
	446610	AV659433	Hs.282984	ESTs, Weakly similar to I38022 hypothe	2.0
	427961	AW293165	Hs.143134	ESTs	2.0
70	455290	U75810		gb:HSU75810 Human Homo sapiens cDNA clon	2.0
	445564	AB028957	Hs.12896	KIAA1034 protein	2.0
	412811	H05382	Hs.21400	ESTs	2.0
	413783	AA314337	Hs.301547	ribosomal protein S7	2.0
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo sapien	2.0
75	429418	AI381028	Hs.118769	ESTs	2.0
	431511	NM_012386	Hs.258581	Homo sapiens p95 paxillin-kinase linker	2.0
	445829	AI452457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
	453123	AI953718	Hs.221849	ESTs	2.0
80	455401	AW936369		gb:QV4-DT0021-301299-071-d07 DT0021 Homo	2.0
	406666	V00495	Hs.184411	albumin	2.0
	445688	AI248205	Hs.153244	ESTs	2.0
	446131	NM_000929	Hs.290	phospholipase A2, group V	2.0
	440388	AI693520	Hs.223000	ESTs	2.0

5	457128	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.0
	404416				2.0
	444187	AW138466	Hs.151274	ESTs	2.0
	431552	AI815863	Hs.259873	axonal transport of synaptic vesicles	2.0
	455814	BE141689		gb:CM1-HT0092-220999-016-b09 HT0092 Homo	2.0
10	454759	AW819455		gb:RC5-ST0293-021299-031-A04 ST0293 Homo	2.0
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	2.0
	404420				2.0
	408112	AW451982	Hs.248613	ESTs	2.0
	432702	AW973953	Hs.293744	ESTs	2.0
15	448587	AI539652	Hs.28338	KIAA1546 protein	2.0
	446854	BE268103	Hs.208914	hypothetical protein MGC10999	2.0
	410569	AA766825	Hs.205675	ESTs	2.0
	432596	AJ224741	Hs.278461	matrilin 3	2.0
	402341				2.0
20	452919	AW962167		gb:EST374240 MAGE resequences, MAGG Homo	2.0
	433632	AA649921	Hs.112553	ESTs	2.0
	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.0
	451927	AL355687	Hs.27261	Homo sapiens mRNA full length insert cDN	2.0
	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	2.0
25	450895	N66727	Hs.10957	ESTs	2.0
	408459	H09701	Hs.278366	ESTs, Weakly similar to I38022 hypothei	2.0
	400942				2.0
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.0
	400859				2.0
30	405829				2.0
	411863	BE075244	Hs.12420	ESTs	2.0
	415258	AW752247	Hs.293853	ESTs	2.0
	416093	R60685	Hs.268698	ESTs, Moderately similar to ALUC_HUMAN I	2.0
	420314	H81671	Hs.320921	ESTs, Weakly similar to T22688 hypothei	2.0
35	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	2.0
	437733	AI792574	Hs.122876	ESTs	2.0
	453118	AW195849	Hs.252757	ESTs	2.0
	457039	H29990	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.0
	454578	AW809178		gb:MR4-ST0118-261099-012-c07 ST0118 Homo	2.0
40	411565	AW851728		gb:MR2-CT0222-011199-007-d06 CT0222 Homo	2.0
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0
	415173	AW501735	Hs.253015	ESTs	2.0
	449011	AI655376	Hs.192693	ESTs	2.0
	410365	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (f	2.0
45	416057	AI927382	Hs.29857	ESTs	2.0
	455688	BE067238		gb:PM1-BT0348-151299-001-a12 BT0348 Homo	2.0
	408531	AW207553	Hs.253639	ESTs	2.0
	434663	AA641972	Hs.130058	ESTs	2.0
	428085	AA421081	Hs.12388	ESTs	2.0
50	425006	R38685	Hs.332622	ESTs	2.0
	446139	H77395	Hs.39749	ESTs	2.0
	400049				2.0
	428333	AW972668	Hs.293044	ESTs	2.0
	429458	BE161832	Hs.292689	ESTs	2.0
55	425087	R62424	Hs.126059	ESTs	2.0
	457122	AI026157	Hs.33728	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
	400310	X63965	Hs.135631	H.sapiens synthetic gene for platelet-de	2.0
	451805	AI968300	Hs.208220	ESTs	2.0
	401986				2.0
60	415318	T06544		gb:EST04433 Fetal brain, Stratagene (cat	2.0
	417756	Z43056		gb:HSC12B021 normalized infant brain cDN	2.0
	418301	AW976201	Hs.53913	hypothetical protein FLJ10252	2.0
	424698	AA164366	Hs.151973	hypothetical protein FLJ23511	2.0
	429110	L29301	Hs.2353	opioid receptor, mu 1	2.0
65	433755	AW085934	Hs.120868	ESTs	2.0
	434118	AF116715	Hs.256256	Homo sapiens PRO2829 mRNA, complete cds	2.0
	435413	AI267476	Hs.46669	ESTs	2.0
	443748	AW206447		gb:UH-BI1-atg-g-02-0-UI.s1 NCI_CGAP_Su	2.0
	445205	D83776	Hs.12413	KIAA0191 protein	2.0
70	458175	AW296024	Hs.150434	ESTs	2.0
	446419	AW576760	Hs.160726	Homo sapiens cDNA FLJ11680 fis, clone HE	2.0
	441627	AA947552	Hs.58085	ESTs	2.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, memba	2.0
	455614	AI693369	Hs.202274	ESTs	2.0
75	449899	AI610700	Hs.103280	ESTs	2.0
	420111	AA255652		gb:zs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	2.0
	437354	AA749215	Hs.291886	ESTs	2.0
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.0
	419691	W03298	Hs.193521	ESTs	2.0
80	439724	AF086565	Hs.60351	EST	2.0
	413362	BE088812		gb:CM2-BT0693-230300-129-d08 BT0693 Homo	2.0
	453652	AW009640	Hs.28368	ESTs, Moderately similar to S65657 alpha	2.0
	434361	AF129755	Hs.117772	ESTs	2.0
	442479	AF069484		gb:AF069484 Homo sapiens astrocytoma lib	2.0
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	2.0
	459323	AW062490		gb:MR0-CT0065-100899-001-d01 CT0065 Homo	2.0
	449438	AA927317	Hs.554	Sjogren syndrome antigen A2 (60kD, ribon	2.0

	400285				2.0
	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
	411459	BE142707		gb:MR0-HT0157-191199-002-g12 HT0157 Homo	2.0
5	417383	W02642	Hs.136102	KIAA0853 protein	2.0
	447153	AA805202	Hs.315562	ESTs	2.0
	447313	U92981	Hs.18081	Homo sapiens clone DT1P186 mRNA, CAG rep	2.0
	455696	BE067870		gb:RC0-BT0362-021299-031-b06 BT0362 Homo	2.0
	456510	AK001652	Hs.99423	ATP-dependent RNA helicase	2.0
10	449815	AI671000	Hs.199739	ESTs	2.0
	425398	AL049689	Hs.156369	hypothetical protein similar to tenascin	2.0
	400238				2.0
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	2.0
	445073	AW291389	Hs.13056	hypothetical protein FLJ13920	2.0
	455221	AW867751		gb:MR0-SN0038-290300-001-a03 SN0038 Homo	2.0
15	413174	AA723564	Hs.191343	ESTs	2.0
	435810	BE349853	Hs.2785	keratin 17	2.0
	418687	R61650	Hs.22581	ESTs	2.0
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	2.0
	431750	AA514986	Hs.283705	ESTs	2.0
20	453242	T98327	Hs.18343	ESTs	2.0
	437074	AJ286235	Hs.128905	hypothetical protein FLJ13204	2.0
	459411	N52920		gb:yv34h09.s1 Soares fetal liver spleen	2.0
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	2.0
	409929	R38772	Hs.172619	myelin transcription factor 1-like	2.0
25	406378				2.0
	459208	BE261314	Hs.149039	ESTs, Weakly similar to I38022 hypothei	2.0
	445260	AJ218133	Hs.147617	ESTs	2.0
	416248	H99169	Hs.23450	mitochondrial ribosomal protein S25	2.0
	445020	AJ205655	Hs.147221	ESTs	2.0
30	402048				2.0
	412695	AW984439		gb:PM3-HN0011-220300-002-c05 HN0011 Homo	2.0
	416408	R94725	Hs.35354	ESTs	2.0
	423347	AJ660412	Hs.234557	ESTs	2.0
	427836	AA416642	Hs.116176	ESTs	2.0
35	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
	436902	AW247145	Hs.192729	ESTs	2.0
	440122	AJ733011	Hs.127678	ESTs	2.0
	442901	AJ023654	Hs.114191	ESTs	2.0
	444097	AW517412	Hs.150757	ESTs	2.0
40	447278	AJ934935	Hs.158669	ESTs	2.0
	451361	AA053854		gb:zf5202.r1 Soares retina N2b4HR Homo	2.0
	451813	NM_016117	Hs.27182	phospholipase A2-activating protein	2.0
	454423	AW603985		gb:RC4-CN0048-140100-011-a04 CN0048 Homo	2.0
45	458801	N98548	Hs.276860	ESTs, Weakly similar to C Chain C, Human	2.0

TABLE 30B

50	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
55	Pkey	CAT number	Accession
	407593	1003161_1	AW044083 AW044094 AW370634
	407594	1003220_1	AW057584 AW057585 AW044153 R34370
	407639	1006924_1	AW205369 AW058599 AW207608
	407676	1008294_1	AW064111 AW064450 AW064429
60	407721	10108_1	Y12735 NM_003582 AW238970 R38268 R41411 R41419 T16717 AA002193 H62028 AJ359545 AW105201 AW087158 AA699728 AJ095264
			AA002065 H62029 AJ289101 AA884804 AA904950 AA609672 AJ139874 H77896
	407726	101126_1	AA435679 AA470655 H22526 AA044031 AA876426 W63767 AJ421140 AJ418990 H42329 H88910 AL041066 H88909 W94610 AW352277 W94648
			W94167 AW952568 AJ419653 AA335501 AA393641 AA044353 H41626 H22525 R58582 AW297645 C75230 AW368034 AW468904 AJ272755
65	407762	101439_1	AW235638 AA346882 AW866803 AA361281 AW963163 AA044373 AA136755
	407764	1014849_1	BE008347 BE008320 BE083307 BE083311 AW075968
	407788	10163_1	BE514982 BE614814 AW393078 AW238480 AA055637 N27644 AA641158 M87068 AA161019 AA161003 AA587315 AA716746 AA593632
			AJ354870 AW183492 Y07755 NM_005978 AW872948 AJ608987 H64656 AF086003 AA643149 AJ819402 H64555 AA858398 AA594885 AJ436747
			BE122811 AA587026 AW857106 AJ950679 AA595012 AA654004 AW238238 AJ971395 AA459074 AA458884 AJ608591 BE181995 BE181970
70			AW195797 C00271 BE182043
	407803	1017498_1	AW081681 N36967 N36959
	407809	1017982_1	AW082279 AW082688
	407811	10180_1	AW190902 AJ802788 AJ041650 AJ037867 AF110137 NM_013372 H99469 N35377 AW151676 AJ678451 AW078795 AW087935 AJ884505
			AW044602 AB032372 AF045800 AJ621183 AJ750578 AA376403 AJ910477 AA373348 AA373673 AJ752124 AL359060 W48619 AA373298 AA373975
75			AW604409 AW604404 AW368603 AA545734 AW361415 AA373557 AW956164 AW853798 AJ750595 AL359059 AA344024 N31127 AW580737
			N27040 AA071138 AJ753050 AA599801 W48852 AA669811 AA112124 AJ940705 W52686 AA084001 C01826 AJ940729 AA373544 AW957491
			AJ383224 AW383164 AW383192 AW383125 AW383194 AW842507 AJ940795 H80042 AW631119 W47324 W42884 AJ750594 AJ754387 AJ753734
			AA372833 AW069006 AJ750577 AW473621 AJ888605 AA600082 AJ041803 W51909 W25447 AJ521673 AJ087351 AA670070 W47325 AA071381
80			W42791 AJ090390 AJ085102 AJ302125 AA788723 AW069430 AW069485 AJ754608 AA373014 BE140150 BE140166 BE140102 BE140143
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	400641	8117693	Plus	4766-4992
	400664	8118496	Plus	13558-13721,13942-14090,14554-14679
	400696	8118812	Minus	77737-77899
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	400706	7249204	Minus	78299-78686
	400816	8569993	Plus	161221-162078
	400842	1927148	Plus	90462-90673
	400859	9757499	Minus	91888-92018,98131-98294,99474-99570
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	401240	3355450	Plus	77433-77636
	401324	9863791	Plus	234057-234174
	401365	9796180	Minus	119572-119672
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	401459	9212270	Minus	182001-183323
	401462	6682291	Plus	112763-112909
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	401645	7657839	Minus	34986-35133
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35	401694	3540172	Minus	64056-64168
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	401878	8099802	Minus	162268-162474,163089-163195
	401887	7229981	Plus	93973-94120
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	401989	4309964	Minus	118611-118821
	401991	4156128	Plus	2398-2513
	402048	8072512	Plus	43936-44078
	402076	8117410	Plus	128316-128627
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	402131	7704961	Minus	33114-33209,33496-33678
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	402341	7656696	Plus	22583-23699
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	402528	7630857	Minus	169609-169742
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	402615	9926801	Plus	131390-132157
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	402942	9368398	Plus	102152-102386
	403011	6693597	Minus	3468-3623
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	403089	8954241	Plus	171964-172239
	403188	9838289	Minus	157618-157755
	403218	7630969	Plus	58039-58149
	403271	7230852	Plus	134283-134485
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	403306	8099945	Plus	127100-127251
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	403317	8318526	Minus	50623-50834
	403329	8516120	Plus	96450-96598
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	403344	8569726	Plus	70823-70990
	403356	8569930	Plus	92839-93036
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	404068	3168621	Minus	18123-18766
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	404193	3881948	Minus	94185-94322
	404196	3805917	Minus	67928-68109
	404249	8655533	Plus	64270-64633
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25	404531	8247909	Plus	20152-20362
	404561	9795980	Minus	69039-70100
	404569	7249169	Minus	104257-104348,104822-104970
	404582	9739220	Plus	53230-53424
	404587	8698840	Minus	69781-70096
30	404588	6456726	Minus	40059-40210
	404593	9944086	Minus	74922-75788
	404595	9958262	Minus	16764-16900
	404638	9796751	Minus	99433-99528,100035-100161
	404652	9796969	Minus	108172-108296
35	404694	9799957	Minus	128092-128227
	404708	9800828	Plus	77522-77658
	404731	7230299	Minus	168609-168781,182951-183081
	404767	7882827	Minus	23244-23759
	404793	7232206	Minus	61087-61590
40	404822	3810614	Plus	7541-8132
	404834	6911603	Minus	37948-38226
	404957	7407927	Plus	147512-148011
	404967	7523744	Minus	89944-90729
	404988	4562677	Minus	72406-72600,72779-72856
45	405001	6015406	Minus	104646-104819
	405008	6088019	Minus	64091-64267
	405090	8072525	Minus	38552-39202
	405120	8099940	Plus	140176-140340
	405229	7249019	Plus	51081-51701
50	405230	7249032	Minus	97493-97682
	405302	2078453	Minus	121688-121840
	405347	2979602	Minus	977-1116
	405443	7408143	Plus	90716-90887,101420-101577
	405455	7656675	Plus	134112-134671
55	405456	7656676	Plus	150052-150208
	405494	8050952	Minus	70284-70518
	405521	9454643	Plus	65096-65247,77508-77637,81242-81364,84246-84395
	405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
	405605	5836195	Minus	117070-117270
60	405608	5815499	Minus	66822-66925
	405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
	405654	4895155	Minus	53624-53759
	405692	4314424	Plus	61379-62562
	405738	9943998	Plus	44370-45410
65	405747	8469069	Minus	153933-154060
	405780	7248203	Minus	48204-48371
	405783	5738434	Minus	27238-27885
	405784	7417368	Minus	77798-78000
	405829	7109593	Minus	15628-16127
70	405820	6758795	Plus	120621-120971
	405935	6758795	Minus	163112-163652
	405970	8247789	Minus	45795-46295
	406005	8247801	Minus	39912-40220
	406018	6758904	Minus	37795-38168
75	406076	9123123	Plus	89972-90319
	406092	9123919	Plus	251370-251797,252168-252882
	406190	7289992	Minus	22395-22901
	406288	7549620	Plus	111718-112008
	406298	5686278	Minus	30084-30770
80	406333	9213235	Plus	64689-64798
	406364	9256114	Minus	50715-50833
	406378	9256142	Minus	126408-126800
	406413	9256407	Plus	43858-44003,46993-47136
	406468	9795553	Plus	4373-4616,6870-9046,11368-11509,11625-11880

406603 8272659 Minus 39506-39694

5 TABLE 31A: ABOUT 1884 GENES UP-REGULATED IN IPF COMPARED TO NSIP

Table 31A lists about 1884 genes whose expression levels are up regulated in idiopathic pulmonary fibrosis (IPF) samples as compared with non-specific interstitial pneumonia (NSIP) samples. These were selected from about 59680 probesets on an Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" idiopathic pulmonary fibrosis sample expression level to "average" non-specific interstitial pneumonia sample expression was greater than or equal to about 2.0. The "average" idiopathic pulmonary fibrosis level was set to the 90th percentile amongst idiopathic pulmonary fibrosis samples. The "average" non-specific interstitial pneumonia level was set to the 90th percentile amongst non-specific interstitial pneumonia samples.

15	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
	R1:	Ratio of IPF (idiopathic pulmonary fibrosis) to NSIP (non-specific interstitial pneumonia)		
20	Pkey	ExAccn	Unigene ID	Unigene Title
	450478	AW451709	Hs.271200	ESTs
	405654			20.2
	432365	AK001106	Hs.274419	hypothetical protein FLJ10244
	403637			16.1
25	431548	AI834273	Hs.9711	novel protein
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon
	439606	W79123	Hs.58561	G protein-coupled receptor 87
	403574			11.9
	416653	AA768553	Hs.74170	metallothionein 1E (functional)
	441233	AA972965	Hs.135668	ESTs
30	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor
	432437	W07088	Hs.293685	ESTs
	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin
35	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor
	403329			8.2
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT
	441519	AA972740	Hs.127092	ESTs
40	453823	AL137967		ESTs
	406590	M29540	Hs.220529	cardioembryonic antigen-related cell ad
	416379	N38857	Hs.203933	ESTs
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca
	407305	AA715284		gb:uv35f03.r1 NCI_CGAP_Br5 Homo sapiens
45	434683	AW298724	Hs.202639	ESTs
	441802	AA968636	Hs.127877	ESTs
	431242	AA987742	Hs.251278	KIAA1201 protein
	442377	AA993807	Hs.167367	ESTs
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-B
50	428908	AW303529	Hs.144955	ESTs
	445898	AF070623	Hs.13423	Homo sapiens clone 24468 mRNA sequence
	457673	AA551589	Hs.272034	hypothetical protein PRO2822
	458771	AW295151	Hs.163512	ESTs
	426800	AA385085		gb:EST88959 Thyroid Homo sapiens cDNA 5'
55	440504	AI948966	Hs.130017	ESTs, Weakly similar to JN0908 H-transp
	415025	AW207091	Hs.72307	ESTs
	438557	AW364104	Hs.143509	hypothetical protein FLJ21924
	416128	AA173632	Hs.22116	CDC14 (cell division cycle 14, S. cerevi
	457242	AA457011		gb:aa90c11.r1 Stratagene fetal retina 93
60	423629	AW021173	Hs.18612	Homo sapiens cDNA: FLJ21909 fis, clone H
	404793			6.2
	435563	AF210317	Hs.95497	solute carrier family 2 (facilitated glu
	415672	N53097	Hs.193579	ESTs
	455488	AA102322		ESTs
65	426230	AA367019	Hs.241395	gb:z190f03.r1 Stratagene colon (937204)
	412282	BE160188		protease, serine, 1 (trypsin 1)
	431622	AW979271	Hs.293184	gb:QV1-HT0413-010200-059-g05 HT0413 Homo
	405523			ESTs
	424693	BE169810	Hs.47557	ESTs
70	436397	AA715013	Hs.169835	ESTs
	456476	AA256753		gb:z522b12.r1 NCI_CGAP_GCB1 Homo sapiens
	434784	AA649051	Hs.164007	ESTs
	422977	AA631498		gb:mp83h04.s1 NCI_CGAP_Thy1 Homo sapiens
	442849	R10099	Hs.269805	ESTs
	451519	AI800600	Hs.209573	ESTs
75	412474	AI791451		gb:mi50c09.y5 NCI_CGAP_Ov2 Homo sapiens
	457081	AA916785	Hs.180510	splicing factor proline/arginine rich (
	444827	R09764	Hs.20416	ESTs
	404822			5.7
	402430			5.7
80	457900	AW976692	Hs.291665	ESTs
	400292	AA250737	Hs.72472	ESTs
	410934	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo
	440172	AA868584	Hs.126154	ESTs

5	431374	BE258532	Hs.251871	CTP synthase	5.7
	409816	AW500954		gb:U1-HF-BP0p-air-h-12-0-U1.r1 NIH_MGC_5	5.6
	447613	AL041057	Hs.33363	DKFZP434N093 protein	5.6
	417919	AI928203	Hs.86379	ESTs	5.6
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.6
10	439063	AF085922	Hs.113968	ESTs	5.6
	406053				5.5
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	5.5
	451830	H18433	Hs.21542	KIAA1035 protein	5.5
	416035	H42314		gb:yo09e02.s1 Soares adult brain N2b5HB5	5.5
15	413849	BE173561	Hs.15384	AP1 gamma subunit binding protein 1	5.5
	459458	AW270957	Hs.254577	ESTs, Weakly similar to B34087 hypotheti	5.5
	416154	Z46122		gb:HSCOV8031 normalized infant brain cDN	5.5
	404561				5.4
	428895	AA437124	Hs.187247	ESTs	5.4
20	419247	S65791	Hs.89764	fragile X mental retardation 1	5.4
	455601	AI368680	Hs.816	SRY (sex determining region Y)-box 2	5.4
	440925	AW511090	Hs.130419	ESTs	5.4
	419249	X14767	Hs.89768	gamma-aminobutyric acid (GABA) A recepto	5.4
	448477	BE612572		gb:601452090F1 NIH_MGC_66 Homo sapiens c	5.4
25	454039	AW079064	Hs.245540	ESTs	5.3
	459664				5.3
	401497				5.3
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	5.3
	444931	AV652066	Hs.75113	general transcription factor IIIA	5.3
30	456680	AL137758	Hs.116072	Homo sapiens mRNA; cDNA DKFZp434H245 (fr	5.3
	452542	AW812256		gb:RC0-ST0174-191099-031-a07 ST0174 Homo	5.2
	411402	BE297855	Hs.69855	NRAS-related gene	5.2
	404957				5.2
	436445	AA922213	Hs.121735	ESTs	5.2
35	442617	AW340093	Hs.130538	ESTs	5.2
	416045	H15990	Hs.31403	ESTs	5.2
	425178	H16097	Hs.161027	ESTs	5.2
	441918	AI733373	Hs.128119	ESTs	5.2
	455464	AW983901		gb:RC1-HN0003-220300-011-f10 HN0003 Homo	5.2
40	420929	AI694143	Hs.296251	programmed cell death 4	5.2
	448844	AI581519	Hs.177164	ESTs	5.2
	430686	NM_001942	Hs.2633	desmoglein 1	5.2
	405229				5.1
	417641	AA205015	Hs.54817	hypothetical protein FLJ20060	5.1
45	434167	AA626334	Hs.116153	ESTs	5.1
	450438	AI696071	Hs.253800	ESTs	5.1
	456394	W28506		gb:48f1 Human retina cDNA randomly prime	5.0
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.0
	417420	T85150	Hs.268814	ESTs	5.0
50	409545	BE296182	Hs.19002	hypothetical protein MGC4675	5.0
	426750	AA383950		gb:EST97403 Thymus II Homo sapiens cDNA	5.0
	440615	AI733055	Hs.130806	ESTs	5.0
	408959	AW890878	Hs.211610	CUG triplet repeat, RNA-binding protein	4.9
	454482	BE147919		gb:RC3-HT0230-160200-016-a08 HT0230 Homo	4.9
55	436508	AW604381	Hs.121121	ESTs, Weakly similar to S00755 pleckstri	4.9
	452046	AB018345	Hs.27657	KIAA0802 protein	4.9
	407415	AF073328		gb:Homo sapiens tetracycline transporter-	4.9
	450090	AW448940	Hs.202259	ESTs	4.9
	406333				4.9
60	434188	AI765848	Hs.281680	peroxisomal trans 2-enoyl CoA reductase;	4.8
	403344				4.8
	446466	H38026	Hs.308	arrestin 3, retinal (X-arrestin)	4.8
	405455				4.8
	411387	AW842339	Hs.130815	hypothetical protein FLJ21670	4.8
65	426097	BE327369	Hs.112238	ESTs	4.8
	427768	T78402	Hs.174890	ESTs	4.8
	411018	AW813428		gb:MR3-ST0192-010200-210-c05 ST0192 Homo	4.8
	415257	F03016	Hs.27513	ESTs	4.8
	441107	AA917075	Hs.190520	ESTs	4.8
70	419519	AI198719	Hs.176376	ESTs	4.8
	410901	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	4.8
	426217	AW131888	Hs.172792	ESTs, Weakly similar to hypothetical pro	4.8
	424188	AW954552	Hs.142634	zinc finger protein	4.8
	456987	AI557290	Hs.173536	ESTs	4.8
75	405303				4.8
	414955	C15506		gb:C15506 Clontech human aorta polyA+ mR	4.8
	451620	AW449888	Hs.257224	ESTs	4.7
	421948	L42583	Hs.334309	keratin 6A	4.7
	424780	U39576	Hs.153058	butyrophilin, subfamily 1, member A1	4.7
80	443271	BE568568	Hs.195704	ESTs	4.7
	417181	L10123	Hs.1071	surfactant protein A binding protein	4.7
	402230				4.7
	422246	AA461032	Hs.5306	hypothetical protein DKFZp586F1122 simil	4.7
	431508	NM_012481	Hs.182979	ribosomal protein L12	4.7
	415236	R41400		gb:y94b12.s1 Soares infant brain 1N1B H	4.7
	413101	BE065215		gb:RC1-BT0314-310300-015-f01 BT0314 Homo	4.6
	444774	AW052174	Hs.196030	ESTs	4.6

5	444414	AW293214	Hs.8752	transmembrane protein 4	4.6
	431291	N25521	Hs.25275	Kruppel-type zinc finger protein	4.6
	436853	BE328074	Hs.148661	ESTs	4.6
	445334	AI610081	Hs.9475	glucose transporter protein 10	4.6
	408172	W02488	Hs.46039	phosphoglycerate mutase 2 (muscle)	4.6
10	426985	BE394849	Hs.131905	ESTs, Moderately similar to Z195_HUMAN Z	4.6
	404638				4.6
	447617	AI400762	Hs.176675	ESTs	4.6
	422182	AL043892	Hs.180582	Homo sapiens cDNA: FLJ21836 fis, clone H	4.6
	442360	AI374621	Hs.29055	ESTs	4.6
15	411738	AW859353		gb:MR1-CT0353-150300-102-a12 CT0353 Homo	4.5
	444157	AI125785	Hs.153351	ESTs	4.5
	401365				4.5
	459592	AL037421	Hs.208746	ESTs, Moderately similar to pot. ORF 1 [4.5
	436269	AA707472	Hs.190760	ESTs	4.5
20	459448	AA416773	Hs.275012	EST	4.5
	452090	AA022684	Hs.124673	Homo sapiens cDNA FLJ11477 fis, clone HE	4.5
	414899	AW975433	Hs.36288	ESTs	4.5
	443764	F23283		gb:HSPD22980 HM3 Homo sapiens cDNA clone	4.5
	444898	AI201548	Hs.308338	ESTs	4.5
25	417428	N87579		gb:LL2030F Human fetal heart, Lambda ZAP	4.5
	428528	AI004034	Hs.98638	ESTs	4.5
	405605				4.5
	457982	AW856093	Hs.183617	ESTs	4.5
	427731	AA411750	Hs.20943	ESTs	4.4
30	420691	AA829433	Hs.275343	ESTs	4.4
	429927	NM_001115	Hs.2522	adenylate cyclase 8 (brain)	4.4
	453080	AI230056	Hs.23921	hypothetical protein DKFZp547A023	4.4
	412147	AW895984		gb:QV4-NN0039-040500-197-e08 NN0039 Homo	4.4
	435747	AI079519	Hs.134398	ESTs	4.4
35	453824	AL138012	Hs.183840	ESTs, Moderately similar to ALU7_HUMAN A	4.4
	458865	T05095	Hs.19597	KIAA1694 protein	4.4
	459037	AW439497	Hs.290656	EST	4.4
	403310				4.4
	425578	U65652	Hs.158313	chromosome 17 open reading frame 1A	4.4
40	427500	AW970017	Hs.293948	ESTs, Weakly similar to S65657 alpha-1C-	4.4
	432020	AI251509	Hs.272345	phosphodiesterase 11A	4.4
	453043	AW136440	Hs.224277	ESTs	4.4
	456293	AW131715	Hs.311561	ESTs, Weakly similar to CYA7_HUMAN ADENY	4.4
	447879	BE503405	Hs.170437	ESTs, Weakly similar to PRP4_HUMAN SALIV	4.4
45	426646	AA382787	Hs.122713	ESTs	4.4
	454864	AW835775		gb:QV4-LT0016-240200-110-d04 LT0016 Homo	4.4
	404898				4.4
	435434	AA680387	Hs.187850	ESTs	4.4
	443314	AW771701	Hs.54646	ESTs	4.3
50	408000	L11690	Hs.620	bulious pemphigoid antigen 1 (230/240kD)	4.3
	441700	AA233556	Hs.126908	hypothetical protein FLJ12994	4.3
	455000	AW850283	Hs.324429	Homo sapiens cDNA FLJ14015 fis, clone HE	4.3
	404767				4.3
	445189	AI936450	Hs.147482	ESTs	4.3
55	452293	H87398	Hs.95858	ribosomal protein L7a	4.3
	428740	AA433838		gb:zw53e12r1 Soares_total_fetus_Nb2HF8_	4.3
	426830	AA385751	Hs.196379	ESTs, Weakly similar to putative p150 [H	4.3
	410615	AW772721		gb:h195c01.x1 NCI_CGAP_Thy8 Homo sapiens	4.3
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.3
60	405692				4.3
	436033	H75391	Hs.255748	ESTs	4.3
	410733	D84284	Hs.66052	CD38 antigen (p45)	4.3
	455587	BE007829		gb:QV0-BN0147-280400-213-d03 BN0147 Homo	4.3
	459084	H01699	Hs.27289	CGI-125 protein	4.3
65	401189				4.3
	435451	AF195420	Hs.303006	ESTs, Weakly similar to gamma-heretulin	4.3
	456407	AW968614		gb:EST380690 MAGE resequences, MAGJ Homo	4.3
	425733	F13267	Hs.159388	Homo sapiens clone Z3578 mRNA sequence	4.3
	447863	AL047611	Hs.288885	Homo sapiens cDNA FLJ14246 fis, clone OV	4.3
70	436659	AI217900	Hs.144464	ESTs	4.3
	435463	AA682507		gb:zj18f08.s1 Soares_fetal_liver_spleen_	4.3
	455675	BE065984		gb:RC3-BT0319-120200-014-a06 BT0319 Homo	4.3
	439481	AF086294	Hs.125844	ESTs	4.3
	405287				4.3
75	405784				4.3
	436461	AW511956	Hs.293261	ESTs	4.3
	437636	AA764781	Hs.291844	ESTs	4.2
	409629	AW449589	Hs.279724	ESTs	4.2
	412999	BE046255		gb:hn38g10.x2 NCI_CGAP_RDF2 Homo sapiens	4.2
80	403281				4.2
	427531	AA405097	Hs.97957	ESTs	4.2
	451882	AI821324	Hs.100445	ESTs	4.2
	418856	AA362858		gb:EST72900 Ovary II Homo sapiens cDNA 5	4.2
	405494				4.2
	456027	BE327387	Hs.13913	KIAA1577 protein	4.2
	414539	BE379046		gb:601236646F1 NIH_MGC_44 Homo sapiens c	4.2

	421106	AA877124	Hs.172844	ESTs	4.2
	409076	N57559	Hs.82273	hypothetical protein	4.2
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	4.2
5	411688	AW953440		gb:EST365510 MAGE resequences, MAGB Homo	4.1
	416614	T83391	Hs.111849	ESTs	4.1
	454434	AA083558	Hs.261286	ESTs	4.1
	404526	AI912555	Hs.157195	peptide YY, 2 (seminalplasmin)	4.1
	446393	AW014174	Hs.301956	zinc finger protein	4.1
	405302				4.1
10	432669	AL043482	Hs.267115	ESTs	4.1
	416972	BE019670		gb:bb28c01.x1 NIH_MGC_5 Homo sapiens cDN	4.1
	423841	AW753967		gb:RC2-CT0304-080100-011-h12 CT0304 Homo	4.1
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	4.1
	430484	D82880	Hs.241548	RAS p21 protein activator 2	4.1
15	403895				4.1
	420457	AA482280	Hs.191656	ESTs	4.1
	438993	AA828995		gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens	4.1
	458421	AI279978	Hs.22547	ESTs	4.1
20	458722	AA741545	Hs.282832	ESTs, Weakly similar to T24961 hypotheti	4.1
	411382	BE067246		gb:PM1-BT0348-151299-001-d04 BT0348 Homo	4.1
	422373	AK001843	Hs.115700	Homo sapiens cDNA: FLJ23515 fis, clone L	4.1
	430749	AJ242956	Hs.25960	v-myc avian myelocytomatosis viral relat	4.1
	403625				4.1
25	401887				4.1
	403667				4.1
	452744	AI267652	Hs.30504	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.0
	421065	AA329711		gb:EST33382 Embryo, 12 week II Homo sapi	4.0
	439294	AW975328	Hs.6523	chromosome 1 open reading frame 12	4.0
30	432792	AA448114	Hs.278950	protocadherin beta 1	4.0
	405443				4.0
	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	4.0
	431822	AA516049		gb:ng65d01.s1 NCI_CGAP_Lip2 Homo sapiens	4.0
	432328	AI572739	Hs.195471	6-phosphofructo-2-kinase/fructose-2,6-bi	4.0
35	448324	AI571356	Hs.34174	ESTs, Moderately similar to ALU8_HUMAN A	4.0
	456536	AW135986	Hs.257859	ESTs	4.0
	415811	AA450191	Hs.172963	hypothetical protein FLJ14624	4.0
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	4.0
	438660	U95740	Hs.6349	Homo sapiens, clone IMAGE:3010666, mRNA,	4.0
40	449327	AI638743	Hs.224672	ESTs	4.0
	426062	N57014	Hs.75874	pregnancy-associated plasma protein A	4.0
	433485	AI93076	Hs.201967	aldo-keto reductase family 1, member C2	4.0
	434849	AW292765	Hs.8053	ESTs	4.0
	400268				4.0
45	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	4.0
	445414	AV653692	Hs.146105	ESTs	4.0
	406470				3.9
	429809	AL162010	Hs.223603	Homo sapiens mRNA; cDNA DKFZp761D09121 (3.9
	453098	Z25935	Hs.86379	ESTs	3.9
50	402867				3.9
	431071	AA491379		gb:aa65f05.r1 NCI_CGAP_GCB1 Homo sapiens	3.9
	436298	AW293496	Hs.180138	ESTs	3.9
	440356	AI933184	Hs.127922	ESTs, Moderately similar to S65657 alpha	3.9
	419091	T85332	Hs.178294	ESTs	3.9
55	422581	L07648	Hs.118630	MAX-interacting protein 1	3.9
	426076	AW962714		gb:EST374787 MAGE resequences, MAGG Homo	3.9
	443682	AI383061	Hs.47248	ESTs, Highly similar to similar to Cdc14	3.9
	444461	R53734	Hs.25978	ESTs, Weakly similar to 2109260A B cell	3.9
	430072	X13294	Hs.300592	v-myb avian myeloblastosis viral oncogen	3.9
60	413499	BE144884		gb:CM0-HT0182-041099-065-e11 HT0182 Homo	3.9
	439818	AL360137	Hs.19934	Homo sapiens mRNA full length insert cDN	3.9
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.9
	424029	AB014594	Hs.137579	KIAA0694 gene product	3.9
	455893	BE179085		gb:RC0-HT0613-140300-021-d06 HT0613 Homo	3.9
65	420111	AA255652		gb:cs21h11.r1 NCI_CGAP_GCB1 Homo sapiens	3.9
	403956	W28077	Hs.79389	nal (chicken)-like 2	3.9
	410318	AA084050	Hs.269259	ESTs, Weakly similar to S23650 retroviru	3.9
	426497	AA379913		gb:EST92807 Skin tumor I Homo sapiens cD	3.9
	430140	AW296771	Hs.221999	ESTs	3.8
70	457042	AI382130	Hs.97703	ESTs	3.8
	450236	AW162998	Hs.24684	KIAA1376 protein	3.8
	417706	T90797	Hs.268623	ESTs	3.8
	428692	AI372822	Hs.110103	RNA polymerase I transcription factor RR	3.8
	413071	BE064032		gb:QV3-BT0296-010300-111-b08 BT0296 Homo	3.8
75	437354	AA749215	Hs.291886	ESTs	3.8
	403381				3.8
	425798	AA364002		gb:EST74529 Pineal gland II Homo sapiens	3.8
	459429	AA278779	Hs.335696	EST	3.8
	426365	AA376667	Hs.10283	RNA binding motif protein 8B	3.8
80	430757	AI458623		gb:tk04g09.x1 NCI_CGAP_Lu24 Homo sapiens	3.8
	430205	AB025904	Hs.235168	carbonic anhydrase XIV	3.8
	433887	AW204232	Hs.279522	ESTs	3.8
	444743	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moi	3.8
	404043				3.8

	431333	AA708488	Hs.120127	Homo sapiens cDNA: FLJ22769 fis, clone K	3.8
	451073	A1758905	Hs.206063	ESTs	3.8
	417663	R07483	Hs.180461	ESTs	3.8
5	432363	AA534489		gb:nt76g11.s1 NCI_CGAP_Co3 Homo sapiens	3.8
	436975	AA740723	Hs.212644	ESTs	3.8
	405959				3.8
	400631	AF173937	Hs.109494	secreted protein of unknown function	3.7
	425937	NM_013240	Hs.163846	putative N5-DNA-methyltransferase	3.7
10	446158	A1277603	Hs.145990	ESTs, Weakly similar to f38022 hypothe	3.7
	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	3.7
	416548	H62953		gb:yr47f06.r1 Soares fetal liver spleen	3.7
	436020	AA778177	Hs.121724	ESTs	3.7
	424989	AA985520	Hs.23575	ESTs	3.7
15	426447	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha po	3.7
	441416	A1990139	Hs.148609	ESTs	3.7
	456443	AW967500	Hs.133543	ESTs	3.7
	402112	R58624	Hs.2186	eukaryotic translation elongation factor	3.7
	404453				3.7
20	451421	W16522	Hs.237689	Homo sapiens cDNA FLJ13539 fis, clone PL	3.7
	421037	A1684808	Hs.197653	ESTs	3.7
	427088	AA398085	Hs.142390	ESTs	3.7
	453375	A1990114	Hs.240091	ESTs	3.7
	453530	AW021633		gb:dl26c02.y1 Morton Fetal Cochlea Homo	3.7
25	406964	M21305		gb:Human alpha satellite and satellite 3	3.7
	432291	AK001108	Hs.274274	hypothetical protein FLJ10246	3.7
	449623	C00719	Hs.120440	EST	3.7
	419691	W03298	Hs.193521	ESTs	3.7
	437597	A1591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.7
	403271				3.7
30	453123	A1953718	Hs.221849	ESTs	3.7
	400462				3.7
	449804	A1535663	Hs.39379	ESTs	3.7
	443305	A1050693	Hs.133318	ESTs	3.7
35	411186	AW821257		gb:PM3-ST0307-231299-001-b11 ST0307 Homo	3.6
	424565	AW102723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	3.6
	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	3.6
	403296				3.6
40	417918	AA209205	Hs.163754	hypothetical protein FLJ12605	3.6
	436026	A1349764	Hs.217081	ESTs	3.6
	429864	AA460039	Hs.286	ribosomal protein L4	3.6
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	3.6
	442910	A1365130	Hs.11307	ESTs, Weakly similar to T19326 hypothe	3.6
	446304	AW104432	Hs.149761	ESTs	3.6
45	441216	BE298830	Hs.192908	ESTs	3.6
	421494	A1763322	Hs.152104	ESTs	3.6
	404476				3.6
	416327	R99822	Hs.36172	ESTs	3.6
50	414146	BE549372	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.6
	417401	AA426026	Hs.187615	ESTs	3.6
	401200				3.6
	411560	AW851186	Hs.179909	hypothetical protein FLJ22995	3.6
	425306	AA447310	Hs.164059	Homo sapiens cDNA FLJ13338 fis, clone OV	3.6
55	437918	A1761449	Hs.121629	ESTs	3.6
	447917	AL048037	Hs.164588	ESTs, Moderately similar to neuronal thr	3.6
	421328	BE466506	Hs.3981	ESTs	3.6
	447290	A1476732	Hs.263912	ESTs	3.6
	417229	AA975096	Hs.19522	hypothetical protein PR02849	3.6
60	425403	AL023753	Hs.156406	Human DNA sequence from clone 1198H6 on	3.6
	403515				3.6
	419917	AA320068	Hs.93701	Homo sapiens mRNA; cDNA DKFZp434E232 (tr	3.6
	435554	AF208502	Hs.185708	early B-cell factor	3.6
	420481	U50525	Hs.98201	Human BRCA2 region, mRNA sequence CG029	3.6
65	410500	R09442		gb:yt26c09.r1 Soares fetal liver spleen	3.6
	439326	W07140	Hs.54721	ESTs	3.6
	426296	R14454	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.6
	411311	AW836491		gb:PM3-LT0032-281299-002-f02 LT0032 Homo	3.6
	418019	R68911	Hs.176275	ESTs	3.6
70	417490	AA203335		gb:zx56g02.r1 Soares_fetal_liver_spleen_	3.6
	423035	AW449679	Hs.156739	H.sapiens XG mRNA (clone PEP11)	3.6
	416575	W02414	Hs.38383	ESTs	3.5
	414400	X06948	Hs.897	Fc fragment of IgE, high affinity I, rec	3.5
	418405	A1868282	Hs.11898	ESTs, Highly similar to KIAA1370 protein	3.5
	450350	T97817	Hs.174880	ESTs	3.5
75	451704	A1755209	Hs.205616	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	421013	M52397	Hs.1345	mutated in colorectal cancers	3.5
	407404	AF040257		gb:Homo sapiens TNF receptor homolog mRN	3.5
	423121	AW864848		gb:PM2-SN0018-290300-003-c09 SN0018 Homo	3.5
	430533	AA480895	Hs.201552	ESTs, Weakly similar to T17288 hypothe	3.5
80	457141	AA521410	Hs.41371	ESTs	3.5
	411772	BE170301		gb:QV4-HT0536-040500-193-f05 HT0536 Homo	3.5
	440737	A1375157	Hs.132221	hypothetical protein FLJ12401	3.5
	452728	A1915676	Hs.239708	ESTs	3.5
	423266	AA323875	Hs.193574	ESTs	3.5

	413543	AA130228	Hs.324611	ESTs, Moderately similar to ALU8_HUMAN A	3.5
	454447	BE163567		gb:CV3-HT0460-230200-101-b08 HT0460 Homo	3.5
	458087	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.5
5	437608	AA761605	Hs.292308	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.5
	415549	F11942		gb:HSC33F061 normalized infant brain cDN	3.5
	420910	AL049437	Hs.100292	Homo sapiens mRNA; cDNA DKFZp586E1120 (f	3.5
	435793	AB037734	Hs.4993	KIAA1313 protein	3.5
	453211	WB4829		gb:zh53f04.r1 Soares_fetal_liver_spleen_	3.5
10	418717	AI334430	Hs.86984	ESTs	3.5
	400641				3.5
	442973	BE567665	Hs.288550	Homo sapiens cDNA: FLJ123156 fis, clone L	3.5
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	3.5
	440364	AA910460	Hs.128626	ESTs	3.5
15	458340	AA57102	Hs.6986	Human glucose transporter pseudogene	3.5
	412281	AI810054	Hs.14119	ESTs	3.5
	443204	AW205878	Hs.29543	Homo sapiens cDNA FLJ13103 fis, clone NT	3.5
	416616	H68270		gb:yr81h09.r1 Soares fetal liver spleen	3.5
	444338	AI937026	Hs.146642	ESTs	3.4
20	436946	AW137748	Hs.125956	ESTs	3.4
	411632	AK000992	Hs.333144	Homo sapiens cDNA FLJ10130 fis, clone HE	3.4
	403306	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	3.4
	422093	AF151852	Hs.111449	CGI-94 protein	3.4
	428816	AA004986	Hs.193852	ATP-binding cassette, sub-family C (CFTR	3.4
25	442137	AA977235	Hs.128830	ESTs, Weakly similar to Z192_HUMAN ZINC	3.4
	405970				3.4
	409434	AF278761	Hs.131581	Homo sapiens testis transcript Y 7 (TTY7	3.4
	416100	H18700	Hs.268799	ESTs	3.4
	431418	X68242	Hs.252722	Hin-1	3.4
30	431954	AK001974	Hs.272242	hypothetical protein FLJ11112	3.4
	440388	AI693520	Hs.223000	ESTs	3.4
	421072	AI215069	Hs.89113	ESTs	3.4
	424578	AK001973	Hs.150890	hypothetical protein	3.4
	436331	AI239495	Hs.120189	ESTs	3.4
35	444063	AI122614		gb:qa96b05.x1 Soares_fetal_heart_NbHH19W	3.4
	444453	AW379394	Hs.145126	ESTs	3.4
	404196				3.4
	421262	AA286746	Hs.9343	Homo sapiens cDNA FLJ14265 fis, clone PL	3.4
40	409555	AW410788	Hs.256185	ESTs	3.4
	417659	T99898		gb:ye68g01.r1 Soares fetal liver spleen	3.4
	416057	AI927382	Hs.29857	ESTs	3.4
	425206	NM_002153	Hs.155109	hydroxysteroid (17-beta) dehydrogenase 2	3.4
	447738	AI871000	Hs.161330	ESTs	3.4
	430664	AW969834	Hs.303303	ESTs	3.4
45	411377	AW841462		gb:RC6-CN0014-080300-012-B09 CN0014 Homo	3.4
	415769	H94186	Hs.5912	F-box only protein 7	3.4
	429382	AI791249	Hs.278054	ESTs, Weakly similar to I38022 hypotheti	3.4
	431474	AL133990	Hs.190642	ESTs	3.4
	456908	AI953671	Hs.220994	hypothetical protein FLJ14129	3.4
50	442826	AI018777	Hs.131241	ESTs	3.4
	400608				3.4
	436111	AI803082	Hs.157212	ESTs	3.4
	452807	AA028933	Hs.162434	ESTs	3.4
55	436577	W84774	Hs.17643	ESTs	3.4
	412209	AW901456		gb:RC0-NN1012-270300-031-c07 NN1012 Homo	3.4
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	3.4
	423871	AA331906		gb:EST35805 Embryo, 8 week I Homo sapien	3.4
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.4
	409623	AW449185		gb:UL-H-B13-akg-e-05-0-ULs1 NCI_CGAP_Su	3.4
60	416182	NM_004354	Hs.79069	cyclin G2	3.4
	420854	AW296927		gb:UL-H-BW0-ajc-c-07-0-ULs1 NCI_CGAP_Su	3.4
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.4
	432404	AA535246	Hs.50852	ESTs	3.4
	458695	AV660159	Hs.282284	ESTs, Weakly similar to I38022 hypotheti	3.4
65	440727	AI073991	Hs.134268	ESTs, Weakly similar to 2109260A B cell	3.3
	428766	AA477989	Hs.98800	ESTs	3.3
	439567	AI056618	Hs.134314	ESTs	3.3
	456231	H73183	Hs.129885	ESTs, Weakly similar to 2004399A chromos	3.3
	454318	AW367764	Hs.7857	erythrocyte membrane protein band 4.1-f	3.3
70	411966	AA099113	Hs.118609	ESTs	3.3
	443644	AI080491	Hs.93270	ESTs, Moderately similar to S65657 alpha	3.3
	437037	T63804		gb:yc21e09.r1 Stratagene lung (937210) H	3.3
	407664	AW063476	Hs.279080	ESTs	3.3
	405780				3.3
75	426567	AA381579	Hs.182962	ESTs	3.3
	400432	AX015809	Hs.287767	Sequence 8 from Patent WO9950285	3.3
	403356				3.3
	404518	AI815601	Hs.79197	CD83 antigen (activated B lymphocytes, i	3.3
80	413581	BE150618		gb:RC3-HT0272-110100-013-c06 HT0272 Homo	3.3
	429875	AI091815		gb:qa58b06.s1 Soares_NhHMPu_S1 Homo sapi	3.3
	433785	BE044593	Hs.112704	ESTs	3.3
	437876	AA770151	Hs.126424	ESTs	3.3
	444870	AI200621	Hs.148504	ESTs	3.3
	453324	W26592	Hs.232089	ESTs	3.3

5	437963	BE396279		gb:601309785F1 NIH_MGC_44 Homo sapiens c	3.3
	425361	AA355933	Hs.132221	hypothetical protein FLJ12401	3.3
	408813	AI580090	Hs.48295	RNA helicase family	3.3
	426692	AK001751	Hs.171835	hypothetical protein FLJ10889	3.3
	407456	AJ237589		gb:Homo sapiens mRNA for T-box transcrip	3.3
10	433183	AF231338	Hs.222024	transcription factor BMAL2	3.3
	435168	AK000883	Hs.301645	Homo sapiens cDNA FLJ10021 fis, clone HE	3.3
	438456	AA913381	Hs.190513	ESTs	3.3
	453242	T98327	Hs.18343	ESTs	3.3
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	3.3
15	412040	D86519	Hs.73086	neuropeptide Y receptor Y6 (pseudogene)	3.3
	435070	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	3.3
	444443	AI149286	Hs.55099	rab6 GTPase activating protein (GAP and	3.3
	434001	AW950905	Hs.3697	serine (or cysteine) proteinase inhibito	3.3
	454145	AA046872	Hs.62798	ESTs	3.3
20	405264				3.3
	411849	AW964970	Hs.18861	ESTs, Moderately similar to KIAA1276 pro	3.3
	416816	T71168	Hs.119567	ESTs, Weakly similar to A47582 B-cell gr	3.3
	435325	AI038388	Hs.119309	ESTs	3.3
	440184	AB002297	Hs.7022	dedicator of cyto-kinesis 3	3.3
25	428356	AL046991	Hs.10338	ESTs	3.3
	429216	AI369472	Hs.65407	ESTs	3.3
	429106	AA446612		gb:zw85g07.s1 Soares_total_fetus_Nb2HF8_	3.3
	405720				3.3
	400889				3.3
30	416294	D86980	Hs.79170	KIAA0227 protein	3.3
	422094	AF129535	Hs.272027	F-box only protein 5	3.3
	425374	AI904013		gb:MR-BT041-220199-104 BT041 Homo sapien	3.3
	418122	R42778	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	3.3
	427374	AI150033	Hs.143686	ESTs	3.3
35	443367	AW071349	Hs.215937	ESTs	3.3
	446645	AI336596	Hs.156294	ESTs	3.3
	457604	AI004397	Hs.334552	Homo sapiens cDNA FLJ14930 fis, clone PL	3.3
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.3
	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	3.3
40	458885	AA411303	Hs.30022	ESTs, Weakly similar to NAH6_HUMAN SODIU	3.3
	429608	U49250	Hs.210862	T-box, brain, 1	3.2
	437454	AL390159	Hs.269812	Homo sapiens mRNA; cDNA DKFZp761M0415 (f	3.2
	430503	AA533574	Hs.152274	ESTs	3.2
	432839	AA579465	Hs.45207	hypothetical protein KIAA1335	3.2
45	421698	T89677	Hs.324323	ESTs	3.2
	412321	AW936913		gb:RC1-DT0029-030200-012-f08 DT0029 Homo	3.2
	422219	AW978073	Hs.1010	regulator of mitotic spindle assembly 1	3.2
	454962	AW847645		gb:IL3-CT0213-280100-056-A04 CT0213 Homo	3.2
	441705	AI087052	Hs.55993	ESTs	3.2
50	403619				3.2
	435608	AW183971	Hs.250896	ESTs	3.2
	426701	AI968103	Hs.209461	Homo sapiens cDNA FLJ12836 fis, clone NT	3.2
	401132				3.2
	407764	BE008347		gb:CM0-BN0154-080400-325-h04 BN0154 Homo	3.2
55	409425	U40462	Hs.54452	zinc finger protein, subfamily 1A, 1 (Ik	3.2
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.2
	443603	BE502601	Hs.134289	ESTs, Weakly similar to KIAA1063 protein	3.2
	419936	AI792768		gb:0191d05.y5 NCL_CGAP_Kid5 Homo sapiens	3.2
	455571	BE003714		gb:QV3-BN0096-200400-161-a01 BN0096 Homo	3.2
60	406592				3.2
	446530	AV658909	Hs.282642	ESTs	3.2
	454466	AA984138	Hs.155101	ATP synthase, H+ transporting, mitochond	3.2
	401449				3.2
	431196	AW974436	Hs.154929	ESTs	3.2
65	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	3.2
	459459	AA460445		gb:zx68h11.r1 Soares_total_fetus_Nb2HF8_	3.2
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	3.2
	427335	AA448542	Hs.251677	G antigen 7B	3.2
	455236	AW875972		gb:CM3-PT0014-071299-051-b05 PT0014 Homo	3.2
70	425156	AA351364		gb:EST59099 Infant brain Homo sapiens cD	3.2
	404588				3.2
	413087	BE064655		gb:RC1-BT0313-301299-012-c09 BT0313 Homo	3.2
	444910	AI201849		gb:xs76g04.x1 NCL_CGAP_Pr28 Homo sapiens	3.2
	426650	NM_002719	Hs.171734	protein phosphatase 2, regulatory subuni	3.2
75	438315	R56795	Hs.82419	ESTs	3.2
	425523	AB007948	Hs.158244	KIAA0479 protein	3.2
	419340	AA236590	Hs.87530	ESTs	3.2
	425636	AK001243	Hs.158370	hypothetical protein FLJ10381	3.2
	430553	AW392821		gb:CM4-ST0275-021299-053-h09 ST0275 Homo	3.2
80	457030	AI301740	Hs.173381	dihydropyrimidinase-like 2	3.2
	447375	AI376660	Hs.257822	ESTs	3.2
	408334	AW514652	Hs.321637	ESTs	3.2
	410085	AA428482	Hs.58589	glycogenin 2	3.2
	410536	N39533		gb:yy27d04.s1 Soares fetal liver spleen	3.2
	448495	AW136516	Hs.208515	ESTs	3.2
	405634				3.2
	431098	AW501465	Hs.249230	ribonuclease L (2',5'-oligoadenylate	3.2

	421581	U89331	Hs.105932	short stature homeobox	3.1
	440633	AI140686	Hs.263320	ESTs	3.1
	453264	AA034137	Hs.271955	ESTs	3.1
5	411656	AW855576		gb:CM4-CT0278-221099-027-001 CT0278 Homo	3.1
	419169	AW851980	Hs.262346	ESTs, Weakly similar to S72482 hypotheti	3.1
	426591	AA431127	Hs.88685	ESTs	3.1
	446956	CO1448	Hs.300611	ESTs	3.1
	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	3.1
10	455170	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	3.1
	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	3.1
	423657	AL045128	Hs.1691	glucan (1,4-alpha), branching enzyme 1	3.1
	400816				3.1
	410307	AF022913	Hs.62187	phosphatidylinositol glycan, class K	3.1
	440046	AW402306	Hs.6877	hypothetical protein FLJ10483	3.1
15	452824	W27643	Hs.73965	splicing factor, arginine/serine-rich 2	3.1
	400315	U46120	Hs.193392	Human expressed unknown mRNA	3.1
	411965	BE467339	Hs.280115	ESTs	3.1
	416316	H58721	Hs.271628	ESTs	3.1
	400613				3.1
20	414819	BE177320	Hs.156148	hypothetical protein FLJ13231	3.1
	434833	AF156548	Hs.192969	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.1
	418693	AI750878	Hs.87409	thrombospondin 1	3.1
	416258	N45661	Hs.90011	adenylosuccinate synthase	3.1
	405093				3.1
25	415273	Z39840	Hs.22229	ESTs	3.1
	450519	AA010066	Hs.224849	Homo sapiens cDNA FLJ12583 fis, clone NT	3.1
	422654	AA314316	Hs.163725	ESTs	3.1
	414605	BE390440		gb:601283601F1 NIH_MGC_44 Homo sapiens c	3.1
30	400441	M15530	Hs.99879	B-cell growth factor 1 (12kD)	3.1
	402790				3.1
	438563	AA810665	Hs.134746	ESTs, Weakly similar to A46010 X-linked	3.1
	447524	D80449	Hs.45177	ESTs	3.1
	448835	BE277929	Hs.11081	UBX domain-containing 2	3.1
35	415979	H16427	Hs.271501	ESTs, Weakly similar to I54374 gene NF2	3.1
	434479	AI138213	Hs.162035	olfactory receptor, family 52, subfamily	3.1
	426724	AA383623	Hs.293616	ESTs	3.1
	418105	AW937488	Hs.178000	ESTs, Weakly similar to FV1 MOUSE FRIEND	3.1
	405608				3.1
	406506				3.1
40	421216	AV649282	Hs.102664	vesicle-associated membrane protein 4	3.1
	452755	AW138937	Hs.213436	ESTs, Weakly similar to A34087 hypotheti	3.1
	404288				3.1
	429878	AA460188	Hs.127263	ESTs	3.1
45	439834	AI754576	Hs.124523	ESTs	3.1
	454564	AW807573		gb:MR1-ST0088-021299-004-g01 ST0088 Homo	3.1
	450491	BE045604	Hs.202301	ESTs	3.1
	409920	BE169746	Hs.12504	likely ortholog of mouse Arkadia	3.1
	400579				3.1
	402953				3.1
50	404285				3.1
	426890	AA393167	Hs.41294	ESTs	3.1
	457770	BE065030	Hs.124179	ESTs	3.1
	435477	BE218708	Hs.117270	hypothetical protein FLJ14345	3.1
55	436391	AJ227892	Hs.146274	ESTs	3.1
	456083	U46922	Hs.77252	fragile histidine triad gene	3.1
	416421	AA134006	Hs.79306	eukaryotic translation initiation factor	3.1
	430101	AF110002	Hs.233363	guanylate cyclase activator 1C	3.1
	449238	AA428229	Hs.331561	muscle-specific RING-finger protein 3	3.1
60	452605	AW968557	Hs.90012	hypothetical protein FLJ23441	3.1
	456323	AW752389	Hs.87296	Homo sapiens cDNA FLJ20269 fis, clone HE	3.1
	429828	AB019494	Hs.225767	IDN3 protein	3.1
	423454	AL110456	Hs.469	succinate dehydrogenase complex, subunit	3.1
	452762	AW501435	Hs.278582	v-akt murine thymoma viral oncogene homo	3.1
	401344				3.1
65	455511	BE144762		gb:CMQ-HT0180-041099-065-b04 HT0180 Homo	3.1
	455280	AW886156		gb:RC5-OT0078-150300-021-E08 OT0078 Homo	3.1
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	3.1
	423600	AI633559	Hs.310359	ESTs	3.1
70	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	3.0
	407257	AB006834		gb:Homo sapiens mRNA for HRV Fab N6-VH,	3.0
	457041	AA399018	Hs.250835	ESTs	3.0
	421482	AL135462	Hs.104715	inversin	3.0
	459062	AA059246	Hs.110293	ESTs	3.0
75	436475	R58806	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.0
	411622	AI807894	Hs.47274	Homo sapiens mRNA; cDNA DKFZp5648176 (fr	3.0
	417489	AW953341	Hs.22573	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	3.0
	409699	BE154650		gb:PM3-HT0344-071299-003-c08 HT0344 Homo	3.0
80	438394	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I	3.0
	443741	AW451759	Hs.145420	ESTs	3.0
	405090				3.0
	432267	AK000872	Hs.274227	Homo sapiens cDNA FLJ10010 fis, clone HE	3.0
	445409	AI949081	Hs.147862	ESTs	3.0

	449347	AV649748	Hs.295901	KIAA0493 protein	3.0
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	3.0
	406364				3.0
5	418409	AA219332	Hs.120869	ESTs, Weakly similar to R107_HUMAN H-REV	3.0
	427050	AA397789	Hs.161803	ESTs	3.0
	431778	AL080276	Hs.268562	regulator of G-protein signalling 17	3.0
	448405	AW207634	Hs.170849	ESTs	3.0
	429846	AB023021	Hs.225945	fucosyltransferase 9 (alpha (1,3) fucosy	3.0
10	438165	AA779344	Hs.138136	ESTs, Weakly similar to 1510254A L1 repe	3.0
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	3.0
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	3.0
	426424	BE081745	Hs.272188	Homo sapiens cDNA FLJ12090 fis, clone HE	3.0
	419505	AA243660	Hs.143061	ESTs	3.0
	403743				3.0
15	415452	F09134	Hs.12839	ESTs	3.0
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	3.0
	447046	AA326187	Hs.17170	G protein-coupled receptor 4	3.0
	455851	BE146879		gb:QV4-HT0222-261099-014-c11 HT0222 Homo	3.0
	400227				3.0
20	436219	AK001695	Hs.146589	hypothetical protein FLJ10701	3.0
	439037	AF075084		gb:Homo sapiens full length insert cDNA	3.0
	439693	AI741816	Hs.125897	ESTs	3.0
	431292	AA370141	Hs.2281	chromogranin B (secrelogranin 1)	3.0
	403513				3.0
25	425745	U44050	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H	3.0
	440122	AI733011	Hs.127678	ESTs	3.0
	448446	AI521251	Hs.171030	ESTs	3.0
	422563	BE299342	Hs.19348	hypothetical protein FLJ13119	3.0
	448130	AW271635	Hs.170717	ESTs	3.0
30	420288	AW071225	Hs.245556	ESTs	3.0
	428201	AA424158	Hs.206461	ESTs	3.0
	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	3.0
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.0
	404513				3.0
35	412074	S74683	Hs.73139	ADP-ribosyltransferase 1	3.0
	407762	AW235638	Hs.29475	ESTs	3.0
	403396				3.0
	436938	AW139680	Hs.161393	ESTs	3.0
	458090	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	3.0
40	400706				2.9
	432779	AW979241		gb:EST391351 MAGE resequences, MAGP Homo	2.9
	444600	R41398	Hs.6996	ESTs	2.9
	403786				2.9
	430187	AI799909	Hs.156989	ESTs	2.9
45	451700	AI470262	Hs.29553	ESTs	2.9
	456649	R74441	Hs.117176	poly(A)-binding protein, nuclear 1	2.9
	457503	AW970244	Hs.162188	ESTs	2.9
	446251	AW867156	Hs.282589	ESTs, Weakly similar to I38022 hypotheti	2.9
	406327				2.9
50	434671	R34758		gb:yg61g02r1 Soares infant brain 1N1B H	2.9
	430175	AA468724		gb:ne09a06.s1 NCI_CGAP_Co3 Homo sapiens	2.9
	454186	BE141030		gb:MR0-HT0067-201099-002-h11 HT0067 Homo	2.9
	449459	BE546846	Hs.195048	ESTs	2.9
	435934	R19382	Hs.117869	ESTs	2.9
55	400325	M85292	Hs.247924	Homo sapiens endogenous HIV-1 related se	2.9
	408408	AF070571	Hs.44690	Homo sapiens clone 24739 mRNA sequence	2.9
	414514	BE327365	Hs.280187	ESTs	2.9
	423717	AA330036	Hs.152003	ESTs	2.9
	424152	AL133591	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	2.9
60	430982	R17432	Hs.22217	Homo sapiens clone IMAGE:32106, mRNA seq	2.9
	424726	AK001007	Hs.138760	Homo sapiens cDNA FLJ10145 fis, clone HE	2.9
	456186	W26642		gb:34b8 Human retina cDNA randomly prime	2.9
	412222	AA528283	Hs.292737	ESTs	2.9
	459201	AW391177		gb:MR3-ST0203-221299-023-d05 ST0203 Homo	2.9
65	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	2.9
	435579	AI332373	Hs.156924	ESTs	2.9
	417027	AA192306	Hs.23926	triadin	2.9
	415533	T74009	Hs.268738	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.9
	445909	BE262656	Hs.32603	hypothetical protein MGC3279 similar to	2.9
70	418343	AA216372	Hs.159501	ESTs	2.9
	459440	BE048054		gb:tz46c03.y1 NCI_CGAP_Bm52 Homo sapien	2.9
	403341				2.9
	445635	AI769774	Hs.209831	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	453830	AA534296	Hs.20953	ESTs	2.9
75	455866	BE149024		gb:CM0-HT0249-291099-084-c04 HT0249 Homo	2.9
	407676	AW064111	Hs.279823	ESTs	2.9
	437913	AI140825	Hs.121623	ESTs	2.9
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	2.9
	457049	AW631495	Hs.27135	B-cell receptor-associated protein BAP29	2.9
80	400491	H25530	Hs.50868	solute carrier family 22 (organic cation	2.9
	456189	H91010	Hs.44940	ESTs	2.9
	441874	AA970389	Hs.128055	ESTs	2.9
	416483	H58311	Hs.165077	ESTs	2.9

	420879	N31165	Hs.238837	ESTs, Weakly similar to S43603 RNA bindi	2.9
	446447	AJ300402	Hs.202250	ESTs	2.9
	439953	AA918129	Hs.124638	ESTs	2.9
	400643				2.9
5	436594	AM419982	Hs.156189	ESTs	2.9
	438402	D16902	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	2.9
	451353	N21043	Hs.42932	ESTs	2.9
	419791	AI579909	Hs.105104	ESTs	2.9
10	415628	F13080		gb:HSC3D041 normalized infant brain cDN	2.9
	423637	AL137279	Hs.130187	Homo sapiens mRNA; cDNA DKFZp434O1214 (f	2.9
	454747	AW818535		gb:RC1-ST0278-140300-016-f05 ST0278 Homo	2.9
	452778	R71338	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	2.9
	457178	AL039101	Hs.194625	dynein, cytoplasmic, light intermediate	2.9
	401526				2.9
15	408751	N91553	Hs.258343	ESTs	2.9
	414140	AA281279	Hs.23317	hypothetical protein FLJ14681	2.9
	417320	AA195667	Hs.86022	ESTs	2.9
	442927	AI024347	Hs.131519	ESTs	2.9
20	444125	AI124882	Hs.118121	ESTs	2.9
	453901	BE065902		gb:RC2-8T0318-150200-011-b09 BT0318 Homo	2.9
	421847	NM_014717	Hs.108884	KIAA0390 gene product	2.8
	434424	AI811202	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.8
	422225	BE245652	Hs.118281	zinc finger protein 266	2.8
	403011				2.8
25	405170				2.8
	435878	R08330	Hs.20152	ESTs	2.8
	436194	AK001074	Hs.333435	Homo sapiens cDNA FLJ10212 fis, clone HE	2.8
	400394	AF040257	Hs.283818	Homo sapiens TNF receptor homolog mRNA,	2.8
30	411244	AW833768		gb:QV4-TT0008-130100-077-e06 TT0008 Homo	2.8
	441817	AW969706	Hs.293332	ESTs	2.8
	456118	AA380267	Hs.78277	DKFZP434F2021 protein	2.8
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	2.8
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	2.8
	402131				2.8
35	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	2.8
	438160	AA779332	Hs.122671	ESTs	2.8
	407594	AW057584	Hs.160681	ESTs	2.8
	417877	AI025829	Hs.86320	ESTs	2.8
40	439235	N45513	Hs.46608	ESTs	2.8
	451257	AA016255	Hs.31856	ESTs, Weakly similar to KIAA1453 protein	2.8
	437113	AA744683		gb:ny26c10.s1 NCL_CGAP_GCB1 Homo sapiens	2.8
	430882	BE174240	Hs.79024	heterogeneous nuclear ribonucleoprotein	2.8
	409978	D31897	Hs.57714	double C2-like domains, alpha	2.8
45	410672	AW794800		gb:RC6-UM0014-170300-022-C05 UM0014 Homo	2.8
	412236	AW902583		gb:QV3-NN1024-260400-171-f10 NN1024 Homo	2.8
	417827	T79366	Hs.108258	actin binding protein; macrophilin (microf	2.8
	420206	M91463	Hs.95958	solute carrier family 2 (facilitated glu	2.8
	449676	AW380579	Hs.209657	ESTs	2.8
50	454778	AW820199		gb:QV2-ST0296-190100-029-a07 ST0296 Homo	2.8
	451203	AW070604	Hs.46517	ESTs	2.8
	450180	AW449644	Hs.257182	ESTs	2.8
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.8
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.8
55	450003	AA777809	Hs.191996	ESTs	2.8
	401602				2.8
	413986	Z43567		gb:HSC1FC021 normalized infant brain cDN	2.8
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	2.8
	415652	T79213	Hs.272073	ESTs	2.8
	404076				2.8
60	409416	AW388359	Hs.10667	ESTs	2.8
	420814	AA721156	Hs.190440	ESTs	2.8
	426960	AA393713		gb:zf71h04.r1 Soares_testis_NHT Homo sap	2.8
	419227	BE537383	Hs.89739	cholinergic receptor, nicotinic, beta po	2.8
65	448597	BE613250	Hs.98265	KIAA1877 protein	2.8
	409928	AL137163	Hs.57549	hypothetical protein dJ473B4	2.8
	433077	AA314262	Hs.301917	YDD19 protein	2.8
	436720	AW975902		gb:EST388011 MAGE resequences, MAGN Homo	2.8
	447410	AI470235	Hs.172698	EST	2.8
70	414652	AI620599	Hs.72068	ESTs	2.8
	430454	AW469011	Hs.105635	ESTs	2.8
	412417	AA102268	Hs.158622	ESTs	2.8
	423130	AW897586	Hs.21213	ESTs	2.8
	430560	R11884	Hs.100826	ESTs	2.8
	401098				2.8
75	454036	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	2.8
	403549				2.8
	414394	AI904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.8
	412323	AW937143		gb:PM1-DT0041-281299-001-f01 DT0041 Homo	2.8
80	433513	AI566356	Hs.171437	ESTs	2.8
	446677	AI800311	Hs.156291	ESTs	2.8
	457756	AA126136	Hs.38125	interferon-induced protein 75, 52kD	2.8
	450895	N66727	Hs.10957	ESTs	2.8
	434352	AF129505	Hs.86492	small muscle protein, X-linked	2.8

	449358	AA001229	Hs.131436	ESTs	2.8
	422816	AA323586	Hs.93235	ESTs	2.8
	420756	AA411800	Hs.189900	ESTs	2.8
5	423532	BE090503		gb:RC6-BT0717-110400-011-F11 BT0717 Homo	2.8
	448870	BE181783	Hs.175358	ESTs, Weakly similar to A47582 B-cell gr	2.8
	451206	H86228	Hs.271780	ESTs, Weakly similar to I38022 hypothei	2.8
	457314	AA479597	Hs.193669	hypothetical protein DKFZp586J1119	2.8
	458023	AW978161	Hs.268555	5'-3' exonuclease 2	2.8
10	422260	AA315993	Hs.105484	regenerating gene type IV	2.8
	429638	AI916662	Hs.211577	kinecin 1 (kinesin receptor)	2.8
	408936	AL138043	Hs.293549	ESTs	2.8
	411762	AW860972		gb:QV0-CT0387-180300-167-h07 CT0387 Homo	2.8
	416192	NM_005036	Hs.968	peroxisome proliferative activated recep	2.8
15	455310	AW893961		gb:RC4-NN0027-050400-011-d11 NN0027 Homo	2.8
	406992	S82472		gb:beta -pol=DNA polymerase beta (exon a	2.7
	421003	T72080	Hs.95567	F-box protein 30	2.7
	429593	AK000332	Hs.209927	Homo sapiens cDNA FLJ20325 fis, clone HE	2.7
	445611	AW418497	Hs.145583	ESTs	2.7
20	445747	AI820863	Hs.145328	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
	445017	AI205493	Hs.176860	ESTs	2.7
	411726	AW858812		gb:CM3-CT0341-190400-152-h12 CT0341 Homo	2.7
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	2.7
	416805	F13271	Hs.79981	Human clone 23560 mRNA sequence	2.7
25	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.7
	427134	AA398409	Hs.173561	EST	2.7
	435689	AA694284		gb:zi35c02.s1 Soares_fetal_liver_spleen_	2.7
	429282	N27596	Hs.21342	ESTs	2.7
	435731	AA699581	Hs.186811	ESTs	2.7
30	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	2.7
	421274	BE160327	Hs.104572	ESTs	2.7
	403776				2.7
	409526	BE298751	Hs.55014	hypothetical protein FLJ10206	2.7
	410201	AA126129		gb:zm78c07.r1 Stratagene neuroepithelium	2.7
35	427839	AA608823	Hs.98244	ESTs	2.7
	447884	H29505		gb:ym60d10.r1 Soares infant brain 1N1B H	2.7
	449396	BE169100	Hs.195029	ESTs	2.7
	422988	AW673847	Hs.97321	ESTs	2.7
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	2.7
40	434890	AF161345	Hs.283930	Homo sapiens HSPC082 mRNA, partial cds	2.7
	412400	AW948066		gb:RC0-MT0012-290300-031-h10 MT0012 Homo	2.7
	413998	AW103807	Hs.243933	ESTs	2.7
	403677				2.7
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	2.7
45	430698	AA492071		gb:ne97b04.s1 NCI_CGAP_Kid1 Homo sapiens	2.7
	432581	AA643238	Hs.146144	ESTs	2.7
	446800	AI341635	Hs.156486	ESTs	2.7
	454938	AW846134		gb:QV0-CT0179-091199-049-d02 CT0179 Homo	2.7
	455869	BE467912	Hs.154294	discs, large (Drosophila) homolog 1	2.7
50	445233	AV653034	Hs.297559	ESTs	2.7
	448756	AI739241	Hs.171480	ESTs	2.7
	418379	AA218940	Hs.137516	fidgetin-like 1	2.7
	435068	H16262	Hs.31415	ESTs	2.7
	406092				2.7
55	422036	AA302647	Hs.271891	ESTs, Weakly similar to ZN91_HUMAN ZINC	2.7
	441541	AA938663	Hs.199828	ESTs	2.7
	451395	AI082419	Hs.114761	ESTs	2.7
	455880	BE153208		gb:PM0-HT0335-050400-007-F10 HT0335 Homo	2.7
	459275	AI808913	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	2.7
60	423949	AI014546	Hs.130912	ESTs	2.7
	435420	AI928513	Hs.59203	ESTs	2.7
	439418	AI282149	Hs.56213	ESTs, Highly similar to FXD3_HUMAN FORKH	2.7
	454790	AW820852		gb:RC2-ST0301-120200-011-F12 ST0301 Homo	2.7
	447453	AW608645	Hs.18800	hypothetical protein FLJ20281	2.7
65	454767	BE069199		gb:QV3-BT0379-010300-105-g03 BT0379 Homo	2.7
	413252	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	2.7
	402429				2.7
	403760				2.7
	433128	AB021923	Hs.23367	EST-YD1 protein	2.7
70	435448	H17132	Hs.27085	ESTs	2.7
	445706	AA305520	Hs.108812	hypothetical protein FLJ22004	2.7
	422171	U50529	Hs.112434	Novel human gene mapping to chromosome 13	2.7
	459023	AW968226	Hs.60798	ESTs	2.7
	443246	T75157	Hs.337603	ESTs, Weakly similar to T08680 hypothei	2.7
	404569				2.7
75	410181	AI468210	Hs.261285	pleiotropic regulator 1 (PRL1, Arabidops	2.7
	422897	AA679784	Hs.4290	ESTs	2.7
	427038	NM_014633	Hs.173288	KIAA0155 gene product	2.7
	449880	AI673006	Hs.231948	ESTs	2.7
	455992	BE179015		gb:RC3-HT0612-080500-013-h10 HT0612 Homo	2.7
80	415268	R53935	Hs.287827	ESTs, Highly similar to MDR3_HUMAN MULTI	2.7
	446554	AA151730	Hs.301769	nudix (nucleoside diphosphate linked moi	2.7
	452512	AW363486	Hs.337635	ESTs	2.7
	440728	AW086077	Hs.153272	Homo sapiens cDNA: FLJ22715 fis, clone H	2.7

	419481	AI879195	Hs.90606	15 kDa selenoprotein	2.7
	454352	AW389668		gb:RC2-ST0168-071299-013-06 ST0168 Homo	2.7
	422831	R02504	Hs.332943	ESTs	2.7
5	413646	BE155042		gb:PMO-HT0349-101299-002-E04 HT0349 Homo	2.7
	426872	AA410446	Hs.112011	ESTs, Weakly similar to unknown [H.sapie	2.7
	459160	AI904723		gb:CM-BT066-120299-092 BT066 Homo sapien	2.7
	421338	AA287443		gb:zs52c10.r1 NCI_CGAP_GCB1 Homo sapiens	2.7
	446002	AI346468	Hs.145789	ESTs	2.7
10	454716	AW850584		gb:IL3-CT0219-160200-063-D12 CT0219 Homo	2.7
	406684	L34041	Hs.9739	glycerol-3-phosphate dehydrogenase 1 (so	2.7
	453128	AW026516	Hs.31791	acylphosphatase 2, muscle type	2.7
	408591	AW250525		gb:2821626.5prime NIH_MGC_7 Homo sapiens	2.7
	454754	AW819191		gb:CM1-ST0283-071299-061-d08 ST0283 Homo	2.7
15	439451	AF086270	Hs.278554	heterochromatin-like protein 1	2.7
	445225	AI216555	Hs.202398	ESTs	2.7
	427175	H06924	Hs.23782	hypothetical protein FLJ12847	2.7
	411816	AW864609		gb:PM3-SN0017-240300-001-h03 SN0017 Homo	2.7
	438135	AI253025	Hs.190426	ESTs	2.7
20	405981				2.7
	406005				2.7
	430762	AI343652	Hs.105667	ESTs	2.7
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	2.7
	412105	H07971	Hs.94319	VPS10 domain receptor protein	2.7
25	434684	AA737282	Hs.190911	ESTs	2.7
	445660	AI702668	Hs.201955	ESTs	2.7
	400844				2.6
	415725	BE219771	Hs.237146	hypothetical protein FLJ12752	2.6
	420159	AI572490	Hs.99785	Homo sapiens cDNA: FLJ21245 fis, clone C	2.6
30	408812	BE397160	Hs.254763	ESTs, Weakly similar to A42442 integrin	2.6
	430052	AF102850	Hs.227933	Alg5, S. cerevisiae, homolog of	2.6
	440310	AA878939	Hs.125406	ESTs	2.6
	425659	AK000590	Hs.158836	hypothetical protein FLJ20583	2.6
	417252	AA195014	Hs.85971	ESTs	2.6
35	427167	AI239607	Hs.99196	hypothetical protein MGC11324	2.6
	431613	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f	2.6
	414546	BE379492		gb:601236215F1 NIH_MGC_44 Homo sapiens c	2.6
	407494	U10072		gb:Human forkhead family (AFX1) mRNA, pa	2.6
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.6
40	442240	AI791883	Hs.292719	ESTs	2.6
	452821	AW471181	Hs.160874	ESTs	2.6
	410238	N94320	Hs.144225	ESTs	2.6
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fis, clone HE	2.6
	440801	AA906366	Hs.190535	ESTs	2.6
	440274	R24595	Hs.7122	scrapie responsive protein 1	2.6
45	411597	AW852925		gb:PMO-CT0248-131099-001-f10 CT0248 Homo	2.6
	417956	AA210704	Hs.190465	ESTs	2.6
	420621	AA278808		gb:zs79c09.r1 NCI_CGAP_GCB1 Homo sapiens	2.6
	425176	AW015644	Hs.155005	TEA domain family member 1 (SV40 transcr	2.6
50	425492	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	2.6
	425698	NM_016112	Hs.159241	polycystic kidney disease 2-like 1	2.6
	426098	NM_014906	Hs.166351	KIAA1072 protein	2.6
	435113	AA665469	Hs.117136	ESTs	2.6
	438188	AA779975	Hs.128859	ESTs	2.6
	445550	AI242754	Hs.137306	ESTs	2.6
55	458804	AL157625		gb:DKFZp761L2016_r1 761 (synonym: hamy2)	2.6
	448299	AA497044	Hs.20887	hypothetical protein FLJ10392	2.6
	436407	T88803	Hs.271507	ESTs, Weakly similar to TIM_HUMAN PROBAB	2.6
	425195	AA352026	Hs.94319	VPS10 domain receptor protein	2.6
60	418282	AA215535	Hs.98133	ESTs	2.6
	442757	AI739528	Hs.28345	ESTs	2.6
	413470	N20934		gb:yx54c11.s1 Soares melanocyte 2NbHM Ho	2.6
	428527	AI902398	Hs.34492	Cyt19 protein	2.6
	441209	AA922939	Hs.135742	ESTs	2.6
65	458679	AW975460	Hs.143563	ESTs	2.6
	442279	AW867006	Hs.159970	ESTs	2.6
	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	2.6
	411880	AW872477		gb:hm30f03.x1 NCI_CGAP_Thy4 Homo sapiens	2.6
	404845				2.6
70	411693	AW857271		gb:CMO-CT0307-210100-158-g09 CT0307 Homo	2.6
	438298	H23542	Hs.181788	ESTs	2.6
	444517	AI939339	Hs.146883	ESTs	2.6
	455870	AW452631	Hs.313803	ESTs, Highly similar to AF157833 1 noncl	2.6
	457630	AI680803	Hs.112627	ESTs	2.6
75	424015	N95696	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	2.6
	417563	AA203701		gb:zx52a10.r1 Soares_fetal_liver_spleen_	2.6
	413174	AA723564	Hs.191343	ESTs	2.6
	438875	AA827640	Hs.189059	ESTs	2.6
	440700	AW952281	Hs.296184	guanine nucleotide binding protein (G pr	2.6
80	423257	AW161039	Hs.125878	synapsin III	2.6
	431086	AI829692	Hs.211561	ESTs	2.6
	409337	H71289	Hs.220535	ESTs	2.6
	442818	AK001741	Hs.8739	hypothetical protein FLJ10879	2.6
	410004	AI298027	Hs.5057	carboxypeptidase D	2.6

	455935	BE158687	gb:CMD-HT0395-280100-169-b09 HT0395 Homo	2.6
	403273			2.6
	445955	AA332209	Hs.158196 transcriptional adaptor 3 (ADA3, yeast h	2.6
	425626	AI537536	Hs.173519 ESTs	2.6
5	451531	AA018311	Hs.114762 ESTs	2.6
	428085	AA421081	Hs.12388 ESTs	2.6
	429761	AI276780	Hs.135173 ESTs	2.6
	437958	BE139550	Hs.121668 ESTs, Moderately similar to PC4259 ferri	2.6
	442666	W74633	Hs.303720 ESTs	2.6
10	413088	BE064962	gb:RC1-BT0313-130400-016-c02 BT0313 Homo	2.6
	419107	AW085152	Hs.292987 ESTs	2.6
	435766	R11673	Hs.186498 ESTs	2.6
	452879	AW905328	Hs.180842 ribosomal protein L13	2.6
	440400	AA994364	Hs.125594 ESTs, Weakly similar to T25472 hypotheti	2.6
15	440460	H92571	Hs.234478 Homo sapiens cDNA: FLJ22648 fis, clone H	2.6
	424146	AA705092	Hs.202368 ESTs	2.6
	439950	AW937417	Hs.293561 ESTs	2.6
	410366	AI267589	Hs.302689 hypothetical protein	2.6
20	417485	AA203304	Hs.32826 CG-130 protein	2.6
	412566	AW962574	gb:EST374647 MAGE resequences, MAGG Homo	2.6
	416498	U33632	Hs.79351 potassium channel, subfamily K, member 1	2.6
	440397	AA884448	Hs.157239 ESTs	2.6
	451236	AI767406	Hs.207026 ESTs, Weakly similar to B56205 transcrip	2.6
25	411819	AW947884	gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.6
	430357	AW976789	Hs.165607 ESTs	2.6
	432869	AW974094	gb:EST386197 MAGE resequences, MAGM Homo	2.6
	427506	AK000134	Hs.179100 hypothetical protein FLJ20127	2.6
	401614			2.6
30	404531	Z25884	Hs.121483 chloride channel 1, skeletal muscle (Th	2.6
	426698	AA394104	Hs.97489 ESTs	2.6
	440479	AA886461	Hs.208161 ESTs	2.6
	443160	AI467915	Hs.36053 ESTs	2.6
	419323	AI092379	Hs.135275 ESTs	2.5
35	442813	AI018435	Hs.270970 ESTs	2.5
	436196	AK001084	Hs.333498 Homo sapiens cDNA FLJ10222 fis, clone HE	2.5
	433561	BE540937	Hs.20104 hypothetical protein FLJ00052	2.5
	434059	AA649162	Hs.236456 ESTs	2.5
	454836	AW833711	gb:QV4-TT0008-251199-043-e11 TT0008 Homo	2.5
40	458589	AV654623	Hs.288141 hypothetical protein MGC3156	2.5
	459716			2.5
	436340	R42246	Hs.21606 ESTs	2.5
	428020	L19058	Hs.181581 glutamate receptor, ionotropic, kainate	2.5
	416951	AA190926	Hs.190785 ESTs, Moderately similar to S65657 alpha	2.5
45	401078			2.5
	410644	AW902125	gb:QV0-NN1022-120500-220-h12 NN1022 Homo	2.5
	411660	AW855718	gb:RC1-CT0279-070100-021-a06 CT0279 Homo	2.5
	425201	AA352111	gb:EST60061 Activated T-cells XX Homo sa	2.5
	455252	AW876627	gb:RC3-PT0028-120200-013-d11 PT0028 Homo	2.5
50	439096	AA830185	Hs.269680 ESTs	2.5
	442627	AI027990	Hs.132303 ESTs	2.5
	457799	AF220188	Hs.236510 uncharacterized hypothalamus protein HTM	2.5
	428799	AI478619	Hs.104677 ESTs	2.5
	450402	BE218027	Hs.89969 ESTs	2.5
55	411156	AW819939	Hs.273629 ESTs	2.5
	431673	AW971302	Hs.293233 ESTs	2.5
	415706	BE182587	Hs.57485 ESTs	2.5
	412882	BE006919	Hs.134105 ESTs	2.5
	441300	R35063	Hs.181536 ESTs	2.5
60	413257	BE075035	gb:PM3-BT0584-260300-002-g05 BT0584 Homo	2.5
	434662	AA641957	gb:ns18d08.r1 NC1_CGAP_GCB1 Homo sapiens	2.5
	455255	AW877139	gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.5
	417137	U46265	Hs.81281 mitochondrial ribosomal protein S21	2.5
	417909	R35614	gb:yg66e08.r1 Soares infant brain 1N18 H	2.5
65	458043	AW979009	Hs.326108 ESTs	2.5
	417008	AW673606	Hs.80758 aspartyl-tRNA synthetase	2.5
	442006	AW975183	Hs.292663 ESTs, Weakly similar to S72482 hypotheti	2.5
	455756	BE079307	gb:RC1-BT0623-120200-011-g09 BT0623 Homo	2.5
	454032	W31790	Hs.194293 ESTs, Weakly similar to I54374 gene NF2	2.5
70	444963	AI916973	Hs.213603 ESTs	2.5
	443526	AW792804	Hs.134002 ESTs	2.5
	454532	AA344685	Hs.58831 regulator of Fas-induced apoptosis	2.5
	428832	AA578229	Hs.324239 ESTs, Moderately similar to ZN91_HUMAN Z	2.5
	442003	AW297497	Hs.201891 ESTs	2.5
75	452768	AW069459	Hs.61539 ESTs	2.5
	411355	AW838479	Hs.22692 ESTs	2.5
	458890	AW865523	gb:PM4-SN0020-010400-009-b05 SN0020 Homo	2.5
	400074			2.5
	405241			2.5
80	413096	BE065209	gb:RC1-BT0314-310300-015-b12 BT0314 Homo	2.5
	414349	BE512968	gb:601172296F1 NIH_MGC_15 Homo sapiens c	2.5
	422884	AW860975	Hs.13256 ESTs	2.5
	429515	AL031228	Hs.204370 DNA segment on chromosome 6 (unique, pse	2.5
	431925	AK000890	gb:homo sapiens cDNA FLJ10028 fis, clone	2.5

	442653	BE269247		gb:601185486F1 NIH_MGC_8 Homo sapiens cD	2.5
	401882				2.5
	458257	U48351	Hs.201219	ESTs, Weakly similar to S18946 ultra hlg	2.5
5	405336				2.5
	439492	AF086310	Hs.103159	ESTs	2.5
	459390	BE385725		gb:601276347F1 NIH_MGC_20 Homo sapiens c	2.5
	435359	Z83806		gb:H.sapiens mRNA for axonemal dynein he	2.5
	429322	D86984	Hs.199243	KIAA0231 protein	2.5
10	431699	NM_001173	Hs.267831	Rho GTPase activating protein 5	2.5
	437107	AA745598	Hs.291840	ESTs, Weakly similar to I78885 serine/th	2.5
	441953	H11695	Hs.322901	disrupter of silencing 10	2.5
	442777	AW341541	Hs.271153	ESTs	2.5
	453361	AA035197	Hs.107375	ESTs	2.5
15	455275	AW977806		gb:EST389810 MAGE resequences, MAGO Homo	2.5
	457824	R84938		gb:yt65f04.r1 Soares retina N2b4HR Homo	2.5
	428550	AW297880	Hs.98661	ESTs	2.5
	445900	AF070526	Hs.13429	Homo sapiens clone 24787 mRNA sequence	2.5
	456359	AI967991	Hs.93574	homeo box D3	2.5
20	414366	BE549143		gb:601076456F1 NIH_MGC_12 Homo sapiens c	2.5
	452528	AA742457	Hs.291479	ESTs	2.5
	408444	AW661839	Hs.253204	ESTs	2.5
	440327	R12581	Hs.191146	ESTs	2.5
	410406	AI969703	Hs.1466	glycerol kinase	2.5
25	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	2.5
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	2.5
	435427	AA682573	Hs.188982	ESTs, Weakly similar to organic anion tr	2.5
	427791	AA412446	Hs.98138	ESTs	2.5
	403509	AF231919	Hs.18759	KIAA0539 gene product	2.5
30	436590	AI393115	Hs.127655	ESTs	2.5
	455556	AW995423		gb:QV0-BN0042-010400-183-g08 BN0042 Homo	2.5
	405869				2.5
	408274	R17315		gb:yg12g11.r1 Soares infant brain 1N1B H	2.5
	448015	AI458065	Hs.23196	ESTs	2.5
35	454190	AW177821		gb:IL3-HT0059-180899-007-C05 HT0059 Homo	2.5
	436154	AA764950	Hs.119898	ESTs	2.5
	406377				2.5
	437030	AA742577	Hs.303781	EST	2.5
	420815	AA280684	Hs.270584	ESTs	2.5
40	418421	R58620	Hs.85050	phospholamban	2.5
	423638	AI003521	Hs.130310	Homo sapiens mRNA for cyclin B3 isoform	2.5
	415425	F08365		gb:HSCZSA121 normalized infant brain cDN	2.5
	404577				2.5
	403568				2.5
45	425967	NM_007159	Hs.4007	Sarcolemmal-associated protein	2.5
	449899	AI610700	Hs.103280	ESTs	2.5
	451078	AI927694	Hs.204470	ESTs	2.5
	453343	AA905353	Hs.121622	ESTs	2.5
	428728	NM_016625	Hs.191381	hypothetical protein	2.5
	409642	AW450809	Hs.257347	ESTs	2.5
50	426235	AI631964	Hs.34447	ESTs	2.5
	452043	H86231		gb:yt03f02.r1 Soares retina N2b5HR Homo	2.5
	401992				2.5
	419910	AA662913	Hs.190173	ESTs, Weakly similar to A46010 X-linked	2.5
55	411036	AA857218	Hs.297007	membrane-bound transcription factor prot	2.5
	444575	AI264847	Hs.22545	Homo sapiens cDNA FLJ12935 fis, clone NT	2.5
	449311	AI657014		gb:tl49a12.x1 NCL CGAP_GC6 Homo sapiens	2.5
	454566	AW807605		gb:MR4-ST0098-120100-001-b06 ST0098 Homo	2.5
	454597	AW809648		gb:MR4-ST0124-261099-015-d01 ST0124 Homo	2.5
60	413875	BE176776		gb:RC3-HT0586-110300-011-g09 HT0586 Homo	2.4
	421583	AA293333		gb:zt53c09.r1 Soares ovary tumor NbHOT H	2.4
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	2.4
	454437	AI248173	Hs.191460	hypothetical protein MGC12936	2.4
	419187	AA234852	Hs.44693	ESTs	2.4
65	444493	R59410	Hs.282094	ESTs, Moderately similar to I38022 hypot	2.4
	405547				2.4
	454086	AW885909	Hs.6975	PRO1073 protein	2.4
	417508	BE163512	Hs.180877	H3 histone, family 3B (H3.3B)	2.4
	416277	W78765	Hs.180145	HSPC030 protein	2.4
70	420976	AI924940	Hs.108082	ESTs, Weakly similar to T31636 hypotheti	2.4
	406468				2.4
	408617	R61736	Hs.124128	ESTs	2.4
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecul	2.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	2.4
75	454137	AW500340	Hs.313876	ESTs, Weakly similar to I38022 hypotheti	2.4
	455328	AW896438		gb:PM1-NN0047-040400-001-d09 NN0047 Homo	2.4
	409500	U08098	Hs.54576	sulfotransferase, estrogen-preferring	2.4
	434138	AA625804		gb:zu86h01.s1 Soares_testis_NHT Homo sap	2.4
	419511	AA429750	Hs.75113	general transcription factor IIA	2.4
80	437980	R50393	Hs.278436	KIAA1474 protein	2.4
	439999	AA115811	Hs.6838	ras homolog gene family, member E	2.4
	403501				2.4
	446845	AI343645	Hs.156108	ESTs	2.4
	401775				2.4

	410845	AW807182		gb:MR4-ST0062-180200-001-b04 ST0062 Homo	2.4
	411836	AW901879	Hs.314453	ESTs	2.4
	412879	BE092219		gb:IL2-BT0734-240400-071-B04 BT0734 Homo	2.4
5	421083	AA283628	Hs.298016	ESTs, Weakly similar to I38022 hypothel	2.4
	423513	AF035960	Hs.129719	transglutaminase 5	2.4
	428882	AA436915	Hs.131748	ESTs, Moderately similar to ALU7_HUMAN A	2.4
	428945	AW192603	Hs.99974	ESTs, Weakly similar to S65824 reverse t	2.4
	434627	AJ221894	Hs.39311	ESTs	2.4
10	435256	AF193766	Hs.13872	cytokine-like protein C17	2.4
	435079	AA664192		gb:ac05b03.s1 Stratagene lung (937210) H	2.4
	458239	BE439877	Hs.283389	ESTs	2.4
	414093	BE544867	Hs.283077	centrosomal P4.1-associated protein; unc	2.4
	441262	AI809130	Hs.176906	ESTs	2.4
	402076				2.4
15	427962	AA946582	Hs.8700	deleted in liver cancer 1	2.4
	400587				2.4
	403053	R58624	Hs.2186	eukaryotic translation elongation factor	2.4
	411203	AW872430	Hs.273743	ESTs	2.4
20	447849	AI538147	Hs.164277	ESTs	2.4
	454201	AB023191	Hs.44131	KJAA0974 protein	2.4
	424131	AA335714	Hs.199665	ESTs	2.4
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	2.4
	440385	AA884283	Hs.192136	ESTs	2.4
25	417976	BE565892	Hs.83077	interleukin 18 (interferon-gamma-inducin	2.4
	447179	AW015633	Hs.157299	ESTs	2.4
	412977	AA125910	Hs.191461	ESTs	2.4
	436958	AA740322	Hs.293539	Homo sapiens mRNA for KIAA1758 protein,	2.4
	401361				2.4
30	403891				2.4
	408419	AW250092	Hs.305953	zinc finger protein 83 (HPF1)	2.4
	417002	T79613	Hs.14613	ESTs	2.4
	439446	AI927629	Hs.57873	ESTs	2.4
	458570	AW971698	Hs.12627	TJ8 protein	2.4
35	458624	AI362790	Hs.278639	KJAA1684 protein; likely homolog of mous	2.4
	459344	AW499533	Hs.257976	ESTs	2.4
	413488	BE144017		gb:MR0-HT0165-191199-004-d09 HT0165 Homo	2.4
	412114	AW893891	Hs.240833	ESTs, Weakly similar to I38022 hypothel	2.4
	423296	AW957193	Hs.3327	Homo sapiens cDNA: FLJ22219 fis, clone H	2.4
40	419983	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	2.4
	428268	AA424957	Hs.294132	ESTs	2.4
	450947	AJ745400	Hs.204662	ESTs	2.4
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	2.4
	438142	T90309	Hs.269651	ESTs	2.4
45	409239	AA740875	Hs.44307	ESTs, Moderately similar to I38022 hypot	2.4
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	2.4
	429063	AW363845	Hs.122142	ESTs, Weakly similar to AA6010 X-linked	2.4
	433868	AA612960	Hs.337300	ESTs	2.4
	401645				2.4
50	432149	AW614326	Hs.157022	ESTs, Weakly similar to T34549 probable	2.4
	453393	AW956392	Hs.110376	ESTs	2.4
	436054	AI076262	Hs.119813	ESTs	2.4
	425433	AA357471		gb:EST66274 LNCAP cells 1 Homo sapiens c	2.4
	417712	AA205569	Hs.194193	ESTs, Moderately similar to ALU1_HUMAN A	2.4
55	420639	AI683116	Hs.25328	ESTs, Moderately similar to ALU7_HUMAN A	2.4
	453369	BE551550	Hs.232630	ESTs	2.4
	405017				2.4
	405385				2.4
	435633	AI248152	Hs.270047	ESTs	2.4
60	457128	AI932995	Hs.183475	Homo sapiens clone 25061 mRNA sequence	2.4
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	2.4
	434544	C05875	Hs.91575	ESTs	2.4
	449432	AW451361	Hs.196529	ESTs	2.4
	455219	AW879403		gb:PM0-OT0019-150300-002-d01 OT0019 Homo	2.4
65	458734	AI554946	Hs.158794	ESTs	2.4
	442179	AA983842	Hs.333555	chromosome 2 open reading frame 2	2.4
	444313	AI140494	Hs.197955	KJAA0704 protein	2.4
	440448	AA885428	Hs.125646	ESTs	2.4
	441498	AI379248	Hs.58742	ESTs	2.4
70	438205	AA780365	Hs.122161	ESTs	2.4
	402615				2.4
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.4
	422306	BE044325	Hs.227280	U6 snRNA-associated Sm-like protein	2.4
	413697	AA131315	Hs.47144	DKFZP586N0819 protein	2.4
75	421755	AW169454	Hs.207422	ESTs, Weakly similar to S71949 metallopr	2.4
	449007	AI620433	Hs.193201	EST, Weakly similar to NIP2_HUMAN BCL2/A	2.4
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	2.4
	418857	D10216	Hs.89394	POU domain, class 1, transcription facto	2.4
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	2.4
80	458914	BE327696	Hs.280922	ESTs	2.4
	435061	AI651474	Hs.163944	ESTs	2.4
	416458	AA180511		gb:zp53i03r1 Stratagene NT2 neuronal pr	2.4
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.4
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase 1, I	2.4

	403003			2.4
	405347			2.4
	406091			2.4
5	428402	AW237531	Hs.326876	Homo sapiens SOX6 mRNA, complete cds
	438762	AW844412	Hs.65450	reticulin 4
	455780	BE088828		gb:CM2-BT0693-230300-129-g09 BT0693 Homo
	457024	AA397546	Hs.119151	ESTs
	404249			2.4
	443921	AI091310	Hs.134848	ESTs
10	407055	X89211		gb:H.sapiens DNA for endogenous retrovir
	417154	AI674701	Hs.21388	ESTs
	419720	AA249131	Hs.337778	hypothetical protein FLJ11068
	405230			2.4
	405935			2.4
15	436998	AA745625	Hs.291414	ESTs, Weakly similar to ALU8_HUMAN ALU S
	445748	U80766	Hs.13252	Human EST clone 22453 mariner transposon
	419233	AA458873	Hs.178306	ESTs
	414277	BE269910		gb:601186291F1 NIH_MGC_8 Homo sapiens cD
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210
20	453736	AL118674	Hs.34871	zinc finger homeobox 18
	410888	AW861207		gb:RC1-CT0302-120200-013-d04 CT0302 Homo
	434239	AF119910	Hs.283047	hypothetical protein PRO2954
	434098	AA625499		gb:af69g08.r1 Soares_NhHMPu_S1 Homo sapi
	414195	BE263293	Hs.89605	cholinergic receptor, nicotinic, alpha p
25	445688	AI248205	Hs.153244	ESTs
	451656	BE327088	Hs.212752	ESTs
	423956	W28203	Hs.136169	Homo sapiens clone 25215 mRNA sequence,
	413445	BE141022		gb:MRD-HT0067-201099-002-d10 HT0067 Homo
30	436149	AI754308	Hs.159452	ESTs
	405629			2.3
	432702	AW973953	Hs.293744	ESTs
	433377	AI752713	Hs.43845	ESTs
	444711	AI188739	Hs.148488	ESTs
	445621	AI733818	Hs.145549	ESTs
35	456432	AW966931	Hs.179662	nucleosome assembly protein 1-like 1
	449236	AI403126	Hs.26373	Homo sapiens cDNA: FLJ23449 fis, clone H
	459024	AA020799	Hs.262869	plasminogen-like
	441037	AA913360	Hs.126468	ESTs
40	431577	T34523	Hs.302040	Homo sapiens DNA sequence from PAC 43401
	438782	AA828380	Hs.126733	ESTs
	412329	AW937445		gb:QV3-DT0043-090200-080-c09 DT0043 Homo
	410999	AW813004		gb:RC3-ST0186-230300-019-h02 ST0186 Homo
	429044	AI261490	Hs.145527	ESTs
45	431655	AW971119		gb:EST383206 MAGE resequences, MAGL Homo
	439642	W81441	Hs.153967	ESTs
	441721	AI288269	Hs.127652	ESTs
	443482	AW188093	Hs.250385	ESTs
	403416	AI744626	Hs.151385	KIAA0564 protein
50	416443	N69469	Hs.194225	ESTs
	419714	AA758751	Hs.98216	ESTs
	415511	AI732617	Hs.182362	ESTs
	412344	AW938384	Hs.264190	vacuolar protein sorting 35 (yeast homol
	449264	AI637649	Hs.196105	ESTs
55	451664	AA889081	Hs.153952	5' nucleotidase (CD73)
	441269	AW015206	Hs.178784	ESTs
	402333			2.3
	453649	Y07494	Hs.34114	ATPase, Na+/K+ transporting, alpha 2 (+)
	430680	AW138724	Hs.168974	ESTs, Highly similar to ALU7_HUMAN ALU S
60	404367			2.3
	403696			2.3
	441622	AW450957	Hs.224864	ESTs
	411004	AW813242		gb:MR3-ST0191-020200-207-g10 ST0191 Homo
	411093	BE067650		gb:MR4-BT0358-090300-003-e01 BT0358 Homo
65	428548	AA430058	Hs.98649	EST
	404059			2.3
	446861	AI696519	Hs.14427	Homo sapiens cDNA: FLJ21800 fis, clone H
	413640	BE158118		gb:MR2-HT0378-240200-205-d09 HT0378 Homo
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin
70	435338	AA678071	Hs.194300	ESTs, Weakly similar to 138022 hypotheti
	442710	AI015631	Hs.23210	ESTs
	444206	AW301017	Hs.146492	ESTs
	451250	AA491275	Hs.236940	hypothetical protein FLJ12542
	454784	AW820626		gb:RC0-ST0299-190100-012-e10 ST0299 Homo
75	458455	AV648310	Hs.213488	ESTs
	458521	AI651039	Hs.148559	ESTs
	407938	AA905097	Hs.85050	phospholamban
	439546	AF088056		gb:Homo sapiens full length insert cDNA
	441274	AW593781	Hs.131357	ESTs
80	454314	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo
	409660	AW452065	Hs.258905	ESTs
	428532	AF157326	Hs.184786	TBP-interacting protein
	411384	AW842115		gb:RC0-CN0026-090200-031-e11 CN0026 Homo
	453687	T55674	Hs.283108	hemoglobin, gamma G

	410140	AL134435	Hs.22269	neurexin 3	2.3
	422443	NM_014707	Hs.116753	histone deacetylase 7B	2.3
	409071	AW316932	Hs.181982	ESTs	2.3
5	421253	AI188102	Hs.31028	ESTs	2.3
	441398	AA932398	Hs.292036	ESTs, Weakly similar to B34087 hypothe	2.3
	448458	AW614367	Hs.171054	ESTs	2.3
	457225	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.3
	443718	AI083580	Hs.221373	ESTs	2.3
10	445568	H00918	Hs.268744	KIAA1796 protein	2.3
	400582				2.3
	411262	AW834480		gb:MR2-TT0014-151199-011-b07 TT0014 Homo	2.3
	401145				2.3
	407440	AF227135		gb:Homo sapiens candidate taste receptor	2.3
15	455121	BE156459		gb:QV0-HT0368-040100-082-f06 HT0368 Homo	2.3
	459077	N20370	Hs.235883	ESTs	2.3
	448117	H49129	Hs.172982	ESTs	2.3
	453331	AI240665	Hs.8895	ESTs	2.3
	443751	AI285839	Hs.153324	EST	2.3
20	402038				2.3
	402176				2.3
	456605	AI827786	Hs.259044	ESTs	2.3
	432479	AL042844	Hs.275675	katanin p80 (WD40-containing) subunit B	2.3
	402527				2.3
25	449272	AW137656	Hs.197645	ESTs	2.3
	411024	BE062590		gb:QV1-BT0260-281099-023-f05 BT0260 Homo	2.3
	455608	BE011437		gb:CM4-BN0220-080500-170-f03 BN0220 Homo	2.3
	458818	AI523857	Hs.232257	ESTs	2.3
	419875	AA853410	Hs.93557	proenkephalin	2.3
	405521				2.3
30	436517	BE080932	Hs.135225	ESTs	2.3
	456801	AW961886	Hs.138263	Homo sapiens clone 24528 mRNA sequence	2.3
	430444	AW296421	Hs.121035	ESTs	2.3
	456208	AW296698	Hs.334625	Homo sapiens cDNA FLJ14890 fis, clone PL	2.3
35	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	2.3
	416509	N57713	Hs.260899	ESTs, Moderately similar to ZN91_HUMAN Z	2.3
	419337	AW291112	Hs.209978	ESTs	2.3
	419699	AA248998	Hs.173044	ESTs, Weakly similar to I38022 hypothe	2.3
	454456	AW850984		gb:IL3-CT0220-150200-068-H08 CT0220 Homo	2.3
40	454633	AW811380		gb:IL3-ST0143-290999-019-D05 ST0143 Homo	2.3
	457028	AW449838	Hs.97562	ESTs	2.3
	458925	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	2.3
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.3
	430850	BE144152		gb:MR0-HT0165-060200-006-e02 HT0165 Homo	2.3
45	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	2.3
	421227	R78581	Hs.266308	mosaic serine protease	2.3
	426902	AI125334	Hs.97408	ESTs	2.3
	430789	AA632577	Hs.310235	ESTs, Weakly similar to I78885 serine/th	2.3
	447475	AI380797	Hs.158992	ESTs	2.3
50	452148	AF007143	Hs.28205	Homo sapiens clone 23738 mRNA sequence	2.3
	430712	AW044647	Hs.196284	ESTs	2.3
	458103	AW780192	Hs.267596	ESTs	2.3
	420959	AA282119	Hs.88975	ESTs	2.3
	444098	AV647969	Hs.109594	KIAA1451 protein	2.3
55	445641	AI245987	Hs.149442	ESTs	2.3
	449276	AW241510	Hs.252713	ESTs	2.3
	452294	AI871925	Hs.117895	ESTs, Moderately similar to A47582 B-cel	2.3
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	2.3
	459497	AA825742	Hs.87517	ESTs	2.3
60	412852	BE004117	Hs.37415	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.3
	437539	AA974573	Hs.121419	ESTs	2.3
	421813	BE048255		gb:tz49b05.y1 NCL_CGAP_Bm52 Homo sapien	2.3
	411994	R67298	Hs.109087	Homo sapiens cDNA: FLJ22845 fis, clone K	2.3
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOT	2.3
65	452463	R36452	Hs.300817	ESTs	2.3
	404936				2.3
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.3
	440836	AW370882	Hs.222080	ESTs	2.3
	405120				2.3
70	400238				2.3
	407809	AW082279	Hs.244106	ESTs	2.3
	412303	AW936336		gb:QV4-DT0021-281299-070-g11 DT0021 Homo	2.3
	420478	AA521259	Hs.193796	ESTs	2.3
	441417	AI733297	Hs.144474	ESTs	2.3
75	445117	AI208754	Hs.147369	ESTs	2.3
	431162	AW971180		gb:EST383268 MAGE resequences, MAGL Homo	2.2
	437036	AI571514	Hs.133022	ESTs	2.2
	455849	BE146866		gb:QV4-HT0222-211099-014-f06 HT0222 Homo	2.2
	447624	AI640326	Hs.62713	ESTs	2.2
80	439780	AL109688		gb:Homo sapiens mRNA full length insert	2.2
	405706				2.2
	447732	AI758398	Hs.161318	ESTs	2.2
	440625	BE539853	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	2.2
	404257				2.2

	437722	AW292947	Hs.122872	ESTs, Weakly similar to JU0033 hypotheli	2.2
	449133	AI631655	Hs.197919	ESTs	2.2
	456555	AW592167	Hs.293299	ESTs	2.2
5	408134	AK000184	Hs.42945	acid sphingomyelinase-like phosphodiester	2.2
	428192	AA424051	Hs.304742	ESTs	2.2
	435634	T82384		gb:yc14f05.r1 Stratagene lung (937210) H	2.2
	438018	AK001150	Hs.5999	hypothetical protein FLJ10298	2.2
	446096	AI276454		gb:ql71a12.x1 Soares_NhHMPu_S1 Homo sapi	2.2
10	448106	AI800470	Hs.171941	ESTs	2.2
	450232	BE300815	Hs.201326	ESTs	2.2
	436134	AK000618	Hs.123784	ESTs	2.2
	448466	AI522109	Hs.171066	ESTs	2.2
	420678	AW593288	Hs.3530	TLS-associated serine-arginine protein 2	2.2
	430692	X80240		gb:HSapiens endogenous retrovirus HERV-	2.2
15	446453	AV658469	Hs.188646	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
	423611	AB011163	Hs.129908	KIAA0591 protein	2.2
	444050	AW138295	Hs.135024	ESTs	2.2
	431532	AI537817	Hs.270311	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.2
20	422669	H12402	Hs.119122	ribosomal protein L13a	2.2
	403388				2.2
	403780				2.2
	419423	D26488	Hs.90315	KIAA0007 protein	2.2
	424719	H90452		gb:yy01c03.r1 Soares fetal liver spleen	2.2
25	431453	AW753917		gb:RC0-CT0299-291199-031-F02 CT0299 Homo	2.2
	442078	AW268583	Hs.262629	ESTs	2.2
	452975	M85521	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.2
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	2.2
	427119	AW680562	Hs.114574	ESTs	2.2
30	400486				2.2
	448482	AW294078	Hs.171092	ESTs	2.2
	402621				2.2
	408363	NM_003389	Hs.44396	coronin, actin-binding protein, 2A	2.2
	424584	H10692	Hs.13310	ESTs	2.2
35	445061	AI253094	Hs.145227	ESTs	2.2
	431065	AA491286	Hs.128792	ESTs	2.2
	411908	L27943	Hs.72942	cytidine deaminase	2.2
	441826	AW503603	Hs.129915	phosphotriesterase related	2.2
	446901	AI347274		gb:tc05d02.x1 NCI_CGAP_Co16 Homo sapiens	2.2
40	422677	AL046388	Hs.208206	hypothetical protein FLJ21162	2.2
	455534	AW991925		gb:PM3-BN0011-130100-002-b07 BN0011 Homo	2.2
	400163				2.2
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.2
	409206	AW364844		gb:QV3-DT0044-221299-045-c03 DT0044 Homo	2.2
45	410556	R32158		gb:yh67a07.s1 Soares placenta Nb2HP Homo	2.2
	432584	AA928829	Hs.47099	hypothetical protein FLJ21212	2.2
	439482	W70045	Hs.58089	ESTs	2.2
	447877	AI435184	Hs.164252	ESTs	2.2
	418297	R91254		gb:yp94e12.s1 Soares fetal liver spleen	2.2
50	403534				2.2
	410594	AW770778	Hs.281238	ESTs	2.2
	414000	BE242814	Hs.323494	ESTs, Weakly similar to T27544 zinc resi	2.2
	432762	NM_014099	Hs.278924	PRO1768 protein	2.2
	437606	AA761594	Hs.122440	ESTs	2.2
55	438550	AW976002	Hs.258402	ESTs	2.2
	439626	N22415	Hs.189080	ESTs	2.2
	444540	AI693927	Hs.265165	ESTs	2.2
	450024	AA005129		gb:zh90h08.r1 Soares_fetal_liver_spleen_	2.2
	456481	AA258033	Hs.108110	DKFZP547E2110 protein	2.2
60	435138	BE314734		gb:601152976F1 NIH_MGC_19 Homo sapiens c	2.2
	412887	BE007420		gb:PM3-BN0142-200300-001-c04 BN0142 Homo	2.2
	454204	AW816498		gb:QV0-ST0236-171299-075-b02 ST0236 Homo	2.2
	408253	AW807476	Hs.21051	Homo sapiens mRNA for FLJ00012 protein,	2.2
	432887	AI926047	Hs.162859	ESTs	2.2
65	448063	AI459108	Hs.159818	ESTs	2.2
	416171	H23896	Hs.125790	leucine-rich repeat-containing 2	2.2
	433098	AW190593	Hs.151143	ESTs	2.2
	409781	AW812266	Hs.15220	zinc finger protein 106	2.2
	423441	R68649	Hs.278359	absent in melanoma 1 like	2.2
70	423646	H02364		gb:yy35d06.r1 Soares placenta Nb2HP Homo	2.2
	436572	AA723274	Hs.279596	ESTs	2.2
	447044	AF030107	Hs.17165	regulator of G-protein signalling 13	2.2
	448928	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	2.2
	444585	AW170015	Hs.6594	ESTs	2.2
75	437334	AL353947	Hs.283780	hypothetical protein DKFZp761N1814	2.2
	431917	D16181	Hs.2868	peripheral myelin protein 2	2.2
	400843				2.2
	455688	BE067238		gb:PM1-BT0348-151299-001-a12 BT0348 Homo	2.2
	449560	AAD01767	Hs.17924	ESTs, Moderately similar to ALU1_HUMAN A	2.2
80	408940	M58583	Hs.662	cerebellin 1 precursor	2.2
	455201	AW947884		gb:PM1-MT0010-200300-001-g08 MT0010 Homo	2.2
	413617	BE155373	Hs.279518	amyloid beta (A4) precursor-like protein	2.2
	459495	BE544158		gb:601076707F1 NIH_MGC_12 Homo sapiens c	2.2
	433225	AW816515	Hs.173540	ATPase, Class V, type 10D	2.2

	444547	AV650207	Hs.282437	ESTs, Weakly similar to I38022 hypothei	2.2
	417156	N49476	Hs.166563	replication factor C (activator 1) 1 (14	2.2
	416761	H85422	Hs.108556	ESTs	2.2
5	408867	AA437199	Hs.656	cell division cycle 25C	2.2
	406748	AW339106	Hs.217493	annexin A2	2.2
	427443	AA402713	Hs.97872	ESTs	2.2
	452843	AI796769	Hs.208320	ESTs	2.2
	427473	AW274439	Hs.252709	ESTs	2.2
10	433919	AA746311		gb:aa56d12.r1 NCI_CGAP_GC81 Homo sapiens	2.2
	431058	AW968865		gb:EST380941 MAGE resequences, MAGJ Homo	2.2
	428679	AA431765		gb:zw80c03.s1 Soares_testis_NHT Homo sap	2.2
	415250	F02614	Hs.27319	ESTs	2.2
	440253	AI651329	Hs.160289	ESTs	2.2
15	434470	AA634818	Hs.298138	ESTs	2.2
	418849	AW474547	Hs.53565	Homo sapiens PIG-M mRNA for mannosyltran	2.2
	432463	AA548518	Hs.186733	ESTs	2.2
	400861				2.2
	407287	AI578812		gb:tu59d08.x1 NCI_CGAP_Gas4 Homo sapiens	2.2
20	414817	AW902892	Hs.23782	hypothetical protein FLJ12847	2.2
	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	2.2
	449808	AA694220	Hs.15403	ESTs, Moderately similar to ALU7_HUMAN A	2.2
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	2.2
	442952	AI743261	Hs.131860	ESTs	2.2
25	425187	AW014486	Hs.22509	ESTs	2.2
	408221	AA912183	Hs.47447	ESTs	2.2
	411480	AW848022		gb:IL3-CT0214-231299-053-A09 CT0214 Homo	2.2
	459681				2.2
	414784	NM_000344	Hs.288986	survival of motor neuron 1, telomeric	2.2
30	442726	AW136066	Hs.19145	ESTs	2.2
	450433	AW444538	Hs.231863	ESTs	2.2
	437642	AL079309		gb:Homo sapiens mRNA full length insert	2.2
	406298				2.2
	409723	AW885757	Hs.257862	ESTs	2.2
35	433266	AI863224	Hs.31476	Homo sapiens cDNA FLJ13872 fs, clone TH	2.2
	435090	BE217923	Hs.149595	ESTs	2.2
	457187	AA443927	Hs.144360	EST	2.2
	446534	AI307356	Hs.175225	ESTs	2.2
	403764				2.2
40	442735	R91949		gb:yq06h06.s1 Soares fetal liver spleen	2.2
	455221	AW867751		gb:MR0-SN0038-290300-001-a03 SN0038 Homo	2.2
	405965				2.2
	408420	NM_006915	Hs.44766	retinitis pigmentosa 2 (X-linked recessi	2.2
45	441679	BE502267	Hs.65996	ESTs	2.2
	432781	NM_014133	Hs.278940	PRO0618 protein	2.2
	448470	AW026226	Hs.309479	ESTs	2.2
	419637	W27493		gb:31h10 Human retina cDNA randomly prim	2.2
	443180	R15875	Hs.258576	claudin 12	2.2
	422213	AA306385	Hs.133160	ESTs	2.2
50	423119	AA322201	Hs.131976	ESTs	2.2
	450192	AA263143	Hs.24596	RAD51-interacting protein	2.2
	428042	AA419529	Hs.76391	myxovirus (influenza) resistance 1, homo	2.2
	400734				2.2
	430499	AW969408	Hs.231991	ESTs	2.2
55	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.2
	401694				2.2
	423531	AW752782	Hs.129750	hypothetical protein FLJ10546	2.2
	424419	AK001563	Hs.146589	hypothetical protein FLJ10701	2.2
	431364	AW971382	Hs.294016	ESTs, Moderately similar to B34087 hypot	2.2
60	436640	AA724411	Hs.156065	ESTs	2.2
	436802	N34486	Hs.170504	ESTs	2.2
	443994	AI094805	Hs.135522	ESTs, Weakly similar to S38038 hypothei	2.2
	445808	R13580	Hs.13436	Homo sapiens clone 24425 mRNA sequence	2.2
	446412	AW135313	Hs.150098	ESTs	2.2
65	448390	AL035414	Hs.21068	hypothetical protein	2.2
	449939	T86420	Hs.272139	ESTs	2.2
	412700	BE222433	Hs.201262	ESTs, Weakly similar to I38022 hypothei	2.2
	453125	AW779544	Hs.115497	hypothetical protein FLJ22655	2.2
	422757	AI090935	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.2
70	452864	AA033714	Hs.287629	hypothetical protein FLJ14260	2.2
	452441	BE222078	Hs.113069	ESTs	2.2
	402395				2.2
	459659				2.2
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	2.2
75	438432	AW444990	Hs.258800	ESTs, Weakly similar to I38022 hypothei	2.2
	409446	AI561173	Hs.67688	ESTs	2.2
	408764	BE087164	Hs.302415	ESTs	2.2
	408908	BE296227	Hs.250822	serine/threonine kinase 15	2.2
	414275	AW970254	Hs.889	Charot-Leyden crystal protein	2.2
80	436992	AA741074	Hs.120750	ESTs	2.2
	439634	W79377	Hs.167	microtubule-associated protein 2	2.2
	444199	AI128931	Hs.260681	ESTs, Moderately similar to ALUF_HUMAN I	2.2
	446009	AI989885	Hs.231926	ESTs	2.2
	435510	BE143837		gb:MR0-HT0164-151299-012-b08 HT0164 Homo	2.1

	403691			2.1
	458333	AI000792	Hs.108209	ESTs
	454560	AW807281		gb:MR4-ST0062-240300-003-g01 ST0062 Homo
5	439343	AF086161	Hs.114611	hypothetical protein FLJ11808
	421498	AA292084	Hs.191575	ESTs, Moderately similar to ALU2_HUMAN A
	414428	BE296906	Hs.182625	VAMP (vesicle-associated membrane protei
	406941	X58140		(NONE)
	445712	AI458246	Hs.167451	ESTs
10	451270	AW341392	Hs.235795	ESTs
	451403	AA885569	Hs.40919	Homo sapiens cDNA FLJ14511 fis, clone NT
	437073	AI885608	Hs.94122	ESTs
	434789	AW292515	Hs.194317	ESTs, Weakly similar to T08680 hypotheti
	430884	AF053748	Hs.248114	glial cell derived neurotrophic factor
	445944	H06336	Hs.13480	Homo sapiens clone 24875 mRNA sequence
15	405233			ESTs
	446512	H30351	Hs.207982	ESTs
	403188			ESTs
	404443			ESTs
20	433645	AI821746	Hs.190258	ESTs, Moderately similar to ALU6_HUMAN A
	414456	H74314		gb:yu56e10.r1 Soares fetal liver spleen
	433479	AW511459	Hs.249972	ESTs
	455482	AW948353		gb:RC0-MT0015-130400-031-d07 MT0015 Homo
	446364	AB006624	Hs.14912	KIAA0286 protein
	452004	AI827815	Hs.277359	ESTs
25	405059			ESTs
	425457	AW964212		gb:EST376285 MAGE resequences, MAGH Homo
	403317	U02687	Hs.385	fms-related tyrosine kinase 3
	413801	M62246	Hs.35406	ESTs, Highly similar to unnamed protein
	415871	R55995	Hs.283309	ESTs, Moderately similar to ALU1_HUMAN A
30	432774	AA564946	Hs.156280	ESTs
	436349	AI445255	Hs.115315	ESTs
	445532	BE138944	Hs.146200	ESTs
	456313	AA225741		gb:nc17b10.s1 NCL_CGAP_Pr1 Homo sapiens
35	412818	NM_003337	Hs.811	ubiquitin-conjugating enzyme E2B (RAD6 h
	450271	AI693900	Hs.200920	ESTs
	401521			ESTs
	422880	AF228704	Hs.121524	glutathione reductase
	448871	BE616709	Hs.159265	kruppel-related zinc finger protein hKf
40	449233	BE048401	Hs.196511	ESTs
	408217	AI433201	Hs.279860	tumor protein, translationally-controlle
	457003	S78234	Hs.172405	cell division cycle 27
	417448	AA203135	Hs.130186	ESTs
	402103			ESTs
45	450579	AW135774	Hs.48614	ESTs
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma
	456596	AA291834	Hs.78950	branched chain keto acid dehydrogenase E
	415333	H24415	Hs.13273	KIAA0592 protein
	457353	X65633	Hs.248144	melanocortin 2 receptor (adrenocorticotr
50	434985	AAG58229	Hs.291228	ESTs
	414729	BE466928	Hs.281901	ESTs
	400510			ESTs
	420844	AA595522		gb:nh22c09.s1 NCL_CGAP_Pr1 Homo sapiens
	427434	BE538374	Hs.301732	hypothetical protein MGC5306
55	432188	AI362952	Hs.2928	solute carrier family 7 (cationic amino
	446296	AA985662	Hs.63131	Homo sapiens cDNA FLJ13155 fis, clone NT
	453853	AL040600	Hs.188083	ESTs
	459108	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti
	430118	AI377255	Hs.183287	ESTs
60	455964	BE166924		gb:CM4-HT0501-240300-519-f01 HT0501 Homo
	437981	AA774445	Hs.192095	ESTs, Weakly similar to KIAA1397 protein
	439957	AI453184	Hs.66357	ESTs
	423734	H02217		gb:cyj38d11.r1 Soares placenta Nb2HP Homo
	450721	AI732271	Hs.25567	ESTs
65	429392	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN
	429986	AF092047	Hs.227277	sinu oculis homeobox (Drosophila) homolo
	432919	AL079800		gb:DKFZp434O2330_r1 434 (synonym: htes3)
	434791	AA649235	Hs.116457	ESTs, Weakly similar to NIP3_HUMAN BCL2/
	445273	AI218441	Hs.153846	ESTs
70	400514			ESTs
	412798	AW998657	Hs.119120	E3 ubiquitin ligase SMURF1
	416085	H18072	Hs.92576	ESTs
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2
	439391	AW975638	Hs.293490	ESTs, Weakly similar to I38022 hypotheti
	428414	AL049980	Hs.184216	DKFZP564C152 protein
75	429430	AI381837	Hs.155335	ESTs
	449689	AF228421	Hs.23889	DKFZP564A032 protein
	430909	AF034632	Hs.248126	G protein-coupled receptor 38
	453116	AI276680	Hs.146086	ESTs
80	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos
	423019	AI640185	Hs.283626	ESTs
	414007	AI733895	Hs.103813	ESTs
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom

	421279	AW664878	Hs.106645	ESTs	2.1
	443167	AI202009	Hs.132087	ESTs	2.1
	459124	AW301478	Hs.184592	protein kinase, lysine deficient 1	2.1
5	448078	AI460117	Hs.170454	ESTs, Highly similar to A53933 myosin I	2.1
	436858	BE545498		gb:601070344F1 NIH_MGC_12 Homo sapiens c	2.1
	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	2.1
	431089	BE041395	Hs.283676	ESTs, Weakly similar to unknown protein	2.1
	407401	AF029325		gb:Homo sapiens laminin beta-4 chain pre	2.1
10	426336	AA375802		gb:EST88135 HSC172 cells II Homo sapiens	2.1
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	2.1
	425541	AA359119		gb:EST68172 Fetal lung II Homo sapiens c	2.1
	406504				2.1
	410626	BE407727		gb:601299771F1 NIH_MGC_21 Homo sapiens c	2.1
15	415186	AA160945	Hs.14479	Homo sapiens cDNA FLJ14199 fis, clone NT	2.1
	416175	H24230	Hs.271498	ESTs, Moderately similar to ALU1_HUMAN A	2.1
	436820	AI684535	Hs.200811	ESTs	2.1
	442095	AI733162	Hs.128470	ESTs	2.1
	451878	AI821027	Hs.8429	ESTs	2.1
20	449178	AI633748	Hs.197597	ESTs	2.1
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	2.1
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	2.1
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	2.1
	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	2.1
25	441543	AI733014	Hs.269715	ESTs	2.1
	403065				2.1
	428811	AA436052	Hs.99487	ESTs	2.1
	451803	BE541174	Hs.252058	ESTs, Moderately similar to PC4259 feni	2.1
	442906	AW296888	Hs.170939	ESTs	2.1
30	409171	R17126		gb:yg09c11.r1 Soares infant brain 1NIB H	2.1
	414175	AI308876	Hs.103849	hypothetical protein DKFZp761D112	2.1
	450785	AA852713	Hs.25459	Homo sapiens, alpha-1 (VI) collagen	2.1
	412039	AW887384		gb:RCO-OT0089-130300-021-d07 OT0089 Homo	2.1
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	2.1
35	443268	AI800271	Hs.129445	hypothetical protein FLJ12496	2.1
	455022	AW850845		gb:IL3-CT0220-111199-028-D11 CT0220 Homo	2.1
	447972	AL137275	Hs.20137	hypothetical protein DKFZp434P0116	2.1
	422942	AF054839	Hs.122540	tetraspan 2	2.1
	400451				2.1
40	406668	T62745	Hs.184411	albumin	2.1
	450159	AI702416	Hs.200771	ESTs, Moderately similar to A Chain A, T	2.1
	404834				2.1
	448732	BE614063	Hs.334689	KIAA1838 protein	2.1
45	423453	AW450737	Hs.128791	CGI-09 protein	2.1
	421447	AB005216	Hs.104481	Nck, Ash and phospholipase C binding pro	2.1
	408774	AW270899	Hs.254569	ESTs, Weakly similar to B34087 hypotheti	2.1
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.1
	405732				2.1
	417848	AA206581	Hs.39457	ESTs, Weakly similar to JC5314 CDC28/bdc	2.1
50	442875	BE623003	Hs.23625	Homo sapiens clone TCCTA00142 mRNA sequ	2.1
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	2.1
	455778	BE088746		gb:CM2-BT0693-210300-123-d09 BT0693 Homo	2.1
	426953	AI769281	Hs.97439	ESTs	2.1
	440454	AI733037	Hs.129990	ESTs	2.1
55	433917	AI809325	Hs.122814	Human DNA sequence from clone RP5-1028D1	2.1
	424872	AA347923		gb:EST54302 Fetal heart II Homo sapiens	2.1
	454658	AW812330	Hs.11123	DKFZP564G092 protein	2.1
	441963	AI733307	Hs.128002	ESTs	2.1
	439498	AA908731	Hs.58297	CLL8 protein	2.1
60	456224	AW292905	Hs.128770	ESTs	2.1
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	2.1
	444702	AI220122	Hs.326560	hypothetical protein MGC2780	2.1
	417787	R14948	Hs.23883	ESTs	2.1
	400612				2.1
65	410878	AW809201	Hs.314248	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.1
	414494	AA768491	Hs.5783	hypothetical protein FLJ22724	2.1
	427027	AI924294	Hs.173259	uncharacterized bone marrow protein BM03	2.1
	451067	BE172186		gb:MR0-HT0559-110300-005-h11 HT0559 Homo	2.1
	455032	AI830890	Hs.192422	ESTs	2.1
70	417945	R29072		gb:F1-101D 22 week old human fetal liver	2.1
	438268	AA782163	Hs.293502	ESTs	2.1
	424754	R09692		gb:yf23b12.r1 Soares fetal liver spleen	2.1
	404599				2.1
	459655				2.1
	402455				2.1
75	459278	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone H	2.1
	421987	AI133161	Hs.286131	CGI-101 protein	2.1
	400339	X57131	Hs.248209	H2A histone family, member F, pseudogene	2.1
	438206	AA780385	Hs.187885	ESTs	2.1
80	458451	AW297181	Hs.195922	ESTs	2.1
	447534	AW953935	Hs.30837	ESTs	2.1
	417687	AI828596	Hs.250691	ESTs	2.1
	412717	W00973	Hs.334728	ESTs	2.1
	405759				2.1

	406413				2.1
	442081	AA401863	Hs.22380	ESTs	2.1
	457938	AJ373638	Hs.133900	ESTs	2.1
5	420687	AA279392	Hs.88605	Homo sapiens cDNA FLJ13427 fis, clone PL	2.1
	428822	W28418	Hs.30715	potassium voltage-gated channel, Isk-rel	2.1
	415635	F13168		gb:HSC3JF101 normalized infant brain cDN	2.1
	411421	BE272110	Hs.21177	ESTs	2.1
	437825	AA769123	Hs.291947	ESTs	2.1
10	437083	AW082597	Hs.244862	ESTs	2.1
	409466	AA436207	Hs.226666	ESTs, Moderately similar to I54374 gene	2.1
	433523	H29882	Hs.162614	ESTs	2.1
	446868	AV660737	Hs.135100	ESTs	2.1
	445882	AJ948717	Hs.225155	ESTs, Weakly similar to A46302 PTB-assoc	2.1
15	438005	BE151746		gb:PM1-HT0305-061299-003-e06 HT0305 Homo	2.1
	406817	AJ936028		gb:wo47a09.x1 NCI_CGAP_Gas4 Homo sapiens	2.1
	410486	AW235094	Hs.69233	zinc finger protein	2.1
	411940	AW876686		gb:CM4-PT0031-180200-507-e05 PT0031 Homo	2.1
	412446	AJ768015	Hs.92127	ESTs	2.1
	457289	AW573204	Hs.137078	ESTs	2.1
20	400335	Y13187	Hs.248067	Homo sapiens dmd gene, intron 11	2.0
	435959	AW296243	Hs.118375	ESTs	2.0
	448188	AW001835	Hs.13323	hypothetical protein FLJ22059	2.0
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	2.0
25	420430	AJ703192		gb:wd92h04.x1 NCI_CGAP_Lu24 Homo sapiens	2.0
	445717	AW664658	Hs.149332	ESTs	2.0
	451862	H09260	Hs.32333	ESTs	2.0
	459686				2.0
	441996	BE349537	Hs.38383	ESTs	2.0
30	412194	AW900282	Hs.115412	hypothetical protein FLJ13881	2.0
	444229	AV648613	Hs.282397	ESTs	2.0
	441635	AJ908538	Hs.133000	ESTs, Weakly similar to S26689 hypotheti	2.0
	421387	AF059566	Hs.103983	solute carrier family 5 (sodium iodide s	2.0
	414373	AW162907	Hs.75969	proline-rich protein with nuclear target	2.0
35	428209	AA424197	Hs.98947	ESTs, Weakly similar to S33496 trypsin [2.0
	443520	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO	2.0
	409248	AB033035	Hs.51965	KIAA1209 protein	2.0
	444518	AJ160278	Hs.146884	ESTs	2.0
	422237	M13149	Hs.1438	histidine-rich glycoprotein	2.0
40	409316	U28251	Hs.53237	ESTs, Highly similar to Z169_HUMAN ZINC	2.0
	402725				2.0
	413783	AA314337	Hs.301547	ribosomal protein S7	2.0
	423867	AA331886		gb:EST35757 Embryo, 8 week I Homo saplen	2.0
	425008	AW675764	Hs.174248	ESTs	2.0
45	427271	AW195922	Hs.188758	connexin 59	2.0
	444102	AV647953	Hs.83077	interleukin 18 (interferon-gamma-inducin	2.0
	445829	AJ452457	Hs.145526	ESTs	2.0
	452366	AK000464	Hs.29276	hypothetical protein FLJ20457	2.0
	457652	AF116656	Hs.273809	Homo sapiens PRO1167 mRNA, complete cds	2.0
50	429540	M85776		gb:EST02297 Fetal brain, Stratagene (cal	2.0
	459456	AA486036	Hs.190124	ESTs	2.0
	409840	AW502122		gb:UL-HF-BR0p-ajr-c-08-0-ULr1 NIH_MGC_5	2.0
	441025	AA913880	Hs.176379	ESTs	2.0
	457802	T78013	Hs.167279	FYVE-finger-containing Rab5 effector pro	2.0
55	445627	AW818475	Hs.7363	ESTs	2.0
	440299	AJ871778	Hs.250112	ESTs	2.0
	401236	H24185	Hs.92918	hypothetical protein	2.0
	429996	N90822	Hs.48969	ESTs	2.0
	455135	AW857989		gb:PM2-CT0328-281299-003-e04 CT0328 Homo	2.0
60	411537	BE073250		gb:MR0-BT0551-060300-102-e05 BT0551 Homo	2.0
	433449	AW772282		gb:hnh71b05.x1 NCI_CGAP_Kd11 Homo sapien	2.0
	454197	BE140966		gb:MR0-HT0065-081199-002-b06 HT0065 Homo	2.0
	445297	BE544163	Hs.87128	hypothetical protein FLJ23309	2.0
	403977				2.0
65	458948	AJ695359	Hs.280943	ESTs	2.0
	418663	AK001100	Hs.41690	desmocollin 3	2.0
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	2.0
	426536	AJ949749	Hs.44441	ESTs	2.0
	442765	BE567353	Hs.99480	ESTs	2.0
70	400859				2.0
	405829				2.0
	411863	BE075244	Hs.12420	ESTs	2.0
	415258	AW752247	Hs.293853	ESTs	2.0
	416093	R60685	Hs.268698	ESTs, Moderately similar to ALUC_HUMAN I	2.0
75	416184	R48481	Hs.269177	ESTs, Weakly similar to ALU6_HUMAN ALU S	2.0
	437733	AJ792574	Hs.122876	ESTs	2.0
	453118	AW195849	Hs.252757	ESTs	2.0
	457039	H29990	Hs.101937	sine oculis homeobox (Drosophila) homolo	2.0
	444292	AJ139794	Hs.145569	ESTs	2.0
80	431360	NM_000427	Hs.251680	loricin	2.0
	407644	D16815	Hs.37288	nuclear receptor subfamily 1, group D, m	2.0
	412029	AW886238		gb:RC5-OT0078-280300-022-F01 OT0078 Homo	2.0
	438522	AA809431	Hs.258886	ESTs	2.0
	422634	NM_016010	Hs.118821	CGI-62 protein	2.0

	418790	H95693		gb:yt95d11.s1 Soares_pineal_gland_N3HPG	2.0
	442950	AI500417	Hs.46764	ESTs	2.0
	457040	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.0
5	436464	AI016176	Hs.269783	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.0
	402674				2.0
	408733	AW264812	Hs.254290	ESTs	2.0
	408767	AA057279	Hs.211928	ESTs	2.0
	432801	NM_016260	Hs.278963	zinc finger DNA binding protein Helios	2.0
10	418205	L21715	Hs.83760	tropoin I, skeletal, fast	2.0
	404604				2.0
	413627	BE182082	Hs.246973	ESTs	2.0
	402341				2.0
	438090	AA777534	Hs.191992	ESTs	2.0
15	421303	T06464		gb:EST04353 Fetal brain, Stratagene (cat	2.0
	411417	AW845481		gb:MR1-CT0056-201199-008-b04 CT0056 Homo	2.0
	401986				2.0
	415318	T06544		gb:EST04433 Fetal brain, Stratagene (cat	2.0
	417756	Z43056		gb:HSC12B021 normalized infant brain cDN	2.0
20	418301	AW976201	Hs.53913	hypothetical protein FLJ10252	2.0
	433755	AW085934	Hs.120868	ESTs	2.0
	435413	AI267476	Hs.46669	ESTs	2.0
	435648	H24347	Hs.27524	ESTs	2.0
	447555	AI391662	Hs.160963	Homo sapiens, clone MGC:12318, mRNA, com	2.0
25	458175	AW296024	Hs.150434	ESTs	2.0
	458433	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypothei	2.0
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	2.0
	447678	BE385257	Hs.336457	Homo sapiens dopamine receptor interacti	2.0
	448150	AI472187	Hs.302739	ESTs	2.0
30	453445	AL036532	Hs.91453	ESTs	2.0
	444420	AI148157	Hs.146766	ESTs	2.0
	431956	AK002032	Hs.272245	Homo sapiens cDNA FLJ11170 fis, clone PL	2.0
	413758	BE162391		gb:PM2-HT0451-090100-002-004 HT0451 Homo	2.0
	428231	U17989	Hs.183105	nuclear autoantigen	2.0
35	455873	BE152239		gb:QV4-HT0316-091199-028-f12 HT0316 Homo	2.0
	430970	AI018210	Hs.144083	ESTs	2.0
	412277	BE277592	Hs.73799	guanine nucleotide binding protein (G pr	2.0
	413025	AA805265	Hs.291646	ESTs	2.0
	424083	AF055018	Hs.139137	Homo sapiens clone 24442 mRNA sequence	2.0
40	427654	AA410183	Hs.137475	ESTs	2.0
	410483	BE163567		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.0
	423942	AF209704	Hs.135723	glycolipid transfer protein	2.0
	430340	AA476777		gb:zw94g11.r1 Soares_tetal_fetus_Nb2HFB_	2.0
	425686	M73531	Hs.1937	retinal degeneration, slow (retinitis pi	2.0
45	425075	AA506324	Hs.1852	acid phosphatase, prostate	2.0
	400285				2.0
	405966				2.0
	407407	AF050198		gb:Homo sapiens putative mitochondrial s	2.0
	411459	BE142707		gb:MR0-HT0157-191199-002-g12 HT0157 Homo	2.0
50	415105	D60166		gb:HUM089G11B Clontech human fetal brain	2.0
	434531	AA642007	Hs.116369	ESTs	2.0
	447153	AA805202	Hs.315562	ESTs	2.0
	447185	AW377092	Hs.99601	hypothetical protein FLJ12553	2.0
	455696	BE067870		gb:RC0-BT0362-021299-031-b06 BT0362 Homo	2.0
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	400617	AF151064	Hs.36069	hypothetical protein	2.0
	418647	AA226198		gb:nc26a07.s1 NCL_CGAP_Pr1 Homo sapiens	2.0
	401785				2.0
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	2.0
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	439509	AF086332	Hs.58314	ESTs	2.0
	430203	L36140	Hs.235069	RecQ protein-like (DNA helicase Q1-like)	2.0
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	2.0
	455540	BE080231		gb:RC4-BT0629-120200-012-f11 BT0629 Homo	2.0
65	437620	AW976930	Hs.128760	ESTs	2.0
	407528	X64990		gb:H.sapiens mRNA HTPCRX16 for olfactory	2.0
	402048				2.0
	403623				2.0
	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	2.0
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	422600	BE143586	Hs.87	retinoblastoma-like 1 (p107)	2.0
	423347	AI660412	Hs.234557	ESTs	2.0
	424560	AA158727	Hs.150555	protein predicted by clone 23733	2.0
	433153	AA578512		gb:nh22e11.s1 NCL_CGAP_Pr1 Homo sapiens	2.0
75	433347	AF023130		gb:Homo sapiens Ras-GRF2 mRNA, partial c	2.0
	435373	AW665538	Hs.117689	ESTs	2.0
	442988	AI026130	Hs.131683	ESTs	2.0
	447505	AL049266	Hs.18724	Homo sapiens mRNA; cDNA DKFZp564F093 (fr	2.0
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Table 31B

	Pkey:	Unique Eos probaset identifier number	
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	Accession:	Genbank accession numbers	
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	409840	1156071_1	AW502122 AW502125 AW501653 AW501720
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	410536	1207322_1	N39533 AW753094 AW753093
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	411417	1245075_1	AW845481 AW845474 AW850849
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	423121	225175_1	BE048255 AA313083 AA298419
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	423646	230597_1	AA319642 AW853758 H56414
	423734	231479_1	AW864848 AA322213 AA322209 AW961624
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	424754	243305_1	AA331886 AW962659 AW962655 T89841
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			R09692 R09414 AA346353
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	431822	338082_1	AA516049 AW004922
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	435079	399783_1	AA664192 H60250 T71388
50	435138	401159_1	BE314734 AA666393
	435463	406582_1	AA682507 AW851124
	435510	407286_1	BE143837 AW749652 AA683327
	435634	409239_1	T82384 R05307 AA693714
	435689	409755_1	AA694284 H68267 H68264
55	436359	41847_1	ZB3806 AJ132091 AJ132090
	436720	425676_1	AW975902 AA729344 AI557342
	436858	428095_1	BE545498 AA830720 AI873015 AA732679
	437037	431828_1	T63804 T63768 AA742849
	437113	433234_1	AA744693 AW750059
60	437642	43997_1	AL079309 AA281819
	437963	44635_1	BE396279
	438005	447553_1	BE151746 BE336853 D63271 T94955 AA774994
	438993	467651_1	AA828995 AA834879 AI926361
	439037	46803_1	AF075084 H53157 H53054
65	439546	47360_1	AF088056 W76297 W72448
	439780	47673_1	AL109688 R23665 R26578
	442653	54812_1	BE269247 BE270032 BE270800 BE566840
	442735	550247_1	R91949 AI016237 BE072329
	443764	579650_1	F23283 AI084941 F35774
	444063	590989_1	AI122614 AW869134
70	444910	624951_1	AI201849 BE069007 AW946544
	445432	63943_1	AV653771 BE089370
	446096	661959_1	AI276454 AI633717 AI275116
	446801	697809_1	AI347274 AW844024
75	447884	740749_1	H28505 R18575 Z43580 T48738 AI435454 BE004683
	448477	76475_1	BE612572 AL040190 F08514
	449311	804513_1	AI657014 AW594035 AI657036 AI638390
	450024	82296_1	AA005129 AA679084 AA694399
	451067	85759_1	BE172186 AA059279 AA020815 AA013437
80	452043	89532_1	H86231 AA021632 H38271
	452542	921410_1	AW812256 AW812257 AI906423 AI906422
	453211	95527_1	W84829 AA033900 AW573557
	453530	97021_1	AW021633 AA036730 AI866854
	453823	982526_1	AL137967 BE064160 BE064186

	453901	986414_1	BE065902 AW749032 AW003637
	454186	1049791_1	BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581 BE141477 BE141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460 BE141749 AW177598
5	454190	1049996_1	AW177821 AW177896 AW177867
	454197	1050392_1	BE140966 BE140961 BE140967 BE141006 BE140985 BE140970 BE141669 BE141653 BE141664 BE141655 BE141661 BE141660 BE140969 BE141673 BE141650 BE141674 BE141550 BE141688 AW178241 BE140994 BE141666 BE140998 BE141008 BE140988 BE141011 BE140975 BE141667 BE141675 BE141657 BE141681 BE141656 BE141672 BE141680 AW178237 BE141012 BE140990 BE141658 BE141648 BE141013 BE141668 BE140973 BE141004 BE140963 BE140984 BE141009 AW178232 BE141007 BE141649 AW178293 BE140993 AW178233 BE141646 BE141005 BE141691 BE141000 BE141652 BE140965 BE141562 BE140960 BE140962 BE141001 BE140978 AW178229 AW178239 BE141671 AW178230 BE141547 AW178235 BE141663 BE141549 BE140996 BE141003 AW178236 BE141002 BE141556
10	454204	1050597_1	AW816498 AW808791 AW808515 AW808379 AW808532 AW808605 AW808977 AW808816 AW178675 AW178486 AW808514 AW178483 AW178485 AW809007 AW808524
15	454314	1108161_1	AW364844 AW364847 AW937534 AW937593 AW937659
	454352	1129667_1	AW389668 AW389657 AW609198 AW389649
	454423	1183079_1	AW603985 AW854350
	454447	1204995_1	BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671
	454456	1207088_1	AW650984 AW752836 M86124
	454482	1215087_1	BE147919 AW794884 BE147847
20	454560	1223940_1	AW807281 AW807092 AW807425 AW807330 AW807174 AW807171 AW807274 AW807278 AW807367
	454564	1224407_1	AW807573 AW807566 AW807572
	454566	1224432_1	AW807605 AW807690 AW807839 AW807752 AW807673 AW807667 AW807955 AW807760 AW807615 AW807898 AW807849 AW807821 AW807832 AW807842 AW807827 AW807822 AW807829 AW807830 AW807825 AW807603 AW807612 AW807908 AW807595 AW807617 AW807678 AW807687 AW807918 AW807921 AW807595 AW807602 AW807688 AW807609 AW807684 AW807770 AW807593 AW807754 AW807679 AW807957 AW807683 AW807763 AW807902 AW807840 AW807819 AW807836 AW807769 AW807685 AW807847 AW807674 AW807686 AW807670 AW807917 AW807677 AW807680 AW807900 AW807669 AW807952 AW807907 AW807846 AW807756 AW807835 AW807608 AW807753 AW807601 AW807956
25	454597	1226059_1	AW809648 AW809704 AW809643 AW809653 AW809709 AW809949 AW809939 AW810010 AW809705 AW809950 AW809822 AW809667 AW810093 AW810076 AW809673 AW810349 AW809895
30	454633	1227504_1	AW811380 AW811385
	454716	1230503_1	AW850684 AW850150
	454747	1233006_1	AW818535 AW818588 AW818651
	454754	1233580_1	AW819191 AW819252 AW819183 AW819175 AW819177 AW819186 AW819180 BE158470 AW819242 AW819269 AW819244 AW819190 AW819265 AW819268 AW819246 BE152602 AW819249 AW819251 AW819263 AW819194
35	454767	1234028_1	BE069199 AW936012 AW877466 AW819782 AW935798 AW835546 AW936042 BE069121 AW835625 AW877536 AW935885 BE069202 AW820019 AW935937 BE160180 AW935946 BE069101 BE069125 AW877527 BE160316 BE160398 AW935794 AW835701 AW935784 AW820199 AW820434 BE174743
	454778	1234343_1	AW820626 AW820621 AW820608
	454784	1234630_1	AW820852 AW820773 AW821088
	454790	1234752_1	AW833711 AW833620 AW833699
40	454836	1236509_1	AW835775 AW845768 AW845764 AW845773 AW845757 AW845758 AW845780
	454864	1237929_1	AW846134 AW846467 AW846468 AW846386 AW846461 AW846211 AW846179 AW846205 AW846320 AW846379 AW846367 AW846561 AW846556
	454938	1245635_1	AW847645 AW847791 AW854083 AW853945
45	454962	1246750_1	AW850845 BE144010 AW855164
	455022	1249160_1	BE156459 BE156469 BE156468 AW857447
	455121	1254339_1	AW857989 AW858016 AW861677 AW861689 AW861691 AW858056
	455135	1254729_1	AW860972 AW862598 AW862599 AW860988 AW860983 AW860898 AW860925 AW860922 AW860986 AW860984 AW860989
	455170	1256906_1	AW947884 AW947918 AW947888 AW947883 AW947897 AW947910 AW947905 AW864751 AW947878
50	455201	1259748_1	AW879403 AW867707
	455219	1261640_1	AW867751 AW867770 AW867763
	455221	1261678_1	AW875972 AW875983 AW875974 AW876000 AW875966 AW876050
	455236	1265662_1	AW876627 AW876630 AW876631 AW876625
	455252	1266222_1	AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
55	455255	1266482_1	AW977806 AW887923 AW886321
	455275	1272255_1	AW886156 AW887926 AW886324 AW886236 AW887906 AW886304
	455280	1272607_1	AW893961 AW893998 AW894034 AW894019
	455310	1278158_1	AW896438 AW896534 AW896500 AW896540 AW896446
	455328	1280063_1	AW983901 AW984485 AW947715
60	455464	1292643_1	AW948353 AW948351 AW948331 AW948303 AW948336 AW948305 AW948299 AW948346 AW948352
	455482	1293183_1	AA102322
	455488	129372_1	BE144762 AW979091
	455511	1321229_1	AW991925 AW991919
	455534	1322942_1	BE080231 AW993284 AW993293 AW993000
65	455540	1323701_1	AW995423 AW995373
	455566	1325658_1	BE003714 BE003721 BE003720 BE003716
	455571	1331885_1	BE007829 BE007815 BE007822 BE007996 BE007835 BE007837 BE007824 BE007836 BE007827
	455587	1335046_1	BE011437 BE011402 BE011395 BE011428 BE011407 BE011421 BE011406
	455608	1337389_1	BE065984 BE065942 BE065955 BE066085
70	455675	1349659_1	BE067238 BE067235 BE067240 BE067256 BE067263 BE067236 BE067260 BE067253 BE067248 BE067252
	455688	1350606_1	BE067870 BE067886 BE165133 BE165334 BE165329 BE165332
	455696	1351077_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
	455747	1355877_1	BE079307 BE079309
	455756	1358603_1	BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952
75	455778	1364506_1	BE088828
	455780	1364580_1	BE146866 BE146865 BE146867
	455849	1375441_1	BE146879 BE146914 BE146918
	455851	1375451_1	BE149024 BE149056 BE152826 BE149025 BE149057 BE152819 BE149030 BE149062 BE149023 BE149055
	455866	1377119_1	BE152239 BE152242 BE152230
	455873	1379498_1	BE153208 BE153146 BE152981
80	455880	1380022_1	BE158687 BE158688
	455935	1384144_1	BE166924 BE166921 BE166925 BE166915 BE166970 BE166968
	455964	1389912_1	BE179015 BE178965 BE179010 BE179002 BE178961 BE179005 BE178964 BE179012 BE179011 BE178963 BE178997
	455992	1398552_1	

	455993	1398665_1	BE179085 BE179084 BE179086 BE179264
	456186	1618618_1	W26642 H88394
	456313	177240_1	AA225741 AI734056 AI820965 AI732153 AA259201 AA225731
5	456394	1843275_2	W28506
	456407	184986_1	AW968614 AA243209 AA281411
	456476	191761_1	AA256753 AW628680
	457242	307984_1	AA457011 AI978850
	457824	41515_6	R84938 AL047151 AA310309 AW063200 AI569528 AI307823 N49975
10	458804	75803_1	AL157625 N72698 BE622492
	458890	812733_2	AW865523 AW865128 AW865467 AW865127 AW865466
	459160	920051_1	AI904723 AI904725 AI904729 AI904722 AI904758 AI904736
	459201	925883_1	AW391177 W45021

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TABLE 31C

20	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	Nt_position
25	400451	8113550	Minus	82189-82320
	400462	9929659	Minus	197610-197785
	400486	8569885	Plus	181108-181605
30	400510	9796540	Minus	139633-139910,140469-140979
	400514	9796594	Minus	78844-79025,80850-80991,89754-89941,93750-93891
	400579	9887603	Plus	21323-21526
	400582	9887609	Plus	88642-88726,89716-89866
	400587	9887626	Plus	25435-25588,25668-25747
35	400608	9887666	Minus	96756-97558
	400612	9929646	Minus	151513-151662
	400613	9864507	Plus	92278-92472
	400641	8117693	Plus	4786-4992
	400643	8117693	Plus	12818-13016
40	400706	7249204	Minus	78299-78686
	400734	8118979	Plus	122853-123971
	400816	8569993	Plus	161221-162078
	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,10634-10789,15254-15403,23827-23958
	400844	9188605	Plus	24746-24872,25035-25204
45	400859	9757499	Minus	91888-92018,98131-98294,99474-99570
	400861	9757506	Plus	163855-164016
	400889	9958234	Minus	169782-170036
	401078	3687273	Plus	105052-105171
	401098	9965518	Minus	85632-86174
50	401132	8705350	Minus	85679-85795
	401145	2547238	Plus	17599-17776
	401189	9690246	Minus	90815-90929
	401200	9743387	Minus	111586-111806,114791-114916,115419-115583,116351-116446,116847-116907,122853-123067,124982-125407
	401344	9926411	Minus	82478-82602,86952-87110
55	401361	9958052	Plus	153093-154106
	401365	9796180	Minus	119572-119672
	401449	8574316	Minus	144928-145030
	401497	7381770	Plus	92607-92813
	401521	7705251	Plus	9127-9234
60	401526	7770561	Plus	91570-93177
	401602	7689963	Plus	101096-101253
	401614	7839924	Plus	17350-17735
	401645	7657839	Minus	34986-35133
	401694	3540172	Minus	64056-64168
65	401775	9966311	Minus	110228-110340
	401785	7249190	Minus	165776-165996,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
	401882	8139716	Plus	86466-87077
	401887	7229981	Plus	93973-94120
	401986	4405829	Minus	31137-31293
70	401992	4153858	Plus	31452-31649
	402038	7684482	Minus	100751-100885
	402048	8072512	Plus	43936-44078
	402076	8117410	Plus	128316-128627
	402103	7249203	Plus	14453-15414
75	402131	7704961	Minus	33114-33209,33496-33678
	402176	7543687	Minus	10-750
	402230	9966312	Minus	29782-29832
	402333	8844110	Minus	165693-165856
	402341	7656696	Plus	22583-23699
80	402395	9929693	Minus	131016-131998
	402429	9796372	Minus	57622-57793,59282-59402,59624-59827
	402430	9796372	Minus	62382-62552
	402455	9796753	Minus	139640-139779,140568-140660
	402527	9800806	Plus	4722-4916,17858-18037,19964-20140,24423-24605,26699-26881

	402615	9926801	Plus	131390-132157
	402621	9930950	Plus	130806-131036
	402674	8077108	Minus	39290-39502
5	402725	8979991	Plus	107231-107383
	402790	4835258	Minus	147744-147861
	402867	5596716	Plus	52806-53106,53500-53818
	402953	9408724	Minus	122603-122743
	403003	5441423	Minus	79403-79560,79712-80021
10	403011	6693597	Minus	3468-3523
	403065	8954197	Minus	71615-71773,73930-74144
	403188	9838289	Minus	157618-157755
	403271	7230852	Plus	134283-134485
	403273	8018055	Plus	133809-134099
15	403281	8072630	Minus	7521-7728
	403296	8096530	Minus	35913-36520
	403310	8139935	Minus	183883-184026
	403329	8516120	Plus	96450-96598
	403341	8569175	Plus	30699-30910
20	403344	8569726	Plus	70823-70990
	403356	8569930	Plus	92839-93036
	403381	9438267	Minus	26009-26178
	403388	9438331	Plus	112733-113001,114599-114735
	403396	9438367	Minus	952-1160
25	403501	7534005	Minus	108903-110438
	403513	7656757	Minus	155310-155436,158402-158535
	403515	7656757	Minus	173358-179553
	403534	8076917	Minus	46652-47332
	403549	8081591	Minus	137150-137362
30	403568	8101145	Minus	85509-85658
	403574	8101156	Plus	5542-6176
	403619	8569810	Plus	62501-62653
	403623	8569879	Minus	3519-5426
	403625	8569879	Plus	6551-7111
35	403637	8671936	Minus	142647-142771,145531-145762
	403667	6850483	Minus	1344-1442,1545-1697
	403677	7331517	Minus	55008-55083,62860-63051
	403691	7387384	Minus	88280-88463
	403696	3135242	Minus	143467-143634
40	403743	7652003	Minus	136463-136646
	403760	7712202	Minus	45910-46260,47563-47824
	403764	7717105	Minus	118692-118853
	403776	7770811	Minus	1414-1513,1624-1756
	403780	8076989	Plus	93160-93409
45	403786	8083636	Minus	73028-73217
	403891	7331467	Minus	191508-193220
	403895	7381715	Minus	3502-4002,4070-4308
	403977	7657840	Minus	115573-115820
	404043	9558573	Plus	29042-29135,46597-46699
50	404059	3548785	Plus	104326-106788
	404076	9931752	Minus	3848-3967
	404196	3805917	Minus	67928-68109
	404249	8655533	Plus	64270-64633
55	404257	9367215	Plus	15262-16227
	404285	2326514	Plus	32282-32416
	404288	2769544	Plus	3512-3691
	404367	9965011	Minus	114391-114628
	404443	7579073	Minus	87198-87441
	404453	7657714	Plus	27768-29179
60	404476	8080699	Plus	101841-102043
	404513	8151941	Minus	112837-113339
	404561	9795980	Minus	69039-70100
	404569	7249169	Minus	104257-104348,104822-104970
	404577	4020145	Plus	17991-18420
65	404588	6456726	Minus	40059-40210
	404599	8705107	Plus	110443-110733
	404604	9212537	Minus	72019-72509
	404638	9796751	Minus	99433-99528,100035-100161
	404767	7882827	Minus	23244-23759
70	404793	7232206	Minus	61087-61590
	404822	3810614	Plus	7541-8132
	404834	6911603	Minus	37948-38226
	404845	7958980	Minus	47174-47326,52928-53146,53312-53602
	404898	7331420	Minus	177015-177328
75	404936	6850774	Plus	191519-191664
	404957	7407927	Plus	147512-148011
	405017	6532084	Plus	35551-35690
	405059	7656683	Plus	349-822
	405090	8072525	Minus	38552-39202
80	405093	8072575	Plus	95878-96020
	405120	8099940	Plus	140176-140340
	405170	9566524	Plus	37047-37198
	405229	7249019	Plus	51081-51701
	405230	7249032	Minus	97493-97682

405233	7249045	Plus	9588-10065
405241	7249178	Minus	69927-70526
405264	7329374	Plus	28566-28684
405287	3928029	Plus	89802-89999
405302	2078453	Minus	121688-121840
405303	2078453	Minus	130607-130802
405336	6094635	Plus	33267-33563
405347	2979602	Minus	977-1116
405385	6562772	Plus	48332-48454
405443	7408143	Plus	90716-90887,101420-101577
405455	7656675	Plus	134112-134671
405494	8050952	Minus	70284-70518
405521	9454643	Plus	65096-65247,77508-77637,81242-81364,84246-84395
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
405547	1054740	Plus	124361-124520,124914-125050
405605	5836195	Minus	117070-117270
405608	5815499	Minus	66822-66925
405629	4508116	Minus	101678-101866
405634	5306288	Plus	17856-17957,18302-18412,18837-18927,22790-22989
405654	4895155	Minus	53624-53759
405692	4314424	Plus	61379-62562
405706	4165003	Plus	44307-44431,49619-49802
405720	9797144	Plus	13409-13861
405732	7534017	Plus	146981-147316
405759	3288022	Minus	18283-18399
405780	7248203	Minus	48204-48371
405784	7417368	Minus	77798-78000
405829	7109593	Minus	15628-16127
405869	6758731	Minus	89867-90358
405935	6758795	Minus	163112-163652
405959	6758815	Plus	1-642
405965	8247786	Minus	179930-180373
405966	8247788	Minus	51762-51978
405970	8247789	Minus	45795-46295
405981	8247790	Plus	4771-5338
406005	8247801	Minus	39912-40220
406053	6758997	Plus	30921-31532
406073	9119150	Plus	60495-60610
406091	9123919	Minus	197370-197935
406092	9123919	Plus	251370-251797,252168-252882
406298	5686278	Minus	30084-30770
406327	9212407	Plus	168241-168492
406333	9213235	Plus	64689-64798
406364	9256114	Minus	50715-50833
406377	9256135	Plus	126826-126979,129755-129942
406413	9256407	Plus	43858-44003,46993-47136
406468	9795553	Plus	4373-4616,8870-9046,11366-11509,11625-11880
406470	9795562	Minus	15532-15697
406504	7711360	Minus	107068-107277
406506	7711374	Minus	6843-8077F
406592	4567182	Plus	352560-352963

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Table 32A lists about 969 genes upregulated in lung fibrosis relative to normal body tissues. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

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Table 33A lists about 800 genes upregulated in lung fibrosis relative to normal lung. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

65

Table 34A lists about 703 genes upregulated in idiopathic pulmonary fibrosis (IPF) relative to hypersensitivity pneumonitis (HP) or non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

70

Table 35A lists about 323 genes upregulated in hypersensitivity pneumonitis (HP) relative to idiopathic pulmonary fibrosis (IPF) or non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

75

Table 36A lists about 52 genes upregulated in non-specific interstitial pneumonitis (NSIP) relative to hypersensitivity pneumonitis (HP) or idiopathic pulmonary fibrosis (IPF). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

80

Table 37A lists about 206 genes downregulated in lung fibrosis relative to normal lung. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

Table 38A lists about 207 genes upregulated in lung fibrosis relative to normal tissues. Types of pulmonary fibrosis samples included in this analysis were idiopathic pulmonary fibrosis (IPF), hypersensitivity pneumonitis (HP), and non-specific interstitial pneumonitis (NSIP). These genes were selected from 59680 probesets on the Eos/Affymetrix Hu30 Genchip array. Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative levels of mRNA expression.

TABLE 32A: About 969 genes upregulated in lung fibrosis relative to normal body tissues

Pkey: Unique Eos probest identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of lung fibrosis AIs divided by 90th percentile of normal tissue AIs, where the minimum value for the numerator and denominator was set to 50.
 R2: 90th percentile of lung fibrosis AIs divided by 90th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator. The minimum value for the numerator and denominator was set to 50.

	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
20	414517	M24461	Hs.76305	surfactant, pulmonary-associated protein	22.45	28.63
	406964	M21305		FGFES predicted novel secreted protein	16.10	7.65
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	15.83	14.86
	442275	AW449467	Hs.54795	ESTs	15.74	21.96
	417204	NB1037	Hs.1074	surfactant, pulmonary-associated protein	13.83	34.53
25	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	12.40	7.38
	431089	BE041395		ESTs, Weakly similar to unknown protein	12.38	6.05
	421110	AJ250717	Hs.1355	cathepsin E	11.86	6.49
	457200	U33749	Hs.197764	thyroid transcription factor 1	11.38	9.79
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	10.89	15.94
30	443709	AI082692	Hs.134562	ESTs	10.84	8.27
	431164	AA493650	Hs.94367	Homo sapiens cDNA: FLJ23494 fis, clone L	10.06	8.92
	445537	AJ245671	Hs.12844	ECF-like-domain, multiple 6	9.96	5.43
	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	9.90	7.87
	421798	N74880		N-acylsphingosine amidohydrolase (acid c	9.38	8.35
35	400269			Eos	9.03	6.48
	444325	AW152618	Hs.16757	ESTs	8.31	6.76
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	8.14	5.51
	413048	M93221	Hs.75182	mannose receptor, C type 1	7.70	4.09
	432985	T92363	Hs.178703	ESTs	7.56	7.83
40	443324	R44013	Hs.164225	ESTs	7.06	4.47
	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	6.90	2.89
	408562	AI436323	Hs.31141	roundabout (axon guidance receptor, Dros	6.88	4.00
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.56	4.25
	421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	6.46	4.47
45	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	6.30	13.57
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	6.28	3.38
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	5.99	13.26
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.88	4.10
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	5.88	3.35
50	442652	AI005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	5.87	5.69
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.84	3.34
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.72	5.90
	421502	AF111856	Hs.105039	solute carrier family 34 (sodium phospho	5.59	6.89
	436954	AA740151	Hs.130425	ESTs	5.58	4.72
55	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	5.48	5.33
	421340	F07783	Hs.1369	decay accelerating factor for complement	5.48	2.69
	420656	AA279098	Hs.187636	ESTs	5.45	3.99
	432441	AW292425	Hs.163484	Intron of hepatocyte nuclear factor-3 al	5.38	3.65
	408380	AF123050	Hs.44532	diubiquitin	5.37	3.11
60	414998	NM_002543	Hs.77729	oxidised low density lipoprotein (lectin	5.30	3.98
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	5.29	4.00
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	5.28	2.48
	442832	AW206560	Hs.253569	ESTs	5.20	3.78
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	5.11	3.81
65	433293	AF007835	Hs.32417	hypothetical protein MGC4309	5.11	2.88
	424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.07	3.46
	428043	T92248	Hs.2240	uteroglobin	5.06	9.46
	431745	AW972448	Hs.163425	ESTs	5.04	4.16
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.04	3.68
70	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	5.02	4.26
	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	4.97	3.35
	426927	AA441837	Hs.90250	ESTs	4.92	3.15
	432222	AI204995		gbr:an03c03.x1 Stratagene schizo brain S1	4.79	3.05
	442994	AI026718	Hs.16954	ESTs	4.76	2.65
75	416030	H15261	Hs.21948	ESTs	4.76	4.26
	438873	AI302471	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	4.73	3.24
	453142	AA033648	Hs.7473	ESTs	4.66	2.92
	424917	AI636208	Hs.96901	hypothetical protein FLJ23049	4.64	4.88
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	4.60	2.60
80	432810	AA863400		ESTs	4.54	2.42
	418259	AA215404		ESTs	4.54	2.54
	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	4.48	4.86
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	4.46	3.62
	423575	C18863	Hs.163443	intron of perostatin(OSF-2os)	4.44	3.41
	428667	AI375550	Hs.346868	nuclear protein p40; homolog of yeast	4.42	3.43

	429228	AI553633	ESTs	4.32	2.98
	432435	BE218886	Hs.282070 ESTs	4.30	2.26
	446932	AA961459	Hs.125644 ESTs	4.30	2.81
5	408369	R38438	Hs.182575 SLC15A2 Solute carrier family 15 (H+/pep	4.30	2.39
	409435	AI810721	Hs.95424 ESTs	4.30	2.60
	419490	NM_006144	Hs.90708 granzyme A (granzyme 1, cytotoxic T-lymp	4.29	2.48
	452561	AI692181	Hs.49169 KIAA1634 protein	4.23	2.26
	427698	AW972594	Hs.335499 ESTs	4.22	3.49
10	431433	X65018	Hs.253495 surfactant, pulmonary-associated protein	4.22	13.34
	446608	N75217	Hs.257846 ESTs	4.20	3.62
	428227	AA321649	Hs.2248 small inducible cytokine subfamily B (Cy	4.18	3.14
	459702	AI204995	gb:an03c03.x1 Stratagene schizo brain S1	4.16	2.64
	445885	AI734009	Hs.127699 KIAA1603 protein	4.16	3.99
	430280	AA361258	Hs.237858 interleukin 7 receptor	4.13	2.79
15	425259	AL049280	Hs.155397 Homo sapiens mRNA; cDNA DKFZp564K143 (tr	4.12	2.19
	427019	AA001732	Hs.173233 hypothetical protein FLJ10970	4.12	3.02
	420556	AA278300	Hs.124292 Homo sapiens cDNA: FLJ23123 fis, clone L	4.08	3.13
	428467	AK002121	Hs.184465 hypothetical protein FLJ11259	4.08	3.48
	432731	R31178	Hs.287820 fibronectin 1	4.06	2.66
20	439398	AA284267	Hs.221504 ESTs	4.06	2.86
	409153	W03754	Hs.50813 hypothetical protein FLJ20022	4.05	3.51
	412584	X54870	Hs.74085 DNA segment on chromosome 12 (unique) 24	4.04	2.44
	436120	AI248193	Hs.119860 ESTs	4.04	3.11
25	407910	AA650274	Hs.41296 fibronectin leucine rich transmembrane p	4.03	2.69
	421462	AF016495	Hs.104624 aquaporin 9	4.00	2.51
	443257	AI334040	Hs.11614 HSPC065 protein	4.00	2.61
	421659	NM_014459	Hs.106511 protocadherin 17	4.00	3.00
	424273	W40460	Hs.144442 phospholipase A2, group X	3.98	2.30
	415457	AW081710	Hs.7369 ESTs, Weakly similar to ALU1_HUMAN ALU S	3.97	3.36
30	450656	AA010539	Hs.18912 ESTs	3.96	4.37
	429784	M89796	Hs.30 membrane-spanning 4-domains, subfamily A	3.94	2.44
	424527	AW138558	Hs.334873 ESTs, Weakly similar to I54374 gene NF2	3.93	3.08
	413385	M34455	Hs.840 indoleamine-pyrole 2,3 dioxygenase	3.92	3.53
	452416	AA026115	Hs.114777 ESTs	3.92	2.90
35	428434	AW363590	Hs.65551 Homo sapiens, Similar to DNA segment, Ch	3.90	5.06
	452281	T93500	Hs.28792 Homo sapiens cDNA FLJ11041 fis, clone PL	3.90	2.00
	453204	R10799	Hs.191990 ESTs	3.90	2.22
	450696	AI654223	Hs.16026 hypothetical protein FLJ23191	3.81	3.82
40	422173	BE385828	Hs.250619 phorbol-in-like protein MDS019(CEM15)	3.80	2.23
	425638	NM_012337	Hs.158450 nasopharyngeal epithelium specific prote	3.78	2.86
	406672	M26041	Hs.198253 major histocompatibility complex, class	3.78	3.70
	457411	AW085961	Hs.130093 iroquois-class homeobox protein IROX2	3.76	2.56
	432606	NM_002104	Hs.3066 granzyme K (serine protease, granzyme 3;	3.76	2.76
45	436260	BE172762	Hs.292710 ESTs, Weakly similar to ALU5_HUMAN ALU S	3.74	2.83
	414821	M63835	Hs.77424 Fc fragment of IgG, high affinity Ia, re	3.72	2.55
	428820	AA436187	Hs.172631 integrin, alpha M (complement component	3.71	2.25
	458079	AI796870	Hs.54277 DNA segment on chromosome X (unique) 992	3.70	2.26
	419556	U29615	Hs.91093 chitinase 1 (chitinotrioidase)	3.69	7.71
50	417412	X16895	Hs.82112 interleukin 1 receptor, type I	3.68	2.17
	426174	AA547959	Hs.115838 ESTs	3.65	2.93
	408727	AL137259	Hs.47115 hypothetical protein DKFZp434D0513	3.64	2.62
	435990	AI015862	Hs.131793 ESTs	3.62	2.27
	427621	BE621182	Hs.179882 hypothetical protein FLJ12443	3.62	3.48
55	425555	AA359291	Hs.130767 Homo sapiens cDNA: FLJ23553 fis, clone L	3.61	3.18
	419086	NM_000216	Hs.89591 Kallmann syndrome 1 sequence	3.60	3.05
	426116	AA868729	Hs.144694 ESTs	3.60	2.80
	419235	AW470411	Hs.288433 neurotrophin	3.58	2.88
	424054	AA334511	Hs.26638 membrane-spanning 4-domains, subfamily A	3.56	2.58
60	422667	H25642	ESTs	3.55	2.44
	406673	M34996	Hs.198253 major histocompatibility complex, class	3.54	3.98
	414142	AW365397	Hs.334485 hemiscentin(fibulin 6)	3.54	3.30
	428330	L22524	Hs.2256 matrix metalloproteinase 7 (matrilysin,	3.54	3.11
	430832	AI073913	Hs.100686 ESTs, Weakly similar to JE0350 Anterior	3.53	2.38
65	417318	AW953937	Hs.240845 ESTs	3.52	2.02
	456034	AW450979	gb:U-H-B13-ata-a-12-0-UI.s1 NCL_CGAP_Su	3.50	3.21
	415992	C05837	Hs.145807 hypothetical protein FLJ13593	3.48	2.35
	430709	R34356	gb:rh85d01.s1 Soares placenta Nb2HP Homo	3.48	2.13
	440273	AI805392	Hs.325335 Homo sapiens cDNA: FLJ23523 fis, clone L	3.47	2.93
70	424711	NM_005795	Hs.152175 calcitonin receptor-like	3.47	2.69
	418832	X04011	Hs.88974 cytochrome b-245, beta polypeptide (chro	3.46	2.31
	416847	L43821	Hs.80261 enhancer of filamentation 1 (cas-like do	3.46	2.37
	448019	AW947164	Hs.195641 ESTs, Moderately similar to I38022 hypot	3.45	2.07
	447183	AI554733	Hs.173182 ESTs	3.42	2.01
	435299	AI745458	Hs.343026 ESTs, Weakly similar to T20593 hypotheti	3.40	3.49
75	425922	AL157466	Hs.162751 Homo sapiens mRNA; cDNA DKFZp761E2423 (f	3.40	2.42
	413714	AI560944	Hs.71428 ESTs	3.38	2.52
	407361	AA744622	Hs.292645 ESTs, Weakly similar to ALU5_HUMAN ALU S	3.36	2.13
80	436043	AW963838	Hs.168930 Homo sapiens cDNA FLJ12136 fis, clone MA	3.36	2.41
	450330	AW500775	Hs.24817 hypothetical protein FLJ20136	3.36	2.06
	407756	AA116021	Hs.38260 ubiquitin specific protease 18	3.35	2.42
	410606	AW418779	Hs.114889 ESTs	3.35	2.39
	450726	AW204600	retinoic acid receptor, alpha	3.34	6.35
	430573	AA744550	Hs.136345 ESTs	3.33	1.94

	421585	U95626	Hs.302043	chemokine (C-C motif) receptor-like 2	3.32	2.75
	433658	U03678	Hs.156110	immunoglobulin kappa constant	3.31	2.22
	454076	AW204712	Hs.61957	ESTs	3.31	1.95
5	452039	AI922988	Hs.172510	ESTs	3.30	2.95
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.30	2.37
	430414	AW365665	Hs.120388	ESTs	3.30	2.48
	417958	AA767382	Hs.193417	ESTs	3.30	2.04
	423001	AA320014	Hs.208503	ESTs	3.29	2.62
10	443774	AL117428	Hs.9740	DKFZP434A236 protein	3.28	2.35
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	3.28	2.05
	424238	AA337401	Hs.137635	ESTs	3.28	2.45
	429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	3.27	2.63
	448669	AI792798	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.26	2.67
15	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020.1 E2IG5	3.26	2.04
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.22	2.36
	440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	3.22	3.87
	422109	S73265	Hs.1473	gastrin-releasing peptide	3.20	2.79
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfamily	3.20	2.30
20	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	3.18	2.42
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	3.18	2.12
	438568	R98865	Hs.11135	major histocompatibility complex, class	3.18	3.86
	451497	H83294	Hs.284122	Wnt inhibitory factor-1	3.18	2.99
	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	3.17	2.02
25	446094	AK001760	Hs.13801	KIAA1685 protein	3.17	2.42
	442048	AA974603		gb:op34f05.s1 Soares_NFL_T_GBC_S1 Homo s	3.17	2.27
	406685	M18728		gb:Human nonspecific crossreacting antig	3.17	2.80
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.16	1.95
	424943	AIJ077260	Hs.153924	death-associated protein kinase 1	3.16	2.18
30	436805	AA731533	Hs.270751	ESTs	3.16	1.95
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	3.15	3.63
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	3.14	1.74
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.13	3.35
	420729	AW964897	Hs.290825	ESTs	3.12	2.09
35	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.12	2.06
	416580	T61572	Hs.79385	Human clone 23574 mRNA sequence	3.12	2.58
	451820	AW058357	Hs.199248	ESTs	3.10	2.26
	440028	AW473675		ESTs, Weakly similar to T17227 hypotheti	3.10	3.01
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	3.10	2.32
40	437866	AA156781		metallothionein 1E (functional)	3.10	1.80
	428513	BE220806	Hs.184697	plexin C1	3.10	2.11
	438607	AW080237	Hs.252884	ESTs	3.10	2.20
	445034	AW293376	Hs.143659	ESTs	3.08	2.81
	458332	AI000341		ESTs	3.08	1.87
45	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	3.08	1.87
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.08	1.94
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	3.07	2.12
	452960	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t	3.07	2.16
	425509	AF079363	Hs.158213	sperm associated antigen 6	3.06	2.75
50	431087	H12723	Hs.290791	ESTs	3.06	2.41
	452235	AL039743	Hs.28514	testes development-related NYD-SP21	3.06	2.64
	449328	AI962493		ESTs	3.06	2.78
	422900	AA641201	Hs.222051	ESTs	3.05	1.87
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.05	1.99
55	430250	NM_016929	Hs.283021	chloride intracellular channel 5	3.05	2.49
	437527	AI241019	Hs.145644	ESTs	3.04	2.17
	432340	AA534222		gb:u21d02.s1 NCI_CGAP_AA1 Homo sapiens	3.04	1.78
	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	3.02	2.43
	445495	BE622641	Hs.38489	ESTs, Weakly similar to I38022 hypotheti	3.02	1.77
60	411252	AB018549	Hs.69328	MD-2 protein	3.02	1.95
	439981	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	3.02	2.24
	420683	AA830168	Hs.271305	ESTs	3.01	2.14
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.00	2.13
	410434	AF051152	Hs.63668	tol-like receptor 2	3.00	2.60
65	436396	AI683487	Hs.152213	wingless-type MMTV integration site fam1	3.00	1.94
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.00	1.81
	435800	AI248285	Hs.118348	ESTs	3.00	1.89
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	3.00	2.08
	449057	AB037784	Hs.22941	KIAA1363 protein	3.00	2.18
70	413195	AA127382	Hs.22404	protease, serine, 12 (neurotrypsin, moto	2.99	2.46
	436198	AK001125		Homo sapiens cDNA FLJ10263 fis, clone HE	2.99	2.76
	411492	T46848	Hs.70337	immunoglobulin superfamily, member 4	2.99	2.16
	444020	R92962	Hs.35052	ESTs	2.98	2.21
	427785	X81053	Hs.180828	collagen, type IV, alpha 4	2.98	2.08
75	432583	AW023624	Hs.162282	potassium channel TASK-4; potassium chan	2.98	2.40
	457675	AF119917	Hs.306574	Homo sapiens PRO3098 mRNA, complete cds	2.96	2.03
	414546	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	2.96	1.74
	429950	AW081608	Hs.105053	ESTs	2.96	2.40
	420394	AB023161	Hs.97403	KIAA0944 protein	2.95	2.45
	406698	X03068	Hs.73931	major histocompatibility complex, class	2.95	4.13
80	419038	AW134924	Hs.190325	ESTs	2.94	1.72
	449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	2.94	2.93
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	2.94	1.94
	400880			NM_000611*:Homo sapiens CD59 antigen p18	2.94	1.74

	430382	AA477908	Hs.282267	ESTs, Moderately similar to I38022 hypol	2.94	2.12
	419034	NM_002110	Hs.89555	hemopoietic cell kinase	2.93	2.25
	439335	AA742697	Hs.62492	NM_052863:Homo sapiens secretoglobulin, fa	2.93	3.72
5	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	2.92	1.91
	419981	AA897581	Hs.128773	ESTs	2.92	2.18
	400419	AF084545		Target	2.92	1.83
	435176	AA744875	Hs.189413	ESTs	2.91	2.15
	413283	R78669	Hs.23756	hypothetical protein similar to swine ac	2.90	2.25
10	444339	T96555	Hs.31562	ESTs	2.90	3.16
	429272	W25140	Hs.110667	ESTs	2.90	2.43
	435047	AA454985	Hs.54973	cadherin-like protein VR20	2.90	2.29
	435080	AB31760	Hs.155111	hypothetical protein FLJ14428	2.90	2.40
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	2.88	2.47
	421554	AW137676	Hs.97775	ESTs	2.88	3.37
15	422770	AL117544	Hs.120021	DKFZP434I092 protein	2.88	2.00
	434658	AF624436	Hs.310286	ESTs	2.88	2.06
	440248	AA876138		ESTs	2.86	2.24
	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	2.86	4.32
20	430515	AA746503	Hs.283313	ESTs	2.86	2.96
	446063	AJ720140	Hs.151079	ESTs	2.86	2.47
	438177	BE327015		ESTs	2.86	1.70
	429083	Y09397	Hs.227817	BCL2-related protein A1	2.85	2.06
	417105	X60992	Hs.81226	CD6 antigen	2.85	3.00
25	433230	AW136134	Hs.220277	ESTs	2.84	1.97
	438676	AA813745	Hs.123446	ESTs	2.84	2.62
	435575	AF213457	Hs.44234	triggering receptor expressed on myeloid	2.82	4.33
	420252	AW270404	Hs.193161	ESTs	2.82	3.22
	415788	AW628686	Hs.78851	KIAA0217 protein	2.82	1.78
30	428065	AI634046	Hs.157313	ESTs	2.81	2.47
	434340	AI193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	2.81	2.67
	451558	NM_001089	Hs.26530	ATP-binding cassette, sub-family A (ABC1	2.78	3.39
	435517	AA928626	Hs.130177	ESTs	2.78	2.36
	439883	AL359652	Hs.171096	Homo sapiens EST from clone DKFZp434A041	2.78	1.82
35	434158	T86534	Hs.14372	ESTs	2.78	1.96
	428923	BE047698	Hs.188785	ESTs	2.78	2.07
	413786	AW613780	Hs.13500	ESTs	2.78	1.97
	406387			Target Exon	2.77	4.22
40	421168	AF182277	Hs.330780	cytochrome P450, subfamily IIB (phenobar	2.76	3.24
	444561	NM_004469	Hs.11392	c-fos induced growth factor (vascular en	2.76	2.11
	427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	2.76	1.94
	417728	AW138437	Hs.24790	KIAA1573 protein	2.76	1.78
	435154	AA668764		ESTs	2.76	2.10
45	429490	AJ971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.76	2.21
	423387	AJ012074		vasoactive intestinal peptide receptor 1	2.76	2.36
	432060	AW971364	Hs.324775	ESTs	2.75	2.02
	434164	AW207019	Hs.148135	serine/threonine kinase 33	2.74	2.48
	423706	U95218	Hs.131924	G protein-coupled receptor 65	2.74	1.93
	442703	AL044949	Hs.116298	ESTs	2.74	1.89
50	450247	AF123303	Hs.24713	hypothetical protein	2.74	1.73
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	2.74	2.85
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	2.74	1.88
	409196	NM_001874	Hs.334873	carboxypeptidase M	2.73	1.86
	422389	AF240635	Hs.115897	protocadherin 12	2.72	2.26
55	444324	AJ301330	Hs.143838	ESTs	2.72	1.74
	417831	H16423	Hs.82685	CD47 antigen (Rh-related antigen, integr	2.72	2.40
	428769	AW207175	Hs.106771	ESTs	2.72	2.19
	404277			NM_019111*:Homo sapiens major histocompa	2.72	3.12
	409653	AW451693	Hs.220826	ESTs	2.72	2.62
60	437211	AA382207	Hs.5509	ecotropic viral integration site 2B	2.72	2.25
	430299	W28673	Hs.105747	serine carboxypeptidase 1 precursor prot	2.72	2.09
	444381	BE387335	Hs.283713	hypothetical protein BC014245	2.71	2.26
	443547	AW271273		hypothetical protein FLJ12666	2.71	1.74
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	2.70	2.39
65	402674			Target Exon	2.70	1.95
	438068	AJ927209	Hs.306210	Homo sapiens cDNA: FLJ23133 fis, clone L	2.70	2.23
	415075	L27479	Hs.77689	Friedreich ataxia region gene X123	2.69	2.11
	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	2.69	2.28
	428656	AB037798	Hs.188790	KIAA1377 protein	2.68	1.91
70	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.68	3.95
	443951	F13272		ferritin, light polypeptide	2.68	2.66
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.68	1.74
	432639	AW973785		gb:EST385886 MAGE resequences, MAGM Homo	2.68	1.78
	446423	AW139655	Hs.150120	ESTs	2.68	2.29
75	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	2.67	2.07
	431779	AW971178	Hs.268571	apolipoprotein C-I	2.67	3.00
	458124	AW005548	Hs.124590	ESTs	2.67	3.78
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-ii	2.66	1.64
	445745	AB007924	Hs.13245	KIAA0455 gene product	2.66	1.64
80	425188	AK002052	Hs.155071	hypothetical protein FLJ11190	2.65	1.92
	432231	AA339977	Hs.274127	CLST 11240 protein	2.64	4.23
	442200	AW590572	Hs.235768	ESTs	2.64	2.45
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	2.64	2.00
	448569	BE382657	Hs.21486	signal transducer and activator of trans	2.63	3.23

	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	2.63	2.48
	411213	AA676939	Hs.69285	neuropilin 1	2.62	1.73
	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	2.62	2.69
5	446570	AV659177	Hs.127160	ESTs	2.61	2.44
	411020	NM_005770	Hs.67726	macrophage receptor with collagenous str	2.60	3.39
	434792	AA649253	Hs.132458	ESTs	2.60	1.74
	426782	R14614	Hs.33846	ESTs	2.60	2.36
	425371	D49441	Hs.155981	mesothelin	2.60	6.97
10	447720	AL038765	Hs.161304	ESTs	2.59	3.06
	444623	AI183829	Hs.202111	ESTs	2.59	2.77
	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	2.58	2.01
	444542	AI161293	Hs.280380	aminopeptidase	2.58	2.31
	439549	AW937885	Hs.137314	ESTs	2.58	2.37
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	2.58	2.56
15	417015	M83772	Hs.80876	flavin containing monooxygenase 3	2.56	2.47
	433308	AA582718	Hs.291650	ESTs	2.56	2.01
	443885	H91806	Hs.15284	ESTs	2.55	1.71
	408170	AW204516	Hs.31835	ESTs	2.55	1.59
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.54	1.63
20	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	2.54	2.98
	428791	AA435661	Hs.264750	ESTs	2.53	2.29
	435472	AW972330	Hs.283022	triggering receptor expressed on myeloid	2.53	3.91
	447357	AI375922	Hs.159367	ESTs	2.52	2.83
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	2.52	1.90
25	424105	AI142336	Hs.43977	Human DNA sequence from clone RP11-196N1	2.52	3.45
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	2.52	1.98
	438698	AW297855		ESTs, Weakly similar to I38022 hypothei	2.52	1.98
	420991	AW504814	Hs.287379	Homo sapiens mRNA for FLJ00111 protein,	2.52	2.41
	424049	AB014524	Hs.138380	KIAA0624 protein	2.51	2.19
30	438543	AA810141	Hs.192182	ESTs	2.51	2.05
	414061	NM_000699	Hs.335493	amylase, alpha 2A; pancreatic	2.51	2.14
	424806	AA382523	Hs.105689	MSTP031 protein	2.51	2.11
	438580	AA811262	Hs.299202	ESTs	2.50	1.83
	434445	AI349306	Hs.11782	ESTs	2.50	3.13
35	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	2.50	1.76
	413638	H71252		gbys12h12.s1 Soares fetal liver spleen	2.50	2.00
	421281	AI299139	Hs.17517	ESTs	2.50	2.40
	441384	AA447849	Hs.288660	retinoic acid induced 3	2.50	2.75
40	436772	AW975688		metallothionein 1E (functional)	2.49	1.80
	433102	AI343966	Hs.158528	ESTs	2.49	2.25
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	2.48	2.09
	445612	N94126	Hs.12969	hypothetical protein	2.48	2.28
	445261	T79759	Hs.250651	ESTs, Weakly similar to I38022 hypothei	2.48	1.87
45	433854	AA610649	Hs.333239	ESTs	2.48	2.09
	447997	H00656	Hs.29792	ESTs, Weakly similar to I38022 hypothei	2.48	2.75
	411069	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	2.48	2.01
	440594	AW445167	Hs.126036	ESTs	2.48	1.57
	450295	AI766732	Hs.210628	ESTs	2.48	1.99
50	431316	AA502663	Hs.145037	ESTs	2.48	1.80
	438564	AA381553	Hs.198253	major histocompatibility complex, class	2.48	2.80
	439593	BE073697	Hs.124863	ESTs	2.48	1.89
	422355	AW403724	Hs.300697	coagulation factor VII (serum prothrombi	2.47	3.74
	453134	AA032211	Hs.118493	ESTs	2.46	2.72
55	417169	R13550	Hs.21388	ESTs	2.46	1.88
	434411	AA632649	Hs.201372	ESTs	2.46	1.95
	440381	AA917808	Hs.190495	ESTs	2.46	2.09
	448782	AL050295		KIAA0758 protein	2.46	2.69
	404240			NM_018950:Homo sapiens major histocompat	2.45	2.83
60	450843	AI741483	Hs.205383	ESTs	2.44	2.25
	434137	AA907734	Hs.124895	ESTs	2.44	2.55
	438315	R56795	Hs.82419	ESTs	2.44	1.94
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.44	1.61
	439402	W02753	Hs.103002	ESTs	2.44	1.90
65	445903	AI347487	Hs.132781	class I cytokine receptor	2.44	2.32
	437323	AA371145	Hs.194397	leptin receptor	2.44	1.70
	433923	AI823453	Hs.146625	ESTs	2.44	1.58
	442201	AW516704	Hs.208726	ESTs	2.43	1.68
	437982	N93466	Hs.121764	ESTs, Weakly similar to testicular tekfi	2.43	3.22
70	452698	NM_001295	Hs.301921	chemokine (C-C motif) receptor 1	2.43	2.21
	407904	W44735	Hs.9286	Homo sapiens cDNA: FLJ21278 fis, clone C	2.43	2.13
	406973	M34996	Hs.198253	major histocompatibility complex, class	2.43	2.68
	428055	AA420564	Hs.101760	ESTs	2.42	2.05
	426970	BE276891	Hs.194691	retinoic acid induced 3 (RAIG1); metabo	2.42	2.79
75	433138	AB029496	Hs.59729	semaphorin sem2	2.42	1.68
	415757	AA830854	Hs.187810	ESTs	2.42	2.02
	438507	AA809052		ESTs	2.42	2.08
	450811	AI739486	Hs.245497	ESTs	2.42	1.97
	424027	AW337575	Hs.201591	ESTs	2.42	2.76
80	423778	Y09267	Hs.132821	flavin containing monooxygenase 2	2.41	3.15
	435978	AF272899	Hs.135118	Homo sapiens PR-domain zinc finger prote	2.41	2.08
	426291	U58913	Hs.169191	small inducible cytokine subfamily A (Cy	2.40	1.76
	416370	N90470	Hs.203697	CD38 antigen (p45)	2.40	1.97
	415688	AA166963		gbz086d01.s1 Stratagene ovarian cancer	2.40	1.63

5	445633	AI453386	Hs.17287	ESTs, Weakly similar to S26689 hypotheti	2.39	1.99
	431300	AA502346		gb:na26b03.s1 NCI_CGAP_Co3 Homo sapiens	2.39	1.79
	407690	R47799	Hs.266957	hypothetical protein FLJ14281	2.39	1.84
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.39	2.21
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	2.38	2.09
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.38	1.78
	437479	R61866	Hs.101277	ESTs	2.38	3.00
	445784	AI253155	Hs.146055	ESTs	2.38	1.61
10	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	2.38	2.25
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kafinin	2.37	1.55
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	2.37	2.41
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	2.37	1.61
	418262	Z38968		ESTs	2.37	2.05
	420943	AI718702	Hs.279930	major histocompatibility complex, class	2.37	2.00
15	442762	AF035119	Hs.8700	deleted in liver cancer 1	2.37	2.05
	429747	M87507	Hs.2490	caspase 1, apoptosis-related cysteine pr	2.37	1.67
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.36	1.88
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	2.36	2.61
20	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	2.36	2.84
	427250	R35941	Hs.25418	ESTs	2.36	2.15
	452194	AI694413		olfactory receptor, family 2, subfamily	2.36	3.41
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	2.36	3.05
	407242	M18728		gb:Human nonspecific crossreacting antig	2.35	2.34
25	418875	W19971	Hs.233459	ESTs	2.35	1.95
	425023	AW956889	Hs.154210	EDG-1 (endothelial differentiation, sph	2.35	1.85
	432608	AI492660	Hs.170935	ESTs	2.35	2.06
	408048	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2	2.35	1.91
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	2.35	2.34
30	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	2.35	2.13
	410577	X91911	Hs.64639	glioma pathogenesis-related protein	2.34	1.73
	422099	AA156022	Hs.111518	hypothetical protein	2.34	1.80
	427337	Z45223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	2.34	2.24
	427541	AI798983	Hs.82921	solute carrier family 35 (CMP-sialic aci	2.33	2.62
35	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	2.32	2.52
	431848	AI378857	Hs.271605	ESTs, Highly similar to AF175283 1 zinc	2.32	2.50
	446354	AW449650		ESTs	2.32	2.21
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	2.32	4.34
40	423981	D13665	Hs.136348	perostin (OSF-2os)	2.31	2.19
	410798	BE178622	Hs.16291	gb:PM3-HT0605-270200-001-a02 HT0605 Homo	2.31	2.34
	457250	AA811987	Hs.125779	ESTs	2.31	1.66
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	2.31	2.96
	426839	M74782	Hs.172689	interleukin 3 receptor, alpha (low affin	2.30	2.12
	422746	NM_004484	Hs.119651	glypican 3	2.30	2.16
45	439920	H05430	Hs.288433	neurotrophin	2.30	4.06
	414942	C14898	Hs.192986	ESTs	2.30	2.02
	419092	J05581	Hs.89603	mucin 1, transmembrane	2.29	3.08
	424878	H57111	Hs.221132	ESTs	2.29	1.84
	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.29	2.76
50	411605	AW006831		ESTs	2.29	1.58
	416965	N26223	Hs.160436	ESTs	2.29	4.71
	428713	AA432067		ESTs, Moderately similar to CYA4 RAT ADE	2.29	1.73
	435106	AA100847	Hs.5978	ESTs, Highly similar to AF174600 1 F-box	2.28	1.90
	420380	AA640891	Hs.102406	ESTs	2.28	2.82
55	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.28	1.52
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.28	2.09
	447160	AA330310	Hs.24181	ESTs	2.28	1.71
	421114	AW975051	Hs.293156	ESTs, Weakly similar to T8885 serine/th	2.27	1.98
	453686	AL110326	Hs.304679	ESTs, Moderately similar to Z195_HUMAN Z	2.27	1.91
60	452114	N22687	Hs.8236	ESTs	2.27	1.88
	417355	D13168	Hs.82002	endothelin receptor type B	2.26	1.63
	434927	H46812	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.26	1.84
	442262	BE170651	Hs.8700	deleted in liver cancer 1	2.26	1.86
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	2.26	1.72
65	425354	U62027	Hs.155935	complement component 3a receptor 1	2.26	1.70
	409190	AU076536	Hs.50984	sarcoma amplified sequence	2.26	1.56
	414221	AW450979		gb:UH-BI3-ata-a-12-0-ULs1 NCI_CGAP_Su	2.26	2.12
	435272	AA906415	Hs.110041	ESTs	2.25	2.15
	414991	CT1898		gb:C17898 Human placenta cDNA (TFujwara	2.24	3.58
70	424623	AW963062	Hs.270737	ESTs	2.24	1.87
	424665	AW368576	Hs.139851	caveolin 2	2.24	2.15
	422426	W79117	Hs.58559	ESTs	2.22	3.33
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	2.22	2.39
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	2.22	3.28
75	447197	R35075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	2.22	1.59
	446142	AI754693	Hs.145968	ESTs	2.22	1.88
	410503	AW975746	Hs.188662	KIAA1702 protein	2.22	1.56
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	2.22	2.49
	437629	AW574774	Hs.121692	ESTs	2.22	1.70
	429688	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	2.21	1.64
80	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.20	2.73
	447033	AI357412	Hs.157601	Predicted gene: Eos cloned; secreted w/v	2.20	2.58
	429496	AA453800	Hs.192793	ESTs	2.20	2.97
	425516	BE000707	Hs.29567	ESTs	2.20	1.58

5	422404	AL133571	Hs.336189	Homo sapiens mRNA; cDNA DKFZp434F1135 (I	2.19	1.92
	423526	AB011086	Hs.129739	KIAA0514 gene product	2.19	2.85
	436485	X59135	Hs.156110	immunoglobulin kappa constant	2.19	2.01
	426251	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	2.19	2.53
	443441	AW291196	Hs.92195	ESTs	2.18	1.73
10	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	2.18	2.53
	408705	AA312135	Hs.46967	HSPC034 protein	2.18	1.54
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	2.18	1.93
	430915	AA488953		gb:aa55e05.r1 NCI_CGAP_GC81 Homo sapiens	2.18	1.57
	418791	AA935633	Hs.194628	ESTs	2.17	2.05
15	432620	AA777749	Hs.5978	LIM domain only 7	2.17	1.75
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	2.17	2.01
	406646	M33600	Hs.308026	major histocompatibility complex, class	2.17	3.12
	424450	AL137526		dynein intermediate chain 2	2.17	4.14
	426410	BE298446	Hs.305890	BCL2-like 1	2.16	2.19
20	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	2.16	1.70
	421077	AK000061	Hs.101590	hypothetical protein	2.16	1.60
	424563	AA446932	Hs.151428	ret finger protein 2	2.16	1.83
	405102			C15001220:gi4469558[gb]AAD21311.1[AF	2.16	1.78
	452435	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-fin	2.15	1.87
25	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	2.15	1.65
	418067	A1127958	Hs.83393	cystatin E/M	2.15	2.40
	436372	AW972301	Hs.310286	ESTs	2.15	2.35
	418728	AW970937	Hs.293843	ESTs	2.14	2.58
	450400	A1694722	Hs.279744	ESTs	2.14	2.06
30	409031	AA376836		ESTs	2.14	2.14
	435143	R12375	Hs.194600	ESTs	2.14	1.69
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	2.14	2.03
	453927	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	2.14	1.57
	418304	AA215702		gb:z97g10.r1 NCI_CGAP_GC81 Homo sapiens	2.14	1.68
35	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.14	2.04
	408996	A1979168	Hs.344096	glycoprotein (transmembrane) nmb	2.13	1.72
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	2.13	1.68
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	2.13	2.47
	452353	C18825	Hs.29191	epithelial membrane protein 2	2.12	2.31
40	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	2.12	2.76
	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	2.12	2.11
	437581	N59284	Hs.288010	ESTs	2.12	2.85
	410976	R36207	Hs.25092	hypothetical protein MGC10744	2.12	2.04
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	2.12	2.00
45	423069	W15613	Hs.1613	adenosine A2a receptor	2.12	1.72
	432860	AW974077	Hs.283349	ESTs	2.12	1.75
	449509	AA001615	Hs.84561	ESTs	2.12	1.84
	456062	A1866285	Hs.71962	ESTs, Weakly similar to B36298 prolina-r	2.11	4.42
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.11	1.65
50	459680	H96982	Hs.42321	ESTs	2.11	2.20
	449677	AA02071		gb:zh85d01.s1 Soares_fetal_liver_spleen_	2.10	2.12
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	2.10	2.48
	443021	AA368546	Hs.8904	lg superfamily protein	2.10	2.42
	437838	A1307229		ESTs	2.10	1.67
55	429421	AL031658		Human DNA sequence from clone RP1-310013	2.10	1.91
	407202	N58172	Hs.109370	ESTs	2.10	1.68
	443669	A1140462	Hs.134587	ESTs	2.10	1.64
	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	2.10	1.71
	408410	AA447438	Hs.44697	ATPase, Class V, type 10C	2.10	2.05
60	436293	A1601188	Hs.120910	ESTs	2.10	2.01
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	2.10	1.66
	427876	A194291		ESTs	2.10	2.48
	459672	AK002016	Hs.114727	Homo sapiens, clone MGC:16327, mRNA, com	2.09	3.11
	434987	AW975114		ESTs	2.09	1.69
65	433735	AA608955	Hs.109653	ESTs	2.09	1.78
	433226	AW503733	Hs.9414	KIAA1488 protein	2.09	1.62
	425787	AA363867	Hs.155029	ESTs	2.09	1.85
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	2.08	3.41
	442369	A1565071		ESTs	2.08	1.60
70	430478	NM_014349	Hs.241535	apolipoprotein L, 3	2.08	2.39
	434421	A1915927	Hs.34771	ESTs	2.08	1.66
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	2.08	1.72
	431728	NM_007351	Hs.268107	multimerin	2.08	1.51
	444929	A1685841	Hs.161354	ESTs	2.08	3.14
75	408873	AL046017		calmodulin 2 (phosphorylase kinase, delt	2.08	2.09
	437634	AW293046	Hs.255158	ESTs	2.08	1.66
	400277			Eos Control	2.08	1.46
	443601	A1078554	Hs.42658	ESTs	2.08	1.87
	432212	AW137742		ESTs	2.08	2.84
80	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	2.07	1.48
	406122			Target Exon	2.06	2.75
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	2.06	1.66
	408788	AL134947	Hs.213956	Homo sapiens BAC clone RP11-10205 from Y	2.06	1.70
	421057	T58283		Homo sapiens cDNA: FLJ22063 fis, clone H	2.06	1.78
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibito	2.06	2.30
	431924	AK000850	Hs.272203	Homo sapiens cDNA FLJ20843 fis, clone AD	2.06	2.31
	449444	AW818436		solute carrier family 16 (monocarboxylic	2.06	1.41

	421464	AA291553	Hs.190086	ESTs	2.06	2.61
	424831	H61453		ESTs	2.06	2.12
	434542	AA769310		hypothetical protein FLJ13164	2.06	1.44
5	418323	NM_002118	Hs.1162	major histocompatibility complex, class	2.05	2.61
	418836	AI655499	Hs.161712	ESTs	2.05	1.73
	431315	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	2.05	1.99
	400750			Target Exon	2.05	1.75
	406851	AA609784		major histocompatibility complex, class	2.05	3.94
10	414936	C14774		gb:C14774 Clontech human aorta polyA mRNA	2.05	2.41
	453459	BE047032	Hs.257789	ESTs	2.04	1.86
	443450	N66045	Hs.133529	ESTs	2.04	2.46
	430015	AW768399		ESTs	2.04	1.63
	429399	AA452244	Hs.16727	ESTs	2.04	1.51
15	411653	AF070578	Hs.71168	Homo sapiens clone 24574 mRNA sequence	2.04	1.73
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	2.04	1.46
	421757	Z20897	Hs.296259	para-oxonase 3	2.04	2.13
	441942	AF182645	Hs.8024	IK cytokine, down-regulator of HLA II	2.04	1.82
	431843	AA516420		ESTs, Weakly similar to I38022 hypothe	2.04	1.67
20	432006	AL137382	Hs.272320	Homo sapiens mRNA; cDNA DKFZp434L1226 (f	2.04	3.23
	414154	AW205314	Hs.323060	ESTs	2.03	2.96
	449987	AW079749	Hs.184719	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.03	1.59
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	2.03	2.01
	406645	M57466	Hs.814	major histocompatibility complex, class	2.03	2.49
25	414516	AI307802		ESTs, Weakly similar to T43458 hypothe	2.02	1.56
	417032	AA192469	Hs.271838	ESTs	2.02	1.48
	414875	H42679	Hs.77522	major histocompatibility complex, class	2.02	2.79
	414522	AW518944	Hs.76325	immunoglobulin J chain	2.02	1.84
	410511	AA743475	Hs.285655	ESTs	2.02	1.87
30	423533	NM_014339	Hs.129751	interleukin 17 receptor	2.02	2.26
	437259	AI377755	Hs.120695	ESTs	2.02	2.34
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypothe	2.02	1.86
	426722	U53823	Hs.171952	occludin	2.02	1.57
	421229	AI056590	Hs.7086	hypothetical protein MGC12435	2.02	1.79
35	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.02	1.97
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	2.02	2.09
	449317	AW293413	Hs.132906	19A24 protein	2.02	1.84
	439556	AI623752	Hs.163603	ESTs	2.02	1.62
	443031	AW134696	Hs.49418	ESTs	2.01	1.58
40	444838	AV651680	Hs.208558	ESTs	2.01	1.69
	453108	AI311457	Hs.99472	ESTs	2.01	1.64
	432967	AA572949	Hs.207566	ESTs	2.01	1.83
	441390	AI692560	Hs.131175	ESTs	2.01	1.63
	448076	AI133123	Hs.20196	adenylate cyclase 9	2.01	1.80
45	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.01	2.32
	414629	AA345824	Hs.76688	carboxylesterase 1 (monocyte/macrophage	2.01	1.90
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.01	1.90
	415443	T07353	Hs.7948	ESTs	2.00	1.54
	424925	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	2.00	2.74
50	404394			ENSP00000241075:TRRAP PROTEIN.	2.00	2.99
	459557	N58315		gb:yy68g06.s1 Soares fetal liver spleen	2.00	1.89
	437204	AL110216		ESTs, Weakly similar to I55214 salivary	2.00	1.46
	429295	AA682377	Hs.99216	ESTs, Moderately similar to ALU8_HUMAN A	2.00	1.37
	440667	BE076969	Hs.7337	hypothetical protein FLJ10936	2.00	1.51
55	431193	AW749505	Hs.295770	KIAA1719 protein	1.99	2.01
	432485	N90866	Hs.276770	CDWS2 antigen (CAMPATH-1 antigen)	1.99	2.11
	450293	N36754	Hs.171118	hypothetical protein FLJ00026	1.98	1.79
	417072	BE243915	Hs.81118	leukotriene A4 hydrolase	1.98	2.47
	429073	AA446167	Hs.47385	ESTs	1.98	1.92
60	448133	AA723157	Hs.73769	folate receptor 1 (adult)	1.98	2.94
	420838	AW118210	Hs.42321	ESTs	1.98	1.67
	436252	AI539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	1.97	2.10
	430702	U56979	Hs.278568	H factor 1 (complement)	1.97	1.84
	456804	AI421645	Hs.139851	caveolin 2	1.97	1.58
65	439195	H89360		gb:yy28d08.s1 Morton Fetal Cochlea Homo	1.97	1.93
	459299	BE094291	Hs.155651	hepatocyte nuclear factor 3, beta	1.97	2.28
	413836	W92003	Hs.70614	ESTs	1.97	1.80
	400417	X72475		Target	1.97	1.75
	427814	W28383	Hs.180900	Williams-Beuren syndrome chromosome regi	1.96	1.46
70	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	1.96	2.18
	446135	AW130288	Hs.170318	hypothetical protein FLJ10147	1.96	2.06
	455615	BE045344	Hs.274923	ESTs, Moderately similar to unnamed prot	1.96	2.21
	414572	AU077174	Hs.288181	cathepsin H	1.96	2.65
	433891	AA613792		gb:nc097h03.s1 NCI_CGAP_Pr2 Homo sapiens	1.95	1.71
75	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	1.95	2.88
	451609	AL046019	Hs.209276	ESTs	1.94	3.26
	447131	NM_004585	Hs.17466	retinoic acid receptor responder (Iazaro	1.94	2.94
	430887	N66801	Hs.260287	KIAA1841 protein	1.94	1.62
80	414700	H63202	Hs.38163	ESTs	1.94	1.72
	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	1.94	1.56
	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	1.93	2.22
	425252	AW391162		calreticulin	1.92	2.14
	428758	AA433988	Hs.98502	CA125 antigen; mucin 16	1.92	2.19
	425810	AI923627	Hs.31903	ESTs	1.92	1.76

	433618	AA602539	Hs.345494	ESTs	1.92	1.84
	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	1.92	2.27
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	1.92	1.76
5	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	1.92	1.72
	409745	AA077391		gb:7B14E12 Chromosome 7 Fetal Brain cDNA	1.91	1.83
	426780	BE242284	Hs.172199	adenylate cyclase 7	1.91	1.67
	452386	R12499	Hs.20468	ESTs	1.91	2.64
	438670	AI275803	Hs.123428	ESTs	1.91	3.12
10	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	1.91	1.82
	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	1.90	2.06
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	1.90	1.85
	444745	AF117754	Hs.11861	thyroid hormone receptor-associated prot	1.90	1.65
	428166	AA423849	Hs.79530	M5-14 protein	1.90	1.70
15	426721	AA383588	Hs.131816	ESTs, Weakly similar to T29012 hypotheti	1.89	3.22
	449271	AW338067	Hs.7869	Homo sapiens cDNA FLJ11946 fis, clone HE	1.88	2.07
	436576	AI458213	Hs.77542	ESTs	1.88	2.25
	437751	AA767373		ESTs, Moderately similar to ALU1_HUMAN A	1.88	2.41
	449618	AI076459	Hs.15978	KIAA1272 protein	1.88	1.63
20	430634	AI860651	Hs.26685	calcyphosine	1.88	3.01
	440663	AW452976	Hs.247112	hypothetical protein FLJ10902	1.88	1.65
	440099	AL080058	Hs.6909	DKFZP564G202 protein	1.88	1.78
	414662	AL036058	Hs.76807	major histocompatibility complex, class	1.88	2.37
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	1.87	2.07
25	414464	AI870175	Hs.13957	ESTs	1.87	2.68
	427792	M63928	Hs.180841	tumor necrosis factor receptor superfam	1.87	2.25
	415801	R24219	Hs.278443	Fc fragment of IgG, low affinity IIb, re	1.87	2.05
	430027	AB023197	Hs.227743	KIAA0980 protein	1.87	1.70
30	425771	BE561776	Hs.159494	Bruton agammaglobulinemia tyrosine kinas	1.87	2.18
	412443	AW951103	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	1.86	2.27
	408771	AW732573	Hs.47584	potassium voltage-gated channel, delayed	1.86	2.31
	420361	N92054	Hs.194718	zinc finger protein 265	1.86	1.63
	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	1.86	2.13
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	1.85	1.77
35	442434	AA995787	Hs.129583	ESTs	1.85	2.15
	422735	AA169685	Hs.119529	Niemann-Pick disease, type C2 gene	1.85	2.77
	444083	AI123195		gb:oo17a10.x1 Soares_NSF_FB_9W_OT_PA_P_S	1.84	1.73
	449679	AI823951	Hs.129700	toll-like 1	1.84	1.57
	418183	NM_001772	Hs.83731	CD33 antigen (gp67)	1.84	2.02
40	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.84	1.72
	414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	1.84	2.47
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	1.84	2.29
	455508	AW976165		gb:EST388274 MAGE resequences, MAGN Homo	1.84	1.69
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	1.83	2.12
45	426457	AW894667	Hs.22660	chimerin (chimaerin) 1	1.83	1.59
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	1.83	1.57
	417086	AA194446		ESTs, Weakly similar to S55024 nebulin,	1.83	1.45
	426175	AF020202	Hs.155001	UNC13 (C. elegans)-like	1.83	2.18
	429952	AF080158	Hs.226573	inhibitor of kappa light polypeptide gen	1.83	1.75
50	438596	AA829427	Hs.243081	ESTs	1.83	2.83
	436486	AA742221	Hs.120633	ESTs	1.82	2.14
	433365	AF026944	Hs.293797	ESTs	1.82	2.50
	449943	AF104266	Hs.24212	latrophilin	1.82	2.08
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	1.82	2.37
55	421563	NM_006433	Hs.105806	granulysin	1.82	2.48
	449161	N53431	Hs.47647	ESTs, Weakly similar to T00057 hypotheti	1.81	2.81
	453107	NM_016113	Hs.279746	vanilloid receptor-like protein 1	1.81	2.66
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	1.81	2.50
	432946	U60899	Hs.279854	mannosidase, alpha, class 2B, member 1	1.81	2.05
60	432297	AW663632	Hs.285625	Homo sapiens mRNA; cDNA DKFZp434A119 (fr	1.80	3.13
	428677	AI657119	Hs.120036	tropomyosin 1, cardiac	1.80	2.94
	409485	S80990	Hs.252136	ficollin (collagen/fibrinogen domain-cont	1.80	2.28
	423081	AF262992	Hs.123159	sperm associated antigen 4	1.80	1.56
	425458	H89317	Hs.182889	ESTs	1.80	2.21
65	425390	AI092634	Hs.156114	protein tyrosine phosphatase, non-recept	1.80	1.41
	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	1.80	2.20
	430570	AI417881	Hs.292464	ESTs	1.80	1.62
	439425	AF086244	Hs.114659	ESTs	1.80	2.37
	408688	AI634522	Hs.152925	KIAA1268 protein	1.80	2.13
70	440675	AW005054	Hs.279788	ESTs, Weakly similar to KCC1_HUMAN CALCI	1.80	1.80
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	1.79	1.57
	406621	X57809	Hs.8997	immunoglobulin lambda locus	1.79	2.18
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.79	1.68
	403421			NM_016369*Homo sapiens claudin 18 (CLDN	1.79	2.47
75	430423	AI190548	Hs.143479	ESTs, Weakly similar to hypothetical pro	1.79	2.92
	416384	AU076903	Hs.79283	selectin P ligand	1.79	1.87
	440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	1.78	1.69
	422003	AA361760	Hs.296326	ESTs	1.78	2.05
	412288	NM_003005	Hs.73800	selectin P (granule membrane protein 140	1.77	1.82
80	432987	AI864771	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	1.77	2.03
	441602	AI655043	Hs.133456	ESTs	1.77	2.01
	458194	AW383618		ESTs, Moderately similar to ALU2_HUMAN A	1.76	2.35
	432565	AA553477	Hs.152428	ESTs	1.76	2.63
	421071	AI311238	Hs.104476	ESTs, Weakly similar to CGHUIE collagen	1.75	2.59

	408989	AW361666	Hs.49500	KIAA0746 protein	1.75	1.66
	414807	A1738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	1.75	1.54
	403903			C5001632*gil10645308[gb]AAG21430.1)AC00	1.75	3.20
5	421461	AW291023		ESTs, Weakly similar to A46010 X-linked	1.74	2.67
	430850	BE144152		gb:MRD-HT0165-060200-006-e02 HT0165 Homo	1.74	2.52
	424377	AF081675	Hs.146322	killer cell lectin-like receptor subfam1	1.74	2.15
	443884	N20617	Hs.194397	leptin receptor	1.74	1.51
	423057	AW961597	Hs.130816	ESTs, Moderately similar to I38022 hypot	1.74	1.63
10	448262	AW880830	Hs.186273	ESTs	1.73	2.57
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	1.73	1.87
	431630	NM_002204	Hs.265829	integrin, alpha 3 (antigen CD49C, alpha	1.73	2.21
	412896	AW804157	Hs.308026	major histocompatibility complex, class	1.72	2.37
	407366	AF026942	Hs.17518	gb:Homo sapiens c1g33 mRNA, partial sequ	1.72	2.16
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	1.72	1.52
15	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	1.71	1.55
	436606	NM_014859	Hs.6336	KIAA0672 gene product	1.71	1.57
	434795	BE620794	Hs.4147	translocating chain-associating membrane	1.71	2.21
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	1.71	1.46
	418307	U70867	Hs.83974	solute carrier family 21 (prostaglandin	1.71	2.49
20	412121	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	1.71	1.57
	423857	N48902	Hs.133481	Homo sapiens mRNA; cDNA DKFZp56400862 (f	1.71	1.56
	408393	AW015318	Hs.23165	ESTs	1.70	1.43
	432409	AA806538	Hs.130732	KIAA1575 protein	1.70	1.54
	440817	A1341423	Hs.288433	neurotrophin	1.70	2.17
25	421445	AA913059	Hs.104433	Homo sapiens, clone IMAGE:4054868, mRNA	1.69	2.54
	453691	H12235	Hs.226505	ESTs	1.69	2.07
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	1.68	1.54
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.68	2.29
	434951	AF161442	Hs.191591	Homo sapiens HSPC324 mRNA, partial cds	1.68	2.24
30	444301	AK000136	Hs.10760	asporin (LRR class 1)	1.68	1.44
	407775	NM_004914	Hs.38772	RAB36, member RAS oncogene family	1.68	2.03
	437119	A1379921	Hs.177043	ESTs	1.68	4.21
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	1.68	2.28
	453498	BE181412	Hs.23245	hypothetical protein FLJ11767	1.68	2.76
35	428289	M26301	Hs.2253	complement component 2	1.67	2.40
	404854			Target Exon	1.67	1.76
	450954	A1904740	Hs.25691	receptor (calcitonin) activity modifying	1.67	2.32
	410048	W76467	Hs.343874	proline oxidase homolog	1.67	3.03
40	407857	A1928445	Hs.92254	synaptotagmin-like 2	1.66	1.51
	447827	U73727	Hs.19718	protein tyrosine phosphatase, receptor t	1.66	2.01
	417193	A1922189	Hs.288390	hypothetical protein FLJ22795	1.66	2.05
	421237	U25029	Hs.102761	Human glucocorticoid receptor alpha mRNA	1.66	2.20
	433350	BE563152	Hs.10362	Homo sapiens cDNA: FLJ20944 fis, clone A	1.66	2.11
45	417451	AW007280	Hs.115537	putative dipeptidase	1.65	2.11
	443791	N64458	Hs.143345	ESTs	1.65	2.11
	440475	A1807671	Hs.24040	potassium channel, subfamily K, member 3	1.65	2.04
	431743	AW972642	Hs.293055	ESTs	1.64	2.64
	400328	X87344		transporter 2, ATP-binding cassette, sub	1.64	2.43
50	451876	T63141		gb:yb99a12.s1 Stratagene lung (937210) H	1.64	2.02
	417321	N68722	Hs.191368	ESTs	1.64	2.53
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.64	2.01
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	1.63	2.17
	432176	AW090386	Hs.112278	arrestin, beta 1	1.63	2.04
55	450708	AA376654		eukaryotic translation initiation factor	1.62	2.05
	429570	BE242256	Hs.2441	KIAA0022 gene product	1.62	1.39
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp5648076 (fr	1.62	1.57
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	1.62	1.44
	452424	A1964028	Hs.48353	ESTs	1.62	2.53
60	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	1.62	1.38
	416316	H58721	Hs.271628	ESTs	1.62	1.39
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	1.62	2.67
	452203	X57522		transporter 1, ATP-binding cassette, sub	1.62	2.45
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a1	1.62	1.51
65	438089	W05391		nuclear receptor subfamily 1, group I, m	1.61	1.45
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	1.61	1.52
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	1.61	2.40
	444009	A1380792	Hs.135104	ESTs	1.60	2.15
	436057	AJ004832	Hs.5038	neuropathy target esterase	1.60	2.60
70	437352	AL353957	Hs.284181	hypothetical protein DKFZp434P0531	1.60	2.57
	433614	W07475	Hs.277101	cytochrome c oxidase subunit IV isoform	1.60	3.30
	410494	M36564	Hs.64016	protein S (alpha)	1.59	1.42
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	1.59	2.02
	446616	R65964	Hs.334873	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.59	2.52
	419918	X80700	Hs.93728	pre-B-cell leukemia transcription factor	1.59	2.04
75	428141	D50402	Hs.182611	solute carrier family 11 (proton-coupled	1.59	1.98
	434308	N51517	Hs.47282	ESTs	1.58	2.29
	447341	AF106941	Hs.18142	arrestin, beta 2	1.58	2.09
	454315	AW373564	Hs.251928	BANP homolog, SMAR1 homolog	1.58	2.10
80	423281	AJ271684	Hs.126355	C-type (calcium dependent), carbohydrate-	1.57	1.75
	433571	AW138797	Hs.132906	19A24 protein	1.57	2.05
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	1.57	2.71
	436906	H95990	Hs.181244	major histocompatibility complex, class	1.57	2.24
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	1.57	1.43

5	406825	AJ982529	Hs.84298	CD74 antigen (invariant polypeptide of m	1.57	2.37
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.56	1.61
	423329	AF054910	Hs.127111	teklin 2 (testicular)	1.56	2.51
	424909	S78187	Hs.153752	cell division cycle 25B	1.55	2.00
	431921	N46466	Hs.58879	ESTs	1.54	3.04
10	437400	AB011542	Hs.55599	EGF-like-domain, multiple 5	1.54	1.44
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfam	1.54	3.04
	415078	AA311223	Hs.283091	found in inflammatory zone 3	1.53	2.61
	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	1.53	2.18
	401854			Target Exon	1.53	2.08
15	406850	AI624300	Hs.172928	collagen, type I, alpha 1	1.52	1.52
	433815	AI696602	Hs.112757	ESTs	1.52	2.57
	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	1.52	1.36
	453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fis, clone L	1.51	1.43
	414763	U97276	Hs.77266	quiascin Q6	1.50	2.07
20	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuo	1.50	1.46
	412870	N22788	Hs.82407	CXC chemokine ligand 16	1.50	2.83
	407601	AC002300	Hs.37129	sodium channel, nonvoltage-gated 1, beta	1.50	2.04
	432894	AW167668	Hs.279772	brain specific protein	1.50	2.25
	457941	AJ004525	Hs.14587	ESTs, Weakly similar to AF151859 1 CGI-1	1.49	2.22
25	442743	AJ801351	Hs.302110	ESTs, Weakly similar to MUC2_HUMAN MUCIN	1.49	2.09
	419542	AA366037	Hs.90911	solute carrier family 16 (monocarboxylic	1.49	2.40
	433124	U51712	Hs.13775	hypothetical protein SMAP31	1.49	1.39
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	1.49	1.39
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.48	1.76
30	417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	1.48	1.41
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	1.48	1.44
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	1.47	1.31
	427872	AA835058		Human DNA sequence from clone RP1-261G23	1.47	2.50
	449853	AF008823	Hs.24040	potassium channel, subfamily K, member 3	1.47	2.21
35	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (1.47	1.50
	415149	X12451	Hs.78056	cathepsin L	1.46	1.84
	447217	BE465754	Hs.17778	neuropilin 2	1.46	1.40
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	1.46	2.16
	445672	AI907438	Hs.282862	ESTs	1.46	2.01
40	432210	AI567421	Hs.273330	Homo sapiens, clone IMAGE:3544662, mRNA,	1.46	2.10
	458208	AI380016		ESTs, Weakly similar to T4S4_HUMAN TRANS	1.46	1.60
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypothetical	1.45	1.40
	419577	L36531	Hs.91296	integrin, alpha 8	1.45	1.40
	439620	AA838727	Hs.124405	ESTs, Weakly similar to A46010 X-linked	1.45	1.57
45	423804	AW403448	Hs.16725	interferon-stimulated transcription fact	1.45	2.10
	424658	NM_002406	Hs.151513	mannosyl (alpha-1,3)-glycoprotein beta-	1.44	2.00
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005	1.44	1.45
	431573	AW971070	Hs.291160	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.44	1.40
	409524	AW402151	Hs.54673	tumor necrosis factor (ligand) superfam	1.43	2.01
50	406787	AW090702	Hs.240615	tubulin alpha 1	1.42	1.86
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	1.42	1.95
	406422			Target Exon	1.41	2.02
	421341	AJ243212		deleted in malignant brain tumors 1	1.41	1.47
	421195	BE464560	Hs.133017	ESTs	1.41	2.42
55	425998	AU076629	Hs.165950	fibroblast growth factor receptor 4	1.41	2.05
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	1.41	1.34
	451220	AF124251	Hs.26054	novel SH2-containing protein 3	1.40	2.10
	409238	AL049990	Hs.51515	Homo sapiens mRNA; cDNA DKFZp564G112 (fr	1.40	3.64
	411880	AW872477		gb:hm30f03.x1 NCL_CGAP_Thy4 Homo sapiens	1.40	3.24
60	432133	AB033088	Hs.272567	KIAA1262 protein	1.40	2.78
	428833	AI928355		ESTs	1.40	2.02
	455797	BE091833		gb:IL2-8T0731-260400-076-F04 BT0731 Homo	1.39	1.55
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	1.39	2.09
	427732	NM_002980	Hs.2199	secretin receptor	1.38	2.44
65	449746	AI668594	Hs.176588	ESTs, Weakly similar to CP4Y_HUMAN CYTOC	1.38	1.85
	407568	AA740964	Hs.62699	ESTs	1.38	3.13
	422573	AW297985	Hs.295726	integrin, alpha V(vitronectin receptor	1.38	1.38
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	1.37	1.12
	457918	AL359590	Hs.162604	hypothetical protein DKFZp762M186	1.36	2.01
70	423696	Z92546	Hs.131819	Sushi domain (SCR repeat) containing	1.36	2.54
	416700	AW498958	Hs.343475	cathepsin D (lysosomal aspartyl protease	1.36	2.04
	407244	M10014		fibrinogen, gamma polypeptide	1.36	1.29
	451109	F11875	Hs.5534	Homo sapiens cDNA FLJ12951 fis, clone NT	1.35	1.34
	406654	M90686	Hs.73885	HLA-G histocompatibility antigen, class	1.35	2.47
75	407603	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,	1.34	1.66
	445417	AK001058	Hs.12680	a disintegrin-like and metalloprotease w	1.34	1.92
	436982	AB018305	Hs.5378	spondin 1, (I-spondin) extracellular mat	1.34	1.86
	427507	AF240467	Hs.179152	toll-like receptor 7	1.34	2.11
	446967	AI899629	Hs.156781	ESTs	1.34	3.75
80	436553	AW407157	Hs.8997	immunoglobulin lambda locus	1.34	2.18
	456637	AW161450	Hs.109201	CGI-86 protein	1.33	1.78
	422129	AU076635	Hs.1478	serine (or cysteine) proteinase inhibito	1.33	1.95
	417785	X59812	Hs.82568	cytochrome P450, subfamily XXVIIA (stero	1.32	2.05
	414849	AW372721	Hs.291623	ESTs, Weakly similar to unnamed protein	1.32	2.08
	436586	AA740983	Hs.210792	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.32	2.06
	410598	AU171130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	1.32	2.08
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	1.31	1.29

5	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	1.30	1.25
	413474	T86312	Hs.334485	Homo sapiens cDNA FLJ14438 fis, clone HE	1.30	1.92
	406659	AA663985	Hs.277477	major histocompatibility complex, class	1.30	2.22
	451049	AA013353		gb:ze28h10.s1 Soares retina N2b4HR Homo	1.30	2.12
	436494	AA720997	Hs.128295	ESTs	1.29	2.30
	438374	AA321866	Hs.6193	hypothetical protein FLJ14590	1.28	2.34
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	1.28	2.39
	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (f	1.28	1.69
10	428458	AA428820	Hs.251399	neurogranin (protein kinase C substrate,	1.27	2.00
	443180	R15875	Hs.258576	claudin 12	1.26	1.25
	421764	AI681535	Hs.148135	serine/threonine kinase 33	1.26	2.01
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	1.26	1.21
	433283	BE041135	Hs.175622	ESTs	1.24	3.05
15	426759	AI590401	Hs.21213	ESTs	1.23	1.20
	436446	AW016809	Hs.119021	ESTs	1.23	1.20
	421467	AA291590	Hs.97252	ESTs	1.22	1.54
	431353	AA828032		ESTs	1.22	3.00
	427403	AA402107	Hs.257145	ESTs, Moderately similar to I38022 hypot	1.22	1.91
20	453037	AA045175	Hs.17914	ESTs	1.22	2.40
	437608	AA761605	Hs.292308	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.22	2.26
	439941	AI392640	Hs.18272	amino acid transporter system A1	1.22	1.22
	451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	1.21	1.49
	400496			ENSP00000224716*:GTP-binding protein SAR	1.20	1.25
25	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	1.20	1.44
	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	1.19	2.06
	426486	BE178285	Hs.170056	Homo sapiens mRNA; cDNA DKFZp586B0220 (f	1.18	2.02
	445033	AV652402	Hs.72901	cyclin-dependent kinase inhibitor 2B (p1	1.17	1.14
	439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	1.14	1.16
30	440555	D31292	Hs.6853	hypothetical protein FLJ22167	1.14	2.19
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	1.13	1.12
	432203	AA305746	Hs.49	macrophage scavenger receptor 1	1.12	2.43
	432798	AA565309	Hs.194015	ESTs	1.10	2.23
	411274	NM_002776	Hs.69423	kalikrein 10	1.10	1.09
35	438856	N40027	Hs.7473	ESTs	1.09	1.52
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	1.09	1.07
	448253	H25899	Hs.201591	ESTs	1.08	2.10
	409718	D86640	Hs.56045	src homology three (SH3) and cysteine ri	1.08	2.08
	409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN !!!	1.06	1.58
	449321	AA001150	Hs.132937	ESTs	1.06	2.06
40	418693	AJ750878	Hs.87409	thrombospondin 1	1.06	1.02
	402333			Target Exon	1.03	1.03
	421814	L12350	Hs.108623	thrombospondin 2	1.02	1.02
	425664	AJ006276	Hs.159003	transient receptor potential channel 6	1.00	2.36
45	458158	AW295778	Hs.144734	Human DNA sequence from clone RP3-416F21	1.00	2.73
	406517			nal (chicken)-like 2	1.00	2.07
	442526	AW277221		ESTs	1.00	2.21
	446164	AW273539		hypothetical protein FLJ23577	1.00	2.52
	449122	AI631310	Hs.196955	ESTs	1.00	2.23
50	438038	AI732629		ESTs, Weakly similar to TA2R HUMAN, BETA	1.00	2.04
	429420	AK001679	Hs.202289	hypothetical protein DKFZp434P1735	1.00	2.02
	453672	U73531	Hs.34526	G protein-coupled receptor	1.00	2.57
	436187	AK000998	Hs.297221	Homo sapiens cDNA FLJ10136 fis, clone HE	1.00	2.64
	438909	AF085839		gb:Homo sapiens full length insert cDNA	1.00	2.23
55	423609	AA328348	Hs.218289	ESTs	1.00	2.19
	419261	X07876	Hs.69791	wingless-type MMTV integration site fami	1.00	2.28
	436284	AA708016	Hs.190389	ESTs	1.00	2.22
	440932	AI801509	Hs.182080	ESTs	1.00	1.66
	403420			Target Exon	1.00	1.86
60	431169	AW971240		gb:EST383329 MAGE resequences, MAGL Homo	1.00	2.02
	425916	NM_006786	Hs.162200	urotensin 2	1.00	2.11
	419721	NM_001650		aquaporin 4	1.00	2.26
	421761	AL120297	Hs.108043	Friend leukemia virus integration 1	1.00	1.86
	425781	AF001622	Hs.159523	class-I MHC-restricted T cell associated	1.00	1.96
65	415094	D59513	Hs.330778	ESTs	1.00	2.32
	434088	AF116677	Hs.249270	hypothetical protein PRO1966	1.00	2.26
	420727	H75701	Hs.99886	complement component 4-binding protein,	1.00	1.84
	430049	AW277085	Hs.99619	ESTs	1.00	1.87
	446868	AV660737		ESTs	1.00	1.79
70	418766	AI796317	Hs.203594	Homo sapiens uncharacterized gastric pro	1.00	1.44
	436391	AJ227892	Hs.146274	ESTs	1.00	1.30
	413059	BE151498		gb:RC0-HT0295-291199-031-E11 HT0295 Homo	1.00	1.42
	427739	AW196755	Hs.98105	NYD-SP14 protein	1.00	2.41
	452788	AW294571	Hs.136040	ESTs	1.00	2.23

TABLE 32B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
431089	125941_2	BG940189 AW063489 AA715980 BF001091 BF880066 AA665102 AA621946 AA491826

5	421798	3042_4	BC017829 AW276546 A1984209 AA563933 AA634104 AA551528 AA634041 AA298038 BG483990 T89297 BF853958 H64685 T90329 T60644 T57747 BF852694 T92529 BG482852 BF883054 BF883056 N74880 AA829796 N90716
10	400269	2726_1	X65018 BC022318 NM_003019 BE465060 A1732255 BF446534 A1820677 A1002217 A1924488 B1821373 B1770406 B1823937 B1820265 B1489632 BG482911 AA617783 A1807697 AW205576 T94427 AA487101 T94513 B1819407 B1822450 B1820618 B1824619 BG542824 BG537862
15	432222	539529_1	BG207209 BE166299 A1204995 BG199355 AW969908 AA528756 AW440776 B1044354
20	432810	101919_1	BG292389 C06094 A1668930 AW104534 AA310513 AA830127 AW134897 AA046953 AW965490 A1810530 BF092924 AA334151 AA334725 D31302 R20723 AA263003 B1824635 A1276287 A1684428 A1524234 A1335035 AW014704 A1911443 AA972102 A1367512 A126670 AW016017 A1286003 A1147163 AA626033 A1539156 AA565542 A1094253 AW512612 BE889628 AA744752 BE646306 AW471324 AA999975 AA863400 H17550 A991439 R46187 BE929954 AA333976 D63102 BF744491
25	418259	133853_1	BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 A1688568 A1453594 AW590589 A1652425 A1827969 BF066946 A1802866 A1393380 A1476224 AW590639 AW136271 A458252 A1524726 AA843768 AA782158 A1336058 A1097532 AW451563 AA459408 AA459633 AA418444 W23607 BG940150 A1493445 AW054729 A1221929 A1868744 AA215405 AA766713 AA621546 BF928317 BE464132 A1909099 AW271459 A1262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689586 R69057 BF766886 BE769254 W05240
30	429228	215430_1	BG676155 BM009591 A1479075 A1025794 A1017967 AA448270 BE466812 AA853422 A1392649 BG952034 AA513384 BF840124 BE714620 AW969605 A1553633
35	459702	539529_1	BG207209 BE166299 A1204995 BG199355 AW969908 AA528756 AW440776 B1044354
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TABLE 32C:

65

Pkey:

Ref:

Strand:

NL_position:

Unique number corresponding to an Eos probeset

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

70

Pkey

Ref

Strand

NL_position

400880

9931121

Plus

29235-29336,36363-36580

402474

7547175

Minus

53526-53628,55755-55920,57530-57757

406387

9256180

Plus

116229-116371,117512-117651

404277

1834458

Minus

91655-91946

75

402674

8077108

Minus

39290-39502

404240

5002624

Minus

116132-116407,116653-116922

405102

8076881

Minus

120922-121296

406122

9144087

Minus

30940-31386

80

400750

8119067

Plus

198991-199168,199316-199548

404394

3135305

Minus

37121-37205,37491-37762,41053-41140,4132

403421

9665041

Minus

126609-126773,139986-140205

403903

7710671

Minus

101165-102597

404854

7143420

Plus

14260-14537

5	401854	7770538	Plus	151483-151637,151902-152008,152146-15231
	406422	9256411	Plus	163003-163311
	400496	9743564	Plus	41515-41695
	402333	8844110	Minus	165693-165856
	406517	7711431	Plus	7151-7402
	403420	9664969	Plus	159835-159938

10 TABLE 33A: About 800 genes upregulated in lung fibrosis relative to normal lung

15 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of lung fibrosis AIs divided by 90th percentile of normal lung AIs, where the minimum value for the numerator and denominator was set to 50

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
20	406964	M21305		FGENES predicted novel secreted protein	16.10
	431089	BE041395		ESTs, Weakly similar to unknown protein	12.38
	421110	AJ250717	Hs.1355	cathepsin E	11.86
25	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	11.62
	431958	X53629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.90
	444381	BE387335	Hs.283713	hypothetical protein BC014245	8.58
30	406850	AI624300	Hs.172928	collagen, type I, alpha 1	8.26
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	8.24
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	7.72
35	408380	AF123050	Hs.44532	diubiquitin	7.24
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	7.15
	456034	AW450979		gb:U1-H-B13-ata-a-12-0-U1.s1 NCL_CGAP_Su	7.12
40	453355	AW295374	Hs.31412	myopodin	6.95
	408562	AI436323	Hs.31141	roundabout (axon guidance receptor, Dros	6.88
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.83
45	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	6.72
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	6.72
	438089	W05391		nuclear receptor subfamily 1, group I, m	6.62
50	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.56
	421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	6.46
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	6.32
55	439195	H89360		gb:yy28d08.s1 Morton Fetal Cochlea Homo	6.29
	444301	AK000136	Hs.10760	asporin (LRR class 1)	6.28
	414061	NM_000699	Hs.335493	amylase, alpha 2A; pancreatic	6.13
60	423057	AW961597	Hs.130816	ESTs, Moderately similar to I38022 hypot	6.11
	430702	U56979	Hs.278568	H factor 1 (complement)	6.10
	424878	H57111	Hs.221132	ESTs	6.00
65	417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	6.00
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23155 fis, clone L	5.94
	408491	AI088063	Hs.7882	ESTs	5.94
70	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	5.92
	432222	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	5.92
	407857	AI928445	Hs.92254	synaptotagmin-like 2	5.90
75	433230	AW136134	Hs.220277	ESTs	5.86
	412719	AW016610	Hs.816	ESTs	5.86
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	5.82
80	426759	AI590401	Hs.21213	ESTs	5.72
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	5.72
	421814	L12350	Hs.108623	thrombospondin 2	5.71
85	430887	N66801	Hs.260287	KIAA1841 protein	5.70
	453870	AW385001	Hs.8042	Homo sapiens cDNA: FLJ23173 fis, clone L	5.62
	436954	AA740151	Hs.130425	ESTs	5.58
90	411573	AB029000	Hs.70823	KIAA1077 protein	5.55
	432441	AW292425	Hs.163484	intron of hepatocyte nuclear factor-3 al	5.38
	410506	AW418779	Hs.114889	ESTs	5.38
95	410800	BE280421	Hs.94499	ESTs	5.32
	413195	AA127382	Hs.22404	protease, serine, 12 (neutrypsin, moto	5.28
	406687	M31126		matrix metalloproteinase 11 (stromelysin	5.26
100	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	5.22
	412622	AW664708	Hs.171959	ESTs	5.22
	439941	AI392640	Hs.18272	amino acid transporter system A1	5.18
105	440675	AW005054	Hs.279788	ESTs, Weakly similar to KCC1_HUMAN CALCI	5.15
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	5.13
	425177	AF127577	Hs.155017	nuclear receptor interacting protein 1	5.12
110	444314	AI140497		gb:ow76b09.s1 Soares_fetal_liver_spleen_	5.11
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.04
	452239	AW379378		protein tyrosine phosphatase, receptor t	4.97
115	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	4.96
	443884	N20617	Hs.194397	leptin receptor	4.94
	444040	AF204231	Hs.182982	golgin-67	4.94
120	428281	AA194554	Hs.183434	ATPase, H transporting, lysosomal (vacuo	4.93
	440687	AL080222	Hs.7358	hypothetical protein FLJ13110	4.92
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	4.92
125	432435	BE218886	Hs.282070	ESTs	4.92

	422573	AW297985	Hs.295726	integrin, alpha V (vitronectin receptor	4.90
	430655	BE350122	Hs.157367	ESTs, Weakly similar to 178885 serine/th	4.90
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	4.90
5	415992	C05837	Hs.145807	hypothetical protein FLJ13593	4.82
	430027	AB023197	Hs.227743	KIAA0980 protein	4.78
	408393	AW015318	Hs.23165	ESTs	4.76
	445509	AA001615	Hs.84561	ESTs	4.72
	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	4.72
10	412828	AL133396	Hs.74521	prion protein (p27-30) (Creutzfeld-Jakob	4.72
	433226	AW503733	Hs.9414	KIAA1488 protein	4.68
	444745	AF117754	Hs.11861	thyroid hormone receptor-associated prot	4.68
	442994	AJ026718	Hs.16954	ESTs	4.66
	430580	AA806105	Hs.300697	immunoglobulin heavy constant gamma 3 (G	4.66
15	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	4.66
	418005	AJ186220	Hs.83164	collagen, type XV, alpha 1	4.65
	433586	T85301		gbyd78d06.s1 Soares fetal liver spleen	4.64
	424917	AJ636208	Hs.96901	hypothetical protein FLJ23049	4.64
	424408	AJ754813	Hs.146428	collagen, type V, alpha 1	4.64
20	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	4.62
	451109	F11875	Hs.5534	Homo sapiens cDNA FLJ12961 fis, clone NT	4.62
	450086	AW016343	Hs.233301	ESTs	4.61
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	4.60
	426552	AJ005163	Hs.201378	ESTs, Weakly similar to T12545 hypotheti	4.59
25	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.58
	418259	AA215404		ESTs	4.54
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.54
	432810	AA863400		ESTs	4.54
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.53
30	436100	AA704806	Hs.143842	ESTs, Weakly similar to 2004399A chromos	4.52
	412652	AJ801777		ESTs	4.52
	438899	AF085833	Hs.135624	ESTs	4.52
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	4.52
	436252	AJ539519	Hs.120969	Homo sapiens cDNA FLJ11562 fis, clone HE	4.52
35	443324	R44013	Hs.164225	ESTs	4.51
	407690	R47799	Hs.266957	hypothetical protein FLJ14281	4.51
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.51
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheti	4.50
	431843	AA516420		ESTs, Weakly similar to I38022 hypotheti	4.50
40	436865	AW880358	Hs.339808	hypothetical protein FLJ10120	4.46
	452561	AJ692181	Hs.49169	KIAA1634 protein	4.46
	440273	AJ805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	4.45
	442048	AA974603		gb:op34f05.s1 Soares_NFL_T_GBC_S1 Homo s	4.44
	436120	AJ248193	Hs.119860	ESTs	4.44
45	423575	C18863	Hs.163443	intron of perostin (OSF-2os)	4.44
	429697	AW286451	Hs.24605	ESTs	4.44
	439866	AA280717	Hs.6727	Ras-GTPase activating protein SH3 domain	4.43
	429688	BE245169	Hs.211610	CUG triplet repeat, RNA-binding protein	4.43
	414452	BE622743	Hs.301064	arlapin 1	4.42
50	428698	AA852773	Hs.334838	KIAA1866 protein	4.42
	420838	AW118210	Hs.42321	ESTs	4.41
	458584	AF217518	Hs.8360	PTD012 protein	4.40
	434340	AJ193043	Hs.128685	ESTs, Weakly similar to T17226 hypotheti	4.40
	400076			Eos Control	4.38
55	431049	AA846576	Hs.103267	hypothetical protein FLJ22548 similar to	4.38
	445773	H73456	Hs.13299	Homo sapiens mRNA; cDNA DKFZp761M0111 (I	4.36
	420298	AJ199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.36
	433339	AF019226	Hs.8036	glioblastoma overexpressed	4.36
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	4.34
60	416391	AJ878927	Hs.79284	mesoderm specific transcript (mouse) hom	4.34
	421221	AW276914	Hs.326714	Homo sapiens clone IMAGE:713177, mRNA se	4.33
	409342	AU077058	Hs.54089	BRCA1 associated RING domain 1	4.33
	429228	AJ553633		ESTs	4.32
	426458	D83032	Hs.169984	nuclear protein	4.30
65	408369	R38438	Hs.182575	SLC15A2 Solute carrier family 15 (H+/pep	4.30
	432476	T94344	Hs.326263	ESTs	4.29
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.28
	436446	AW016809	Hs.119021	ESTs	4.27
	439556	AJ623752	Hs.163603	ESTs	4.26
70	428179	AJ127772	Hs.279696	serum/glucocorticoid regulated kinase-li	4.26
	428411	AW291464	Hs.10338	ESTs	4.26
	434936	AJ285970	Hs.183817	ESTs	4.23
	413048	M93221	Hs.75182	mannose receptor, C type 1	4.23
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	4.22
75	413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	4.22
	409977	AW805510	Hs.97056	hypothetical protein FLJ21634	4.22
	441297	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	4.21
	421229	AJ056590	Hs.7086	hypothetical protein MGC12435	4.20
	456844	AJ264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	4.20
80	423578	AW960454	Hs.222830	ESTs	4.20
	446608	N75217	Hs.257845	ESTs	4.20
	424238	AA337401	Hs.137635	ESTs	4.19
	450747	AJ064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	4.18
	420674	NM_000055	Hs.1327	butyrylcholinesterase	4.18

	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	4.18
	439593	BE073597	Hs.124863	ESTs	4.17
	442369	AI565071		ESTs	4.16
5	445885	AI734009	Hs.127699	KIAA1603 protein	4.16
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	4.16
	452960	AK001335	Hs.31137	protein tyrosine phosphatase, receptor I	4.16
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	4.15
	407347	AA829847		gb:ad40d07.s1 NCI_CGAP_GCB1 Homo sapiens	4.14
10	409153	W03754	Hs.50813	hypothetical protein FLJ20022	4.13
	430168	AW968343	Hs.145582	DKFZP434I1735 protein	4.12
	451184	T87943		transcription factor 7-like 2 (T-cell sp	4.12
	426174	AA547959	Hs.115838	ESTs	4.12
	431562	AI884334	Hs.11637	ESTs	4.12
15	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.12
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.12
	449437	AI702038	Hs.100057	Homo sapiens cDNA: FLJ22902 fis, clone K	4.12
	425053	AF046024	Hs.154320	ubiquitin-activating enzyme E1C (homolog	4.10
	444020	R92962	Hs.35052	ESTs	4.10
20	439424	AI478667	Hs.118183	hypothetical protein FLJ22833	4.10
	416987	D86957	Hs.80712	KIAA0202 protein	4.10
	457121	AI743770	Hs.180513	ESTs, Weakly similar to KIAA0822 protein	4.09
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	4.09
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.08
25	431193	AW749505	Hs.296770	KIAA1719 protein	4.08
	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	4.08
	433308	AA582718	Hs.291650	ESTs	4.08
	445756	AA290690	Hs.300776	ESTs	4.08
	431745	AW972448	Hs.163425	ESTs	4.08
30	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	4.07
	440099	AL080058	Hs.6909	DKFZP564G202 protein	4.06
	439398	AA284267	Hs.221504	ESTs	4.06
	432731	R31178	Hs.287820	fibronectin 1	4.06
	415075	L27479	Hs.77889	Friedreich ataxia region gene X123	4.05
35	433626	AF078859	Hs.86347	hypothetical protein	4.05
	428055	AA420564	Hs.101760	ESTs	4.04
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	4.04
	413243	AA769266	Hs.193657	ESTs	4.02
	431214	AA294921	Hs.348024	v-rat simian leukemia viral oncogene hom	4.02
40	453753	BE252983	Hs.35086	ubiquitin specific protease 1	4.02
	414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	4.02
	434404	AW445034	Hs.256578	ESTs	4.02
	407604	AW191962		collagen, type VIII, alpha 2	4.02
	429412	NM_005235	Hs.2407	POU domain, class 2, associating factor	4.02
45	436772	AW975689		metallothionein 1E (functional)	4.00
	443257	AI334040	Hs.11614	HSPC065 protein	4.00
	450187	AA736788	Hs.78521	KIAA1717 protein	3.98
	433913	AI694106	Hs.72325	ESTs, Weakly similar to I38022 hypothe	3.98
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEF5_HUMAN TRANS	3.98
50	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	3.98
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	3.98
	426818	AA554827	Hs.292996	DKFZp434A0131 protein	3.98
	440118	AB040893	Hs.6968	KIAA1460 protein	3.98
	413836	W92003	Hs.70614	ESTs	3.97
55	442647	AL038436	Hs.31388	ESTs	3.96
	449188	AW072939	Hs.347187	myotubularin related protein 1	3.96
	450656	AA010539	Hs.18912	ESTs	3.96
	410817	AI262789	Hs.93659	protein disulfide isomerase related prot	3.94
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	3.94
60	408483	AA464836	Hs.291079	ESTs, Weakly similar to T27173 hypothe	3.94
	407879	AA045464	Hs.6557	zinc finger protein 161	3.93
	438146	Z36842	Hs.57548	ESTs	3.93
	433658	L03678	Hs.156110	immunoglobulin kappa constant	3.93
	429355	AW973253	Hs.292689	ESTs	3.92
65	437210	AA311443	Hs.293563	Homo sapiens mRNA; cDNA DKFZp586E2317 (f	3.92
	432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	3.92
	452416	AA026115	Hs.114777	ESTs	3.92
	413873	AI310151	Hs.173524	ESTs	3.91
	400196			Eos Control	3.91
70	437175	AW968078	Hs.87773	protein kinase, cAMP-dependent, catalyti	3.90
	453204	R10799	Hs.191990	ESTs	3.90
	454076	AW204712	Hs.61957	ESTs	3.90
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	3.90
	437158	AW090198		KIAA1150 protein	3.90
75	443970	AI280341	Hs.166571	ESTs	3.90
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	3.90
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.90
	444057	AA316896	Hs.257267	FYVE and coiled-coil domain containing 1	3.89
	411495	AP000693	Hs.70359	KIAA0136 protein	3.88
80	438452	AI220911	Hs.288959	hypothetical protein FLJ20920	3.88
	410297	AA148710		lumican	3.88
	427698	AW972594	Hs.335499	ESTs	3.88
	436769	AA748675		ESTs	3.86
	417819	AI253112	Hs.133540	ESTs	3.86

	445800	AA126419	Hs.32944	inositol polyphosphate-4-phosphatase, ty	3.86
	425838	NM_014071	Hs.159513	nuclear receptor coactivator RAP250; per	3.86
	422173	BE385828	Hs.250619	phorbol-like protein MDS019 (CEM15)	3.86
5	428147	AW629965	Hs.234983	ESTs, Weakly similar to 2109260A B cell	3.85
	445693	AW800444	Hs.76507	LPS-induced TNF-alpha factor	3.85
	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma	3.85
	412636	NM_004415		desmoplakin (DPI, DPII)	3.84
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	3.84
10	418876	AA740616		gb:ny97f11.1.s1 NCI_CGAP_GCB1 Homo sapiens	3.84
	436110	AA704899	Hs.291651	ESTs, Weakly similar to I38022 hypothe	3.84
	430317	AB020645	Hs.239189	glutaminase	3.84
	442806	AW294522	Hs.149991	ESTs	3.84
	414320	U13616	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	3.82
15	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSm8	3.82
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	3.82
	430573	AA744550	Hs.136345	ESTs	3.82
	453394	AW960474	Hs.40289	ESTs	3.81
	431266	AW149321	Hs.105411	ESTs	3.80
20	434987	AW975114		ESTs	3.80
	452685	AI634651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	3.79
	435176	AA744875	Hs.189413	ESTs	3.78
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	3.77
	430709	R34356		gb:yh85d01.s1 Soares placenta Nb2HP Homo	3.77
25	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.76
	441989	AA306207	Hs.286241	protein kinase, cAMP-dependent, regulato	3.76
	417228	AL134324	Hs.7312	ESTs	3.76
	418546	AA224827		gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens	3.76
	450779	AW204145	Hs.156044	ESTs	3.75
30	412408	D51103	Hs.73851	ATP synthase, H transporting, mitochondr	3.75
	443879	Z28462	Hs.9927	Homo sapiens mRNA; cDNA DKFZp564D156 (fr	3.75
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.75
	429494	AA769365	Hs.126058	ESTs	3.75
	447118	AB014599	Hs.330988	Homo sapiens, Similar to Bicucdial D (Dro	3.75
35	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	3.74
	419591	AF090900	Hs.91393	Homo sapiens cDNA: FLJ21887 fis, clone H	3.74
	448121	AL045714	Hs.128653	hypothetical protein DKFZp564F013	3.74
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.74
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	3.73
40	414883	AA926960		CDC28 protein kinase 1	3.72
	416178	AB08527	Hs.192822	serologically defined breast cancer anti	3.72
	452250	BE618654	Hs.28607	hypothetical protein A-211C6.1	3.72
	444099	D87432	Hs.10315	solute carrier family 7 (cationic amino	3.72
	438607	AW080237	Hs.252684	ESTs	3.72
45	408221	AA912183	Hs.47447	ESTs	3.72
	418599	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.70
	419900	AA69960	Hs.170698	ESTs	3.70
	445342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	3.70
	445100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	3.70
50	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	3.70
	413283	R78669	Hs.23756	hypothetical protein similar to swine ac	3.70
	447846	AA324057	Hs.77955	Homo sapiens cDNA: FLJ23527 fis, clone L	3.70
	436198	AK001125		Homo sapiens cDNA FLJ10263 fis, clone HE	3.70
	418300	AA433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	3.69
55	408495	W68796	Hs.237731	ESTs	3.69
	424452	N41367	Hs.173002	ESTs, Weakly similar to I38022 hypothe	3.68
	448479	H96115	Hs.21293	UDP-N-acetylglucosamine pyrophosphorylas	3.68
	431974	AW972689	Hs.200934	ESTs	3.68
	416354	NM_006633	Hs.79241	B-cell CLL/lymphoma 2 (BCL2)	3.68
60	417412	X16896	Hs.82112	interleukin 1 receptor, type I	3.68
	413645	AA130992		gb:zo15e02.s1 Stratagene colon (937204)	3.67
	416221	BE513171	Hs.79086	mitochondrial ribosomal protein L3	3.67
	419111	AA234172	Hs.137418	ESTs	3.67
	423979	AF229181	Hs.136644	CS box-containing WD protein	3.66
65	418875	W19971	Hs.233459	ESTs	3.66
	451690	AW451469	Hs.209990	ESTs	3.66
	423032	AI684746	Hs.119274	RAS p21 protein activator (GTPase activa	3.66
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	3.66
	428347	AI264161	Hs.183773	golgi autoantigen, golgin subfamily a, 4	3.66
70	426779	AA384577	Hs.93714	ESTs, Weakly similar to T00365 hypothe	3.66
	435335	AI693150	Hs.137928	ESTs	3.66
	410577	X91911	Hs.64639	glioma pathogenesis-related protein	3.66
	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	3.65
	429105	D87077	Hs.196275	KIAA0240 protein	3.64
75	407813	AL120247	Hs.40109	KIAA0872 protein	3.64
	425863	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	3.64
	451678	AA374181	Hs.26799	DKFZP564D0764 protein	3.64
	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	3.64
	452408	AA306477	Hs.29379	hypothetical protein FLJ10687	3.64
80	441466	AW573081	Hs.54828	ESTs	3.63
	414013	AA766605	Hs.47099	hypothetical protein FLJ21212	3.62
	420056	AW043684	Hs.99804	ESTs	3.62
	424886	H88584	Hs.96900	hypothetical protein; KIAA1830 protein	3.62
	431774	BE348813	Hs.268561	hypothetical protein FLJ10726	3.62

	435990	AI015862	Hs.131793	ESTs	3.62
	417821	BE245149	Hs.82643	protein tyrosine kinase 9	3.62
	414715	AA587891	Hs.904	amylase-1,6-glucosidase, 4-alpha-glucanot	3.62
5	444484	AK002126	Hs.11260	hypothetical protein FLJ111264	3.62
	417008	AA191708	Hs.325825	Homo sapiens cDNA FLJ20848 fis, clone AD	3.62
	413823	AL341417	Hs.29406	ESTs	3.61
	435354	AA678267	Hs.117115	ESTs	3.60
	427832	AF038362	Hs.180930	TBP-associated factor 172	3.60
10	427846	AW499770	Hs.180948	KIAA0729 protein	3.60
	426116	AA868729	Hs.144694	ESTs	3.60
	457635	AV660976	Hs.3569	hypothetical protein	3.60
	443998	AI620661	Hs.296276	ESTs	3.60
	417867	AW952547	Hs.194603	ESTs, Moderately similar to I38022 hypot	3.58
15	418182	AW016405	Hs.16648	ESTs	3.58
	434941	AW073202	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT	3.58
	424831	H61453		ESTs	3.58
	448410	AK000227	Hs.21126	hypothetical protein FLJ20220	3.58
	421823	N40850	Hs.28625	ESTs	3.58
20	414781	D50917	Hs.77293	KIAA0127 gene product	3.57
	427393	AB029018	Hs.177635	KIAA1095 protein	3.57
	415664	NM_004939	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	3.56
	425465	L18964	Hs.1904	protein kinase C, iota	3.56
	417124	BE122762	Hs.25338	ESTs	3.56
25	416602	NM_006159	Hs.79389	Protein kinase C-binding protein NELL2	3.56
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	3.55
	421097	AI280112	Hs.125232	Homo sapiens cDNA FLJ13266 fis, clone OV	3.55
	410390	AA876905	Hs.125286	ESTs	3.54
	442073	AW973443	Hs.8086	RNA (guanine-7-) methyltransferase	3.54
30	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	3.54
	441499	AW298235	Hs.101689	ESTs	3.54
	453256	AI565587	Hs.32556	KIAA0379 protein	3.54
	414142	AW368397	Hs.334485	hemiscentin (fibulin 6)	3.54
	438023	AF204883	Hs.6048	FEM-1 (C.elegans) homolog b	3.54
35	412245	AI952669	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	3.54
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	3.53
	446682	AW205632	Hs.211198	ESTs	3.52
	431392	AI371223	Hs.288671	Homo sapiens cDNA FLJ11997 fis, clone HE	3.52
	433430	AI653735		ESTs	3.52
40	420394	AB023161	Hs.97403	KIAA0944 protein	3.52
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.52
	443547	AW271273		hypothetical protein FLJ12665	3.52
	420676	AI434780	Hs.4248	vav 2 oncogene	3.51
	410690	AA322979	Hs.130266	ESTs	3.50
45	459645	AA074346		ESTs	3.50
	401403			Target Exon	3.50
	451166	T98171	Hs.185675	ESTs	3.50
	418836	AI655499	Hs.161712	ESTs	3.50
	421462	AF016495	Hs.104624	aquaporin 9	3.50
50	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	3.50
	432401	NM_013330	Hs.274479	NME7	3.49
	408392	U28831	Hs.44566	KIAA1641 protein	3.49
	425836	AW955695	Hs.90960	ESTs	3.48
	452327	AK000196	Hs.29062	hypothetical protein FLJ20189	3.48
55	418721	NM_002731	Hs.87773	protein kinase, cAMP-dependent, catalyti	3.48
	433627	AF078866	Hs.284296	Homo sapiens cDNA: FLJ22993 fis, clone K	3.48
	422860	AW890487		cadherin 13, H-cadherin (heart)	3.48
	430570	AI417881	Hs.292464	ESTs	3.48
	406387			Target Exon	3.47
60	416585	X54162	Hs.79386	kelomodulin 1, smooth muscle (LMOD1) (Thy	3.46
	432340	AA534222		gbln]21d02.s1 NCI_CGAP_AA1 Homo sapiens	3.46
	412240	H72176		hypothetical protein FLJ13159	3.46
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	3.46
	443634	H73972	Hs.134460	ESTs	3.46
65	422963	M79141	Hs.13234	ESTs	3.46
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	3.46
	433437	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr	3.46
	425100	AF051850	Hs.154567	supervillin	3.45
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.45
70	444250	R40815	Hs.12396	ESTs, Weakly similar to 2004399A chromos	3.44
	428386	R17298	Hs.295923	seven in absentia (Drosophila) homolog 1	3.44
	447764	NM_003776	Hs.19500	nuclear localization signal deleted in v	3.44
	411251	R19774	Hs.22835	HHGP protein	3.44
	432648	AA557952		gbln]17c05.s1 NCI_CGAP_HSC1 Homo sapiens	3.44
75	428708	NM_014897	Hs.190386	KIAA0924 protein	3.44
	437233	D81448	Hs.339352	Homo sapiens brother of CDO (BOC) mRNA,	3.43
	451743	AW074266	Hs.23071	ESTs	3.42
	453258	AW293134	Hs.32597	ring finger protein (C3H2C3 type) 6	3.42
	448705	H05072	Hs.124984	ESTs, Moderately similar to ALU7_HUMAN A	3.42
80	414489	AI620577	Hs.73105	ESTs	3.42
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	3.41
	435841	R28522	Hs.186937	ESTs	3.41
	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	3.40
	451198	AW964541		hypothetical protein FLJ21127	3.40

	429952	AF080158	Hs.226573	inhibitor of kappa light polypeptide gen	3.40
	436023	T81819	Hs.302251	ESTs	3.40
	449656	AA002008	Hs.188633	ESTs	3.40
5	437739	AW579216	Hs.264610	ESTs, Moderately similar to lbd1 [H.sapi	3.40
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	3.40
	448474	AJ792014	Hs.13809	hypothetical protein FLJ10648	3.40
	456505	AA504595		ESTs	3.40
	439867	AA847510	Hs.161292	ESTs	3.40
10	442113	BE622187		ESTs, Weakly similar to I38022 hypotheti	3.40
	425922	AL157466	Hs.162751	Homo sapiens mRNA; cDNA DKFZp761E2423 (I	3.40
	435299	AJ745458	Hs.343026	ESTs, Weakly similar to T20593 hypotheti	3.40
	421263	AB020638	Hs.103000	KIAA0831 protein	3.40
	410300	AW903988	Hs.62119	hypothetical protein FLJ14800	3.39
	440028	AW473675		ESTs, Weakly similar to T17227 hypotheti	3.39
15	454070	N79110	Hs.21276	collagen, type IV, alpha 3 (Goodpasture	3.38
	432572	AI660840	Hs.191202	ESTs, Weakly similar to ALUE_HUMAN !!!!	3.38
	442426	AJ373062	Hs.332938	hypothetical protein MGC5370	3.38
	428412	AA428240	Hs.126083	ESTs	3.38
20	448772	AW390822	Hs.301528	L-tryptophan/alpha-aminoadipate aminotra	3.38
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.38
	413714	AI560944	Hs.71428	ESTs	3.38
	415663	AW296841	Hs.313332	ESTs	3.38
	407904	W44735	Hs.9286	Homo sapiens cDNA: FLJ21278 fis, clone C	3.37
25	421114	AW975051	Hs.293156	ESTs, Weakly similar to I78885 serine/th	3.37
	440214	AA247118	Hs.7049	hypothetical protein FLJ11305	3.37
	440980	AL042005	Hs.11117	tripeptidyl peptidase II	3.36
	411975	AI916058	Hs.144583	ESTs	3.36
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	3.36
30	414783	AW069569		inactive progesterone receptor, 23 kD	3.36
	436043	AW963838	Hs.168830	Homo sapiens cDNA FLJ12136 fis, clone MA	3.36
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.36
	411213	AA676939	Hs.69285	neuropilin 1	3.36
	420613	AJ873871	Hs.7041	ESTs, Weakly similar to A47582 B-cell gr	3.35
35	417534	NM_004998	Hs.82251	myosin IE	3.35
	431698	AI492369		ESTs	3.35
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.35
	441623	AA315805		desmoglein 2	3.34
	420729	AW964897	Hs.290825	ESTs	3.34
40	440010	AA534930	Hs.127236	hypothetical protein FLJ12879	3.34
	448369	AW268962	Hs.111335	ESTs	3.34
	452820	N46161	Hs.35274	ESTs	3.34
	453271	AA903424	Hs.6786	ESTs	3.34
	428839	AJ767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	3.34
45	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	3.34
	443291	AA325633	Hs.136102	KIAA0853 protein	3.33
	418720	AJ381687	Hs.39526	ESTs	3.33
	452107	AB020681	Hs.27973	KIAA0874 protein	3.33
	439943	AW083789	Hs.124620	ESTs	3.33
50	433282	BE539101		hypothetical protein	3.33
	410344	AW978436	Hs.62515	KIAA0494 gene product	3.33
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	3.32
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.32
	434210	AA665612		ESTs	3.32
55	431923	AJ741770	Hs.292690	ESTs, Weakly similar to I38022 hypotheti	3.32
	453199	AI336266	Hs.32353	mitogen-activated protein kinase kinase	3.32
	419534	AA443691	Hs.90858	Homo sapiens clone 25023 mRNA sequence	3.32
	448939	BE267795	Hs.22595	hypothetical protein FLJ10637	3.32
	433312	AJ241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	3.32
60	422092	AB007883	Hs.111373	KIAA0423 protein	3.32
	412262	W26406		seven in absentia (Drosophila) homolog 1	3.32
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.32
	446094	AK001760	Hs.13801	KIAA1685 protein	3.32
	446493	AK001389	Hs.15144	hypothetical protein DKFZp564O043	3.32
65	420339	AW968259	Hs.186647	ESTs	3.31
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	3.31
	432331	W37862	Hs.274368	MSTP032 protein	3.31
	433697	AA600357	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.31
	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	3.31
70	430950	AA489525		ESTs	3.30
	409758	AW474960	Hs.182258	ESTs, Weakly similar to I78885 serine/th	3.30
	417958	AA767382	Hs.193417	ESTs	3.30
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	3.30
	419543	AA244170		gbnc05h02.s1 NCL_CGAP_P1 Homo sapiens	3.30
75	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.30
	452039	AI922988	Hs.172510	ESTs	3.30
	443798	R07848	Hs.188522	ESTs	3.29
	449378	AW664026	Hs.59892	ESTs	3.29
	455657	BE065029		gb:RC1-BT0314-310300-015-b12 BT0314 Homo	3.28
80	420126	NM_016255	Hs.95260	Autosomal Highly Conserved Protein	3.28
	444291	AI588022	Hs.193989	TAR DNA binding protein	3.28
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	3.28
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (I	3.28
	443774	AL117428	Hs.9740	DKFZP434A236 protein	3.28

	425657	T89839	Hs.119471	ESTs	3.28
	405672	M26041	Hs.198253	major histocompatibility complex, class	3.28
	419905	AW248229	Hs.93659	protein disulfide isomerase related prot	3.27
5	425332	AA633306	Hs.127279	ESTs	3.27
	418529	AW005695	Hs.250897	TRK-fused gene	3.27
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.27
	433618	AA602539	Hs.345494	ESTs	3.27
	408630	AA748009	Hs.173328	ESTs	3.26
10	415914	AA306033	Hs.78915	GA-binding protein transcription factor,	3.26
	415102	M31899	Hs.77929	excision repair cross-complementing rode	3.26
	432626	AA471098	Hs.278544	acetyl-Coenzyme A acetyltransferase 2 (a	3.26
	429493	AL134708	Hs.145998	ESTs	3.26
	445860	AA332145	Hs.13392	lethuring factor SEC34	3.26
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	3.26
15	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020.1 E2IG5	3.26
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	3.26
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	3.26
	436758	AW977167	Hs.155272	ESTs	3.26
20	438011	BE466173	Hs.145696	splicing factor (CC1.3)	3.26
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	3.25
	426860	U04953	Hs.172801	isoleucine-tRNA synthetase	3.25
	437830	AB020658	Hs.5867	KIAA0851 protein; suppressor of actin 1	3.25
	453368	W20296	Hs.288178	Homo sapiens cDNA FLJ11968 fis, clone HE	3.25
25	409939	AA463437	Hs.11556	Homo sapiens cDNA FLJ12558 fis, clone NT	3.25
	413715	AW851121	Hs.75497	Homo sapiens cDNA: FLJ22139 fis, clone H	3.24
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	3.24
	418283	S79895	Hs.83942	cathepsin K (pseudosostosis)	3.24
	414405	AI362533		KIAA0306 protein	3.24
30	445893	AI610702	Hs.202613	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.24
	434423	NM_006769	Hs.3844	LIM domain only 4	3.24
	408951	AW407227	Hs.227591	hypothetical protein FLJ11088	3.24
	408949	AF189011	Hs.49163	putative ribonuclease III	3.24
	410337	M83822	Hs.62354	cell division cycle 4-like	3.24
35	409010	AI648675		Homo sapiens, Similar to RIKEN cDNA 1700	3.24
	400419	AF084545		Target	3.24
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	3.24
	422461	NM_003417	Hs.117077	zinc finger protein 264	3.24
	441604	AI683049	Hs.201282	ESTs	3.24
40	411960	R77776	Hs.18103	ESTs	3.24
	414895	AW894856	Hs.116278	Homo sapiens cDNA FLJ13571 fis, clone PL	3.23
	430522	N75750	Hs.242271	KIAA0471 gene product	3.23
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	3.23
	405268			ENSP00000223174-KIAA0783 PROTEIN.	3.23
45	429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.22
	427196	AW967522	Hs.191593	ESTs	3.22
	439776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	3.22
	417727	AL133623	Hs.82501	similar to mouse Xmi1 / Dhml2 protein	3.22
	410853	H04588	Hs.30469	ESTs	3.22
50	411862	AA099050		gb:z85d12.r1 Soares_pregnant_uterus_NbH	3.22
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.22
	440452	AI925136	Hs.55150	ESTs, Weakly similar to CAYP_HUMAN CALCY	3.22
	427480	BE148769	Hs.334477	hypothetical protein FLJ11328	3.22
	444623	AI183829	Hs.202111	ESTs	3.21
55	424006	AF054815	Hs.137548	CD84 antigen (leukocyte antigen)	3.21
	435874	AA868688	Hs.93102	ESTs	3.20
	443801	AW206942	Hs.253594	intron of trichorhinophakangeal syndro	3.20
	434982	AW975084		gb:EST387190 MAGE resequences, MAGN Homo	3.20
	430929	AA489166	Hs.156933	ESTs	3.20
60	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced transl	3.20
	430378	Z29572	Hs.2556	tumor necrosis factor receptor superfam	3.20
	422109	S73265	Hs.1473	gastrin-releasing peptide	3.20
	451119	AA805417	Hs.64753	ESTs	3.20
	414893	AA215295	Hs.77578	ubiquitin specific protease 9, X chromos	3.20
65	432678	AI187366		gb:ql29c01.x1 Soares_testis_NHT Homo sap	3.19
	428820	AA436187	Hs.172631	integrin, alpha M (complement component)	3.19
	422040	AA172106	Hs.110950	Rag C protein	3.18
	437838	AI307229		ESTs	3.18
	408761	AA057264	Hs.238936	ESTs, Weakly similar to (define not ava	3.18
70	420789	AI670057	Hs.199882	ESTs	3.18
	419135	R61448	Hs.106728	ESTs, Weakly similar to KIAA1353 protein	3.18
	446019	AI362520		histone deacetylase 3	3.18
	430848	AW021726	Hs.345490	gb:dl27e02.y1 Morton Fetal Cochlea Homo	3.18
	425375	AA631977	Hs.155995	KIAA0643 protein	3.18
75	424075	AI807320	Hs.227630	RE1-silencing transcription factor	3.18
	413802	AW964490	Hs.32241	ESTs, Weakly similar to S65657 alpha-1C-	3.18
	453111	AB014598	Hs.31720	hephaestin	3.18
	454042	H22570		hypothetical protein FLJ20093	3.18
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	3.18
80	447183	AI554733	Hs.173182	ESTs	3.18
	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	3.18
	431831	AW023204	Hs.302743	ESTs	3.18
	420664	AI681270	Hs.99824	BCE-1 protein	3.18
	451582	AI963026	Hs.289958	ESTs, Weakly similar to putative p150 [H	3.17

	432954	AI076345		ESTs	3.17
	444990	AI912410	Hs.27475	Homo sapiens cDNA FLJ12749 fis, clone NT	3.17
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	3.17
5	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.17
	441889	AI090455	Hs.268371	hypothetical protein FLJ20274	3.17
	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	3.16
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.16
	420623	BE245485	Hs.99437	Homo sapiens mRNA; cDNA DKFZp586G1924 (f	3.16
10	451475	T19093	Hs.25450	KIAA0725 protein	3.16
	452066	AA772149	Hs.16979	ESTs, Weakly similar to A43932 mucin 2 p	3.16
	429556	AW139399	Hs.98988	ESTs	3.16
	448514	AB020626	Hs.301866	KIAA0819 protein	3.16
	443732	AI188803	Hs.153944	ESTs	3.16
15	436805	AA731533	Hs.270751	ESTs	3.16
	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	3.16
	417511	AL049176	Hs.82223	chordin-like	3.16
	423595	R82826	Hs.220702	ESTs	3.16
	445837	AI261700	Hs.145544	ESTs	3.16
20	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUS protein d	3.16
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.16
	414183	AW957446	Hs.301711	ESTs	3.16
	433194	AB040883	Hs.83243	KIAA1450 protein	3.16
	453915	AA588721	Hs.286218	ribosomal protein L44	3.15
25	407725	BE388094	Hs.21857	ESTs	3.15
	437412	BE069288	Hs.34744	Homo sapiens mRNA; cDNA DKFZp547C136 (fr	3.14
	440937	AF202724	Hs.7531	KIAA0810 protein	3.14
	449057	AB037784	Hs.22941	KIAA1363 protein	3.14
30	446126	AW085909		pleckstrin homology domain interacting p	3.14
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.14
	419145	N99638		gb:za39g11.1 Soares fetal liver spleen	3.14
	418757	AI864193	Hs.169728	hypothetical protein FLJ13150	3.14
	430000	AW205931	Hs.99598	hypothetical protein MGC5338	3.14
	437296	AA350994	Hs.20281	KIAA1700	3.14
35	441381	H22195	Hs.31874	ESTs	3.14
	457250	AA811987	Hs.125779	ESTs	3.14
	422900	AA641201	Hs.222051	ESTs	3.14
	442787	W93048	Hs.250723	hypothetical protein MGC2747	3.14
40	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.14
	419355	AA428520	Hs.90061	progesterone binding protein	3.14
	409509	AL036923	Hs.322710	ESTs	3.14
	417308	H60720	Hs.81892	KIAA0101 gene product	3.14
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	3.14
	429160	AW663083	Hs.144469	ESTs	3.14
45	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	3.14
	451107	AA235108	Hs.17639	Homo sapiens ubiquitin protein ligase (U	3.14
	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	3.14
	451518	AW340925	Hs.174918	ESTs	3.14
	435702	AI033647	Hs.121001	Homo sapiens, clone IMAGE:3460280, mRNA	3.13
50	439208	AK000299	Hs.180952	dynactin 4 (p62)	3.13
	451838	AW005866	Hs.193969	ESTs	3.13
	426369	AF134157	Hs.169487	Kreister (mouse) maf-related leucine zip	3.13
	446945	AI193115	Hs.16611	tumor protein D52-like 1	3.13
	453920	AI133148	Hs.35602	I factor (complement)	3.13
55	411529	AA403348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.13
	417105	X60992	Hs.81226	CD6 antigen	3.12
	433854	AA610649	Hs.333239	ESTs	3.12
	408089	H59799	Hs.42644	thioredoxin-like	3.12
	453686	AL110326	Hs.304679	ESTs, Moderately similar to Z195_HUMAN Z	3.12
60	426167	AF039023	Hs.167496	RAN binding protein 6	3.12
	452195	AA994712	Hs.116878	ESTs	3.12
	416580	T61572	Hs.79385	Human clone Z3574 mRNA sequence	3.12
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.12
	424001	W67883	Hs.137476	paternally expressed 10	3.12
65	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.12
	433401	AF039698	Hs.284217	serologically defined colon cancer antig	3.12
	409245	AA361037		(RNA isopentenylpyrophosphate transferas	3.12
	414290	AI568801	Hs.71721	ESTs	3.12
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	3.12
70	429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	3.11
	448873	NM_003677	Hs.22393	density-regulated protein	3.11
	428471	X57348	Hs.184510	stratfin	3.11
	436288	AI361722	Hs.192410	ESTs	3.10
	433376	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	3.10
75	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	3.10
	453468	W00712	Hs.32990	DKFZP566F084 protein	3.10
	412340	AA101809	Hs.182685	ESTs	3.10
	438716	AA814903	Hs.155113	ESTs	3.10
	419440	AB020689	Hs.90419	KIAA0882 protein	3.10
80	433017	Y15067	Hs.279914	zinc finger protein 232	3.10
	428513	BE220806	Hs.184697	plexin C1	3.10
	437866	AA155781		metallothionein 1E (functional)	3.10
	451027	AW519204	Hs.40808	Homo sapiens, Similar to RIKEN cDNA 2810	3.10
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	3.10

	435445	AA737345	Hs.294041	ESTs	3.10
	420997	AK001214	Hs.100914	hypothetical protein FLJ10352	3.09
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	3.09
5	406122			Target Exon	3.09
	435272	AA906415	Hs.110041	ESTs	3.09
	410726	AI623859	Hs.15935	ESTs	3.09
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.08
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.08
10	417538	AW050865	Hs.275711	hypothetical protein MGC2452	3.08
	434938	AW500718	Hs.8115	Homo sapiens, clone MGC:16169, mRNA, com	3.08
	434733	AI334367	Hs.159337	ESTs	3.08
	434421	AI915927	Hs.34771	ESTs	3.08
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.08
15	424839	AK000059	Hs.153881	Homo sapiens NY-REN-62 antigen mRNA, par	3.08
	456332	AI000341		ESTs	3.08
	445034	AW293376	Hs.143659	ESTs	3.08
	446570	AV659177	Hs.127160	ESTs	3.08
	429920	AW473208	Hs.115572	ESTs, Weakly similar to I38022 hypotheti	3.08
20	459513	AI032946		gb:ox08g09.s1 Soares_fetal_liver_spleen_	3.06
	419038	AW134924	Hs.190325	ESTs	3.06
	451079	AI827988	Hs.240728	ESTs, Moderately similar to PC4259 ferri	3.06
	417386	AL037228	Hs.82043	D123 gene product	3.06
	453108	AI311457	Hs.99472	ESTs	3.06
25	449328	AI962493		ESTs	3.06
	428656	AB037798	Hs.188790	KIAA1377 protein	3.06
	425509	AF079363	Hs.158213	sperm associated antigen 6	3.06
	447957	NM_014821	Hs.20126	KIAA0317 gene product	3.06
	417226	AW505054	Hs.4283	ESTs	3.05
30	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	3.05
	426279	AI648520	Hs.169084	tubby like protein 3	3.05
	433814	AA609738	Hs.16525	ESTs	3.05
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	3.05
	431341	AA307211	Hs.251531	proteasome (prosome, macropain) subunit,	3.04
35	441789	D52059	Hs.7972	KIAA0871 protein	3.04
	456437	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.04
	438771	NM_016289	Hs.6406	MO25 protein	3.04
	448497	BE613269	Hs.21893	hypothetical protein DKFZp761N0624	3.04
	416240	NM_001981	Hs.79095	epidermal growth factor receptor pathway	3.04
40	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	3.04
	424776	AI857931	Hs.164595	ESTs	3.03
	408409	AW838181	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.03
	429693	BE254962	Hs.211612	SEC24 (S. cerevisiae) related gene famil	3.03
	425960	AW410646	Hs.164649	hypothetical protein DKFZp434H247	3.03
45	431625	AW750627	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	3.03
	451144	AW956103	Hs.61712	pyruvate dehydrogenase kinase, isoenzyme	3.02
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.02
	408683	R58665	Hs.46847	TRAF and TNF receptor-associated protein	3.02
	427735	AA916785	Hs.180610	splicing factor proline/glutamine rich (3.02
50	440603	AL121733	Hs.7299	Novel human gene mapping to chromosome 1	3.02
	415443	T07353	Hs.7948	ESTs	3.02
	439981	AI348408	Hs.124675	ESTs, Weakly similar to T14742 hypotheti	3.02
	406685	M18728		gb:Human nonspecific crossreacting antig	3.02
55	446013	AI360167	Hs.152774	ESTs	3.02
	433902	AW292820	Hs.144906	ESTs	3.02
	412610	X90908	Hs.74126	fatty acid binding protein 6, foal (gas	3.02
	432505	AW274526	Hs.277721	KIAA0049	3.01
	440040	BE219431	Hs.302031	zinc finger protein, subfamily 1A, 4 (Eo	3.01
	433255	AI274270	Hs.96840	KIAA1527 protein	3.01
60	419726	U50330	Hs.1274	bone morphogenetic protein 1	3.01
	417258	N58885		gb:yy60a09.s1 Soares_multiple_sclerosis_	3.00
	435800	AI248285	Hs.118348	ESTs	3.00
	444838	AV651680	Hs.208558	ESTs	3.00
	456760	AW961251	Hs.127828	guanine nucleotide binding protein (G pr	3.00
65	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	3.00
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.00
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	3.00
	410434	AF051152	Hs.63668	toll-like receptor 2	3.00
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.00
70	425955	T96509	Hs.248549	ESTs, Moderately similar to S65657 alpha	2.98
	450247	AF123303	Hs.24713	hypothetical protein	2.98
	417865	AW086059	Hs.6529	ESTs, Weakly similar to I78885 serine/th	2.98
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.98
	438543	AA810141	Hs.192182	ESTs	2.98
75	415503	U36601	Hs.78473	N-deacetylase/N-sulfotransferase (hepara	2.98
	429138	AB020657	Hs.197298	NS1-binding protein	2.98
	447881	BE620886		GCN1 (general control of amino-acid synt	2.96
	425481	AW978162		ESTs	2.96
	453315	BE544203	Hs.24831	ESTs	2.96
80	440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	2.95
	433208	AW002834	Hs.24095	ESTs	2.95
	442495	AI184717		ESTs	2.94
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	2.94
	408170	AW204516	Hs.31835	ESTs	2.94

5	430382	AA477908	Hs.282267	ESTs, Moderately similar to I38022 hypot	2.94
	449765	N92293	Hs.206832	ESTs, Moderately similar to ALU8_HUMAN A	2.94
	407361	AA744622	Hs.292645	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.94
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.93
	436005	BE551650	Hs.158126	Homo sapiens cDNA FLJ13350 fis, clone OV	2.93
	449458	AI805078	Hs.208261	ESTs	2.93
	449317	AW283413	Hs.132906	19A24 protein	2.92
	411118	N27944	Hs.221476	ESTs, Weakly similar to AF108460 1 ubinu	2.92
10	449494	AW237014	Hs.315369	Homo sapiens cDNA: FLJ23075 fis, clone L	2.91
	416311	D80529		gb:HUM081H05B Human fetal brain (TFujiwa	2.91
	433068	NM_006456	Hs.288215	sialyltransferase	2.90
	429272	W25140	Hs.110667	ESTs	2.90
	432519	AI221311	Hs.130704	ESTs, Weakly similar to BCHUIA S-100 pro	2.90
15	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.88
	426782	R14614	Hs.33846	ESTs	2.88
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	2.88
	413882	AA132973	Hs.184492	ESTs	2.88
	421554	AW137676	Hs.97775	ESTs	2.88
20	446488	AB037782	Hs.15119	KIAA1361 protein	2.84
	421391	AW304350	Hs.191958	immunoglobulin superfamily receptor tran	2.84
	424527	AW138558	Hs.334873	ESTs, Weakly similar to I54374 gene NF2	2.82
	419284	AW820869	Hs.215658	ESTs, Moderately similar to ZN91_HUMAN Z	2.82
	415788	AW628686	Hs.78851	KIAA0217 protein	2.82
25	448481	W15284	Hs.74832	ESTs	2.82
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.80
	443441	AW291196	Hs.92195	ESTs	2.80
	422725	AA315703	Hs.199993	ESTs, Weakly similar to ALUB_HUMAN !!!	2.80
	431926	AW972724		gb:EST384816 MAGE resequences, MAGL Homo	2.80
30	420406	AA741024	Hs.88378	ESTs	2.79
	437678	AA829860	Hs.122834	ESTs	2.78
	440115	R41808	Hs.144924	ESTs, Weakly similar to B Chain B, Solut	2.78
	439883	AL359652	Hs.171096	Homo sapiens EST from clone DKFZp434A041	2.78
	446428	AW082270	Hs.12496	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.77
35	451273	NM_014811	Hs.26163	KIAA0649 gene product	2.76
	435154	AA668764		ESTs	2.76
	432451	AW972771	Hs.292471	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.75
	442703	AL044949	Hs.116298	ESTs	2.74
	419341	N71463	Hs.118888	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.74
40	435861	AF254956	Hs.16608	candidate tumor suppressor protein	2.72
	420137	AA305478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	2.70
	438441	AW664960	Hs.205319	ESTs	2.70
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.67
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-ii	2.66
45	416239	AL038450	Hs.48948	ESTs	2.62
	434792	AA649253	Hs.132458	ESTs	2.60
	424852	AI222779	Hs.144848	ESTs	2.58
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	2.57
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	2.56
50	450571	AF158240	Hs.60397	ESTs	2.56
	442435	AI986208	Hs.244760	ESTs, Highly similar to B34087 hypotheti	2.56
	424148	BE242274	Hs.1741	integrin, beta 7	2.56
	445784	AI253155	Hs.146065	ESTs	2.53
	408072	BE005566	Hs.16773	Homo sapiens clone TCCCA00427 mRNA sequ	2.52
55	434779	AF153815	Hs.50151	potassium inwardly-rectifying channel, s	2.52
	450295	AI766732	Hs.210628	ESTs	2.48
	440381	AA917808	Hs.190495	ESTs	2.46
	433923	AI823453	Hs.146625	ESTs	2.44
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	2.44
60	429670	L01087	Hs.211593	protein kinase C, theta	2.44
	437908	AI082424		ESTs	2.43
	438676	AA813745	Hs.123446	ESTs	2.37
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	2.28
	444969	AI203334	Hs.160628	ESTs	2.28
65	446423	AW139655	Hs.150120	ESTs	2.27
	435517	AA928626	Hs.130177	ESTs	2.27
	425354	U62027	Hs.155935	complement component 3a receptor 1	2.26
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	2.00
	428073	AA446167	Hs.47385	ESTs	1.98
70	433834	AA620742	Hs.130786	ESTs	1.72
	417365	D50683	Hs.82028	transforming growth factor, beta recepto	1.52
	414521	D28124	Hs.76307	neuroblastoma, suppression of tumorigen	1.30
	402550			Target Exon	1.09

TABLE 33B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

80	Pkey	CAT Number	Accession
	431089	125941_2	BG940189 AW063489 AA715960 BF001091 BF880066 AA666102 AA621946 AA491826
	456034	685586_1	AA136653 AA136656 AW450979 AA584358 AA809054 AW238038 AA492073 BE168945
	407192	2200202_1	AA602964 AA609200

436089	22448_4	BM475665 BE644917 AW770789 AW952971 N64663 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AAB09472 AV564440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899564 H91240 R60548 N41701
5	439195 432222 405687 444314 452239	21979_1 539529_1 0_0 1027984_1 10116_4
10	433586 418259	32908_1 133853_1
15	432810	101919_1
20	412652	18858_2
25	431843	445334_1
30	442048 429228 442369 459702 407347 451184	750422_1 215430_1 2691713_1 539529_1 810943_1 1531_4
35	444610 407604	2145292_1 43771_1
40	436772 437158	1239464_1 59575_1
45	410297	2990_1
50	436769 412636	1239572_1 1438_1
55		
60		
65		
70		
75		
80		

5	118876	121279_1	434987	121985_1	437079	1234627_1	148546	242836_1	414883	8371_2
10	436198	28727_1	413645	1234345_1	424831	1227834_1	433430	2181751_1	434547	137089_2
20	459645	722255_1	422960	11862_2	432340	1619980_1	412240	8235_1		
30	432648	129028_1	451198	18351_1						
40	456505	15472_2	442113	43919_1						
50	440028	598730_1	414783	262554_1	431698	6468_7				
55	441623	3362_1								
60	433282	759_1								
65										
70	434210	54521_1								
75	412262	4362_1								
80	430950	594908_1								

419543	251903_1	AJ018087 AA244170 AA244355
455657	1490185_1	BE065209 BE065364 BE065110 BE065111
414405	112689_1	AL047596 AA393792 AJ670731 AJ037957 AW874364 AJ038137 N62286 AJ241379 BE501096 AW090666 A927369 A1669226 A1369437 AJ371075
5		AW612409 AJ685711 AJ183289 AA477717 AJ076122 AA635190 AA700984 AA781508 D81020 BF575223 AJ356183 D79312 AJ375558 H61111
		BG283489 BE090666 BE090664 BE090662 H26545
409010	10331_1	AL575207 AL551714 BMD14781 BG542863 BG771232 AA429722 AJ377511 AJ770155 AA716665 BG003427 AA810811 AA442760 AA128610
		AA059411 AJ796263 AJ494075 AJ572127 AA420992 BF436083 AJ648575 AA878813 BJ488614 BG700886 AA128609 AV702879 AA731146
10		AJ580336 AJ373224 AA919169 AJ758175 AA976350 BG701414 BF057794 AW135598 AA062583 BJ549631 AJ185077 AA933879 AW024454
		AA193289 AA045194 BG928396 BE856883 BF435859 AA196423 AW237471 R99289 D61992 BE856637 BF368270 AA194235 N51319 AA383499
		N53065 BG548812 BF027898 BG779448
411962	2307710_1	AA099050 AA099526 T47733
434982	121871_1	AW975084 T90204 AA658177
432876	3503_22	AJ187366 AA618478 AA558869
437838	2512601_1	AJ308202 AJ307229 AA769348
15	446019	658727_1
		AJ362520 D25917 AJ670784 AJ742347 AW269789 AJ270700 AW610541 AW793036 AW793035 AW610540 AW362220 AW362166 AW362214
		AW362225 AW362228 AL119827
454042	30254_1	AJ420458 AJ018523 AA708686 BF949633 AL119553 BF945960 AJ081305 AA041432 AJ921013 AJ684910 AJ654847 AW874199 AJ206120
		AW241428 R43035 T66767 AW103715 W28478 BF953052 H45926 BF807568 AW903943 BE170143 BJ040435 BF931989 BJ600000 AV722350
20		W27787 H45331 BJ549761 R53955 BJ549855 BG991583 BJ491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199
		AJ431587 BE858679 AW292267 AJ421678 AA041195 BE466753 AJ243913 AJ358894 AW137298 AJ366468 N64350 AA779107 AW025969 R49056
		AA347011 R55722 AW771106 F04969 Z38381 F01659 H17396 BJ93714 AJ880103 AW771447 AJ202561 AA788851 AJ494436 BF856114 H22570
432954	2159612_1	AJ076345 AJ887648 AA572691
446126	610_2	BF946219 BF946218 BF851494 AL536879 AA457150 AJ590194 AJ582629 AA464515 AA916242 AA337109 AA336509 NA6906 AA336322
25		AA336407 AA337222 AA319240 BJ026817 BJ027058 AL536880 AJ693827 AA651730 AJ701013 BMD68789 AW339506 AA293021 BF691108
		AJ458885 AW361203 AW974652 AJ761251 AJ655763 AA628063 BE047125 AW085916 AJ129587 N52070 AW172361 AA052951 AW085909
		AJ000008 AA962570 AJ371342 AJ364207 AA464514 AJ962506 AJ824503 AW376300 AA058439 AW361192 AV656660 N50282 BF820514 BF891008
		H40784 BF891112 BE708029 AW043567 AA056762
419145	248375_1	BM456602 AV706711 BF379357 H90994 AA234435 AA558020 BF351723 AJ328271 R94815 N99638 BG223375 AW973750 N59599
409245	3199_2	AF030234 BC017465 BG008526 AW505550 BM460141 N47324 AA361037 AA321632 N45606 AV572798 AV657116 AA296632 AJ137857
30		AW467027 AJ742080 AJ624350 H58206 AA478518 AW439997 AW393555 AW393523 AJ559753 AJ808732 R66856 H01374 BJ257369 BJ259830
		AW960845 BM466252 AW956813 BE768647 AV658853 BM055248 BF372070 BF372055 BF372061 AA347852 AA905863 BG505078 AV654024
		BF093291 AW021929 H22650 AA459715 BG496341 BE697763 BJ254209 BG499543 H42946 BJ059780 BJ086741 H87696 H87599 BF691752
		BE768511 BG940948 W37195 BF372041 BE883796 BF372082 BF367329 BF509744 AW966003 AV714014 BJ492868 BJ495144 AA921845
35		AJ693426 AJ652147 AJ435449 N47325 AJ434429 AA573137 AJ183429 AJ829962 AJ332526 BF513937 AJ189561 AJ221962 AJ378034 AW118897
		AW665247 AW340077 N41605 AA478519 AA463875 AJ858260 AA463379 AJ292305 BE045947 AA971089 AJ125820 BG940947 AJ080245
		AA884954 AJ125702 AJ382934 AA931835 AJ358631 AW439905 AJ027833 AJ399648 AJ014533 AA347851 AA738261 N67374 N69081 AJ768667
		AA948472 AJ19214 AA293133 AJ186725 AA889214 AJ222635 BJ485143 N29605 N48812 AA769041 AJ492769 D56771 AA095911 BE222062
		D56772 AW372265 BM054985 D12465 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 BJ255749 BJ492848
40	437886	34287_1
		H16217 H21980 H22651 H88179 H87354 H44052 H25165 H44128
		US2054 AL581000 AA156850 AW293839 BJ335865 AA024963 BF149420 BE073977 AW602574 BE164012 BE163992 BE163974 AW402161
		BM194134 AW966609 W84374 BF916380 AA385173 W84366 AA383743 BF903598 AA043776 W84421 AA778446 AW444904 BF446960
		AA837481 AV755539 AW468444 AW468002 AA811830 AA581806 AJ866686 AJ572124 AA687333 D20160 AA812489 AJ185248 AJ186004
		AA156781 AJ536733 BM144850 AJ471883 AA040926 BF507639 AA043777 AW874142 BE832523 BE163972 BJ022546 BJ021204
45	458332	1139685_1
	459513	417837_1
	493328	3030726_1
	405685	0_0
	417258	400835_1
	447881	44623_1
50		AJ000341 AJ766341 AW873274
		AV704062 BE162284 AJ032946 BF360636
		AJ884781 AJ652306 AJ651694 AJ638744 AJ962493
		M18728
		BG116781 BJ914326 BJ030196 N58885 N53406 AV683374 N58892 BG110501 AA333708 AA359583 AW963123 N59562 N59596 N59587
		AK074291 AW293424 BE676135 AJ832125 BE019146 BE465019 AJ761124 AA617778 AJ279232 AW575897 AJ672039 F28618 BF924261
		AA722184 BF934174 BE004328 AV749301 BE880282 BJ019798 BJ019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119
		AW814195 BE879126 AJ697926 BF594155 BE205787 BF063513 N35828 AJ948557 AJ433839 AJ379679 BG056182 AJ589094 N23123 AA588805
		AW316581 AJ080272 AJ421980 AJ493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H96592 N28741 BJ035539 BF747723
		BF171066 W01350 H05495 AJ243785 Z39622 AA887432 AJ350659 R46102
55	425481	334120_2
	440638	371165_1
	442495	928718_1
	416311	1280744_1
	431926	1237041_1
	435154	126605_1
60	437908	13268_11
		AL520496 AW978162 AJ610475 AJ688990 AW470054 AA609426 AJ167391 AA815231 AA358241
		BG009500 AJ376551 AA897445 T87714
		AJ184717 AW518883 AF121173
		AA179446 AA357794 D81719 D80529 C14833
		AW972724 AA877998 AA522631 AJ185388
		AW972053 AA686764 AA804491 AW665688 AA765069
		AJ740586 AA771806 BE500996 AW204531 AJ082424 AJ033879 BF093176 AA771764 D38676

TABLE 33C:

65

Pkey:Unique number corresponding to an Eos probeset

Ref:Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) [Nature](#) 402:489-495.

Strand:Indicates DNA strand from which exons were predicted.

Nt_position:Indicates nucleotide positions of predicted exons.

70

Pkey	Ref	Strand	Nt_position
401403	7710966	Plus	146180-146294
406387	9256180	Plus	116229-116371,117512-117651
405268	4156151	Minus	24404-24521
406122	9144087	Minus	30940-31386
402550	7652009	Minus	80413-80673

75

80 TABLE 34A: About 703 genes upregulated in idiopathic pulmonary fibrosis relative to hypersensitivity pneumonitis or non-specific interstitial pneumonitis

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number		Unigene Title: Unigene gene title				
R1: 90th percentile of IPF AIs divided by 90th percentile of HP AIs, where the minimum value for the numerator and denominator was set to 50						
R2: 90th percentile of IPF AIs divided by 90th percentile of NSIP AIs, where the minimum value for the numerator and denominator was set to 50						
	Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
10	405443			Target Exon	9.66	7.50
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	7.23	3.66
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	6.63	3.03
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	4.84	2.81
	406984	M21305		FGENES predicted novel secreted protein	4.73	5.69
15	425259	AL049280	Hs.155397	Homo sapiens mRNA: cDNA DKFZp564K143 (tr	4.34	4.34
	407244	M10014		fibrinogen, gamma polypeptide	4.14	5.88
	421823	N40850	Hs.28625	ESTs	4.12	1.80
	419875	AA853410	Hs.93557	proenkephalin	3.90	2.01
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.88	2.90
20	418310	AA814100	Hs.86693	ESTs	3.66	2.84
	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	3.60	3.13
	438315	R56795	Hs.82419	ESTs	3.49	3.70
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.47	1.38
	409532	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	3.46	3.46
25	434233	AF119903	Hs.138453	hypothetical protein PRO2834	3.28	2.51
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	3.26	3.26
	447033	AJ357412	Hs.157601	Predicted gene: Eos cloned; secreted w/V	3.19	2.12
	420185	AL044056	Hs.251385	ESTs	3.18	3.01
	420195	N44348		Homo sapiens cDNA FLJ11177 fis, clone PL	3.16	3.16
30	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	3.08	3.18
	408221	AA912183	Hs.47447	ESTs	3.07	1.98
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	3.02	2.36
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	2.98	1.72
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	2.87	1.48
35	422404	AL133571	Hs.336189	Homo sapiens mRNA: cDNA DKFZp434F1135 (f	2.80	2.66
	445745	AB007924	Hs.13245	KIAA0455 gene product	2.78	1.65
	407938	AA905097	Hs.85050	phospholamban	2.78	2.46
	423575	C18863	Hs.163443	intron of perostin (OSF-2os)	2.78	1.55
	446659	AJ335361	Hs.226376	ESTs	2.74	1.56
40	425383	D83407	Hs.156007	Down syndrome critical region gene 1-like	2.74	1.85
	437620	AW976930		ESTs	2.72	2.72
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.67	2.05
	416585	X54162	Hs.79386	leiomyodin 1, smooth muscle (LMOD1) (Thy	2.66	1.47
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	2.66	2.66
45	430712	AW044647		ESTs	2.62	2.62
	453111	AB014598	Hs.31720	hephaestin	2.61	1.72
	451039	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.59	1.27
	414290	AJ568801	Hs.71721	ESTs	2.59	1.23
	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	2.58	2.58
50	412639	AW961284	Hs.203838	ESTs	2.58	2.29
	423720	AL044191	Hs.23388	hypothetical protein DKFZp434F0318	2.57	1.74
	429757	AW452355	Hs.256037	ESTs	2.57	1.60
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	2.57	1.00
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.56	1.12
55	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.56	1.25
	411880	AW872477		gb:hm30f03.x1 NCL CGAP_Thy4 Homo sapiens	2.54	2.54
	401645			C16001440:gi 12330704 gb AAG52890.1 AF3	2.53	3.38
	401673			C16001416:gi 12743112 ref XP_010131.2	2.47	2.83
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	2.46	1.18
60	416316	H58721	Hs.271628	ESTs	2.42	3.44
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	2.40	1.69
	451149	AL047586		RNA binding motif protein 8B	2.40	1.95
	421190	U95031	Hs.102482	mucin 5, subtype B, tracheobronchial	2.40	1.61
	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	2.40	2.40
65	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	2.39	1.27
	405120			C4001445:gi 12697999 dbj BAB21818.1 (AB	2.38	2.38
	432224	AW189460	Hs.208358	ESTs	2.38	2.00
	418663	AK001100	Hs.41690	desmocollin 3	2.38	2.38
	412622	AW564708	Hs.171959	ESTs	2.37	1.63
70	424012	AW388377	Hs.137569	tumor protein 63 kDa with strong homolog	2.37	1.52
	442767	AI017208	Hs.131149	ESTs	2.36	1.22
	401785			NM_002275: Homo sapiens keratin 15 (KRT1	2.35	1.79
	411800	N39342	Hs.103042	microtubule-associated protein 1B	2.35	1.18
	427535	R29543	Hs.2164	pro-platelet basic protein (includes pla	2.34	2.34
75	444009	AI380792	Hs.135104	ESTs	2.34	2.07
	435143	R12375	Hs.194600	ESTs	2.33	1.68
	402333			Target Exon	2.33	3.15
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	2.33	1.10
	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	2.32	1.30
80	452242	R50856	Hs.159993	glycosyltransferase	2.32	1.45
	418693	AI750878	Hs.87409	thrombospondin 1	2.32	2.32
	428411	AW291464	Hs.10338	ESTs	2.32	1.54
	459702	AI204995		gb:an03c03.x1 Stratagene schizo brain S1	2.31	1.98
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	2.31	2.49
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	2.31	1.32

	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	2.30	2.30
	456536	AW135986	Hs.257859	ESTs	2.28	2.28
	428166	AA423849	Hs.79530	M5-14 protein	2.27	1.88
5	456936	M81349	Hs.1955	serum amyloid A4, constitutive	2.25	2.16
	417728	AW138437	Hs.24790	KIAA1573 protein	2.25	1.37
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.24	2.42
	409159	AW673312	Hs.50848	hypothetical protein FLJ20331	2.24	2.24
	404942			splicing factor, arginine/serine-rich 9	2.24	2.64
10	410286	A1739159	Hs.61898	DKFZP586N2124 protein	2.24	2.46
	440516	S42303	Hs.161	cadherin 2, type 1, N-cadherin (neuronal	2.24	1.94
	421574	AJ000152	Hs.105924	defensin, beta 2	2.23	1.36
	418005	A186220	Hs.83164	collagen, type XV, alpha 1	2.22	1.37
	421948	L42583	Hs.334309	keratin 6A	2.20	2.20
15	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	2.19	1.61
	417563	AA203701		gb:zc52a10.r1 Soares fetal liver spleen	2.18	2.40
	431089	BE041395		ESTs, Weakly similar to unknown protein	2.16	2.46
	447333	BE090580	Hs.70704	hypothetical protein DJ61688.3	2.16	2.00
	455797	BE091833		gb:IL2-BT0731-260400-076-F04 BT0731 Homo	2.16	1.26
20	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.16	1.99
	403362			NM_001615: Homo sapiens actin, gamma 2,	2.16	1.61
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	2.15	2.11
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	2.15	2.24
	402641			C1002296:gi 6677817 ref NP_033126.1 rep	2.14	2.14
25	418236	AW994005	Hs.337534	ESTs	2.14	2.14
	413059	BE151498		gb:RCO-HT0295-291199-031-E11 HT0295 Homo	2.14	2.14
	432437	W07088	Hs.293685	ESTs	2.14	2.14
	428398	AJ249368	Hs.98558	ESTs	2.14	2.14
	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.12	1.43
30	421853	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	2.12	1.93
	435391	AJ227892	Hs.146274	ESTs	2.12	2.12
	417430	AA984546		gb:am88e08.s1 Stratagene schizo brain S1	2.11	2.17
	407443	AF227138		gb:Homo sapiens candidate taste receptor	2.11	2.36
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	2.10	1.29
35	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	2.10	2.10
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	2.10	2.00
	440273	AJ805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	2.10	1.37
	450271	AJ693900	Hs.200920	ESTs	2.09	2.34
	432222	AJ204995		gb:an03c03.x1 Stratagene schizo brain S1	2.09	1.40
40	458208	AJ380016		ESTs, Weakly similar to T4S4_HUMAN TRANS	2.08	2.00
	405600			C12001673:gi 9631264 ref NP_048045.1 or	2.07	1.97
	434654	AJ825942	Hs.139366	Homo sapiens clone L5 polyadenylated HER	2.07	2.52
	439261	AJ126020	Hs.145674	basic transcription factor 3	2.05	1.45
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	2.04	2.04
45	457741	BE044740		gb:hms55g10.x1 NCI_CGAP_RDF1 Homo sapiens	2.04	2.04
	423161	AL049227	Hs.124776	downstream of cadherin 6 (by 3.3kb)	2.02	1.33
	412505	AA974491	Hs.21734	ESTs	2.02	2.02
	443180	R15875	Hs.258576	claudin 12	2.02	2.02
	431605	AW972407	Hs.124370	gb:EST384498 MAGE resequences, MAGL Homo	2.02	2.02
50	415938	BE383507	Hs.78921	A kinase (PKA) anchor protein 1	2.02	2.17
	452571	W31518	Hs.34665	ESTs	2.02	2.09
	405061			Target Exon	2.01	2.52
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	2.01	2.41
	402327			Target Exon	2.00	2.44
55	418786	AJ796317	Hs.203594	Homo sapiens uncharacterized gastric pro	2.00	2.00
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	2.00	2.00
	438634	AW340400	Hs.126728	ESTs	1.99	2.43
	416127	N49843	Hs.79022	GTP-binding protein overexpressed in ske	1.97	1.41
	423961	D13666	Hs.136348	periostin(OSF-2os)	1.96	1.48
60	430397	AJ924533	Hs.105607	bicarbonate transporter related protein	1.96	1.31
	411010	AW813339		gb:MR3-ST0192-101299-013-c05 ST0192 Homo	1.96	2.73
	439628	W81007	Hs.58628	ESTs	1.96	1.28
	444301	AK000136	Hs.10760	asporin (LRR class 1)	1.96	1.58
	431726	NM_015361	Hs.268053	KIAA0029 protein	1.95	1.72
65	410418	D31382	Hs.63325	transmembrane protease, serine 4	1.95	1.87
	452814	AJ092790	Hs.334703	hypothetical protein FLJ14529	1.95	1.06
	417562	AW888754	Hs.134126	crystallin, gamma S	1.95	2.14
	424480	AA341442	Hs.205299	ESTs	1.94	1.94
	404342			C7002192:gi 7299207 gb AA54404.1 (AE0	1.92	1.32
70	443320	AJ051607	Hs.16335	ESTs	1.91	2.18
	449780	AA443241		ribosomal protein L44	1.90	1.76
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	1.89	2.16
	434416	AA805903	Hs.59498	cell division cycle 2-like 5 (cholinese	1.89	2.04
	457505	AL044659	Hs.43791	ESTs	1.89	2.34
75	425912	AL137629	Hs.162189	serine/threonine kinase with Dbf- and pt	1.88	1.26
	413585	AJ133452	Hs.75431	fibrinogen, gamma polypeptide	1.88	1.88
	428231	U17989	Hs.183105	nuclear autoantigen	1.88	1.88
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	1.88	1.88
	404429			Target Exon	1.88	2.18
80	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	1.88	3.04
	406641	AJ235667		gb:Homo sapiens mRNA for immunoglobulin	1.86	2.57
	417059	AL037672	Hs.81071	extracellular matrix protein 1	1.86	1.48
	454565	BE141231		gb:MR0-HT0075-081199-003-a09 HT0075 Homo	1.86	1.21
	415115	AA214228	Hs.127751	hypothetical protein	1.85	1.23

	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	1.85	1.45
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	1.84	1.44
	403344			NM_000341: Homo sapiens solute carrier fa	1.84	1.84
5	447245	AK001713	Hs.17860	hypothetical protein FLJ10851	1.84	2.33
	446006	NM_004403	Hs.13530	deafness, autosomal dominant 5	1.84	2.02
	401593			Target Exon	1.83	2.34
	434392	AW983709	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	1.83	2.12
	406461			hypothetical protein, clone 24751	1.83	2.01
10	455657	BE065209		gb:RC1-BT0314-310300-015-b12 BT0314 Homo	1.83	1.26
	400609			C10001147:gi12698926[gb]AAK01739.1[AF33	1.82	2.08
	422095	A1868872	Hs.282804	hypothetical protein FLJ22704	1.81	1.14
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	1.81	1.22
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	1.81	2.10
15	426521	AF161445	Hs.170219	hypothetical protein	1.81	2.08
	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	1.81	1.64
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	1.80	1.34
	439606	W79123	Hs.58561	G protein-coupled receptor 87	1.80	1.80
	459189	A1909090		gb:IL-BT198-010499-007 BT198 Homo sapien	1.80	1.80
20	412429	AV650262	Hs.75765	GRO2 oncogene	1.80	2.55
	402674			Target Exon	1.80	3.41
	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	1.79	1.57
	454824	AW833646		gb:QV4-TT0008-161199-033-d09 TT0008 Homo	1.78	1.94
	401677			BAI1-associated protein 3	1.78	2.28
25	426291	U58913	Hs.169191	small inducible cytokine subfamily A (Cy	1.78	1.53
	430028	BE564110	Hs.227750	Target CAT	1.78	1.59
	445988	BE007663	Hs.13503	Inactivation escape 2	1.78	2.10
	452272	AW292249	Hs.252739	hypothetical protein DKFZp434P0316	1.78	2.08
	418205	L21715	Hs.83760	troponin I, skeletal, fast	1.78	2.70
30	400425	AY004252	Hs.287385	PR domain containing 12	1.77	2.02
	400419	AF084545		Target	1.77	2.67
	447169	A1989803	Hs.157289	ESTs	1.77	2.21
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	1.77	2.12
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	1.76	2.54
35	432808	NM_015985	Hs.278973	angiotensin-3	1.76	1.76
	437400	AB011542	Hs.55599	EGF-like domain, multiple 5	1.75	2.00
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	1.75	1.47
	444986	AJ204197		ESTs	1.75	2.48
	451027	AW519204	Hs.40808	Homo sapiens, Similar to RIKEN cDNA 2810	1.74	1.69
40	413524	BE145837		gb:MR0-HT0208-101299-202-c07 HT0208 Homo	1.74	1.74
	409099	AK000725	Hs.50579	hypothetical protein FLJ20718	1.74	2.26
	405579			C22000151:gi16806921[ref]NP_004165.1[so	1.74	2.12
	405797			CX001015:gi11322384[emb]CAC16687.1[AJ	1.73	2.66
	405159			ENSP0000024337*:cDNA FLJ13984 fis, clone	1.73	2.01
45	450569	AW192334	Hs.38218	ESTs	1.73	2.08
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	1.73	1.24
	445261	T79759	Hs.250651	ESTs, Weakly similar to I38022 hypotheti	1.73	2.52
	445231	AW450669	Hs.45068	hypothetical protein DKFZp434I143	1.73	1.64
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytolactin)	1.72	1.37
50	422259	AA307584		gb:EST178498 Colon carcinoma (HCC) cell	1.72	1.72
	456034	AW450979		gb:UL-H-B13-ata-a-12-0-UL.s1 NCL_CGAP_Su	1.72	1.34
	451862	H09260	Hs.32333	ESTs	1.71	2.16
	403520			Target Exon	1.71	1.39
	456596	AA291834	Hs.78950	branched chain keto acid dehydrogenase E	1.71	2.26
55	426603	AA382291		gb:EST95683 Testis 1 Homo sapiens cDNA 5	1.70	1.70
	418387	R18085	Hs.22279	gb:yg16b12.r1 Soares infant brain 1N1B H	1.70	1.70
	433417	AA587773	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	1.70	1.87
	402538			C1001634:gi12621136[ref]NP_076245.1[Ba	1.69	1.57
	414844	AA296874	Hs.77494	deoxyguanosine kinase	1.69	2.06
60	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	1.69	1.63
	446563	AB021179	Hs.15299	HMBA-inducible	1.68	2.02
	456235	AA203637		gb:zx58b12.r1 Soares_fetal_liver_spleen_	1.68	2.12
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	1.68	2.03
	433930	AA620338		ESTs	1.68	2.28
65	404151			Target Exon	1.68	1.80
	429392	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	1.67	2.18
	430070	AF197927	Hs.231957	ALL1 fused gene from 5q31	1.66	2.16
	400496			ENSP00000224716*:GTP-binding protein SAR	1.66	2.13
	413464	AL121500		ESTs	1.66	2.03
70	411188	BE161168		gb:PM0-HT0425-170100-002-a10 HT0425 Homo	1.66	2.12
	446281	H69416	Hs.14606	hypothetical protein FLJ20271	1.65	2.28
	443282	T47764	Hs.132917	ESTs	1.65	2.04
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	1.65	1.67
	453355	AW295374	Hs.31412	myopodin	1.65	1.66
75	432375	BE538069	Hs.2862	S100 calcium-binding protein P	1.65	1.54
	437929	T09353	Hs.106642	ESTs, Weakly similar to T09052 hypotheti	1.65	2.04
	410295	AA741357		nidogen (enactin)	1.64	2.30
	437767	AA830103	Hs.293331	ESTs	1.64	1.26
	416580	T61572	Hs.79385	Human clone Z3574 mRNA sequence	1.64	3.38
80	450795	AW173371	Hs.60435	ESTs	1.64	1.64
	421847	NM_014717	Hs.108884	KIAA0390 gene product	1.64	2.75
	403010			C21000152:gi16226483[sp]Q52118[YM03_ERWS	1.64	2.03
	406387			Target Exon	1.64	1.78
	440423	AW293995	Hs.192277	ESTs	1.63	2.05

	444381	BE387335	Hs.283713	hypothetical protein BC014245	1.63	2.07
	442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.63	1.65
	442424	AJ342715	Hs.129569	ESTs, Moderately similar to B34087 hypot	1.62	2.40
	402885			Target Exon	1.62	1.18
5	408786	AA773187	Hs.294027	ESTs	1.62	1.59
	448719	AA033627	Hs.21858	linucleotide repeat containing 3	1.62	1.63
	414684	AW630023	Hs.76693	3-hydroxybutyrate dehydrogenase (heart,	1.62	2.10
	406838	AA827569	Hs.153	ribosomal protein L7	1.61	1.41
10	441600	AA939347	Hs.127223	Homo sapiens cysteine knot protein (ZSIG	1.61	2.32
	420693	NM_001972	Hs.99863	elastase 2, neutrophil	1.60	2.37
	412649	NM_002206	Hs.74369	integrin, alpha 7	1.60	1.23
	432331	W37852	Hs.274368	MSTP032 protein	1.60	1.23
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.60	1.69
15	400279			NM_004581*:Homo sapiens Rab geranylgeran	1.60	1.56
	437865	AI472305	Hs.19565	ESTs	1.60	2.42
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	1.60	1.29
	442993	BE018682	Hs.166195	ATPase, Class I, type 8B, member 1	1.60	2.11
	410684	AA088500	Hs.170298	ESTs	1.59	1.46
20	433149	BE257672	Hs.42949	hypothetical protein HES6	1.59	2.22
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	1.59	1.41
	426457	AW694667	Hs.22660	chimerin (chimerin)	1.59	1.26
	427654	AA410183	Hs.137475	ESTs	1.59	2.83
	411662	D60541	Hs.285519	Homo sapiens cDNA FLJ11904 fis, clone HE	1.59	2.18
25	440383	AA884208	Hs.30484	ESTs	1.58	2.19
	406650	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	1.58	1.58
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	1.58	1.47
	407857	AJ928445	Hs.92254	synaptotagmin-like 2	1.58	1.51
	411573	AB029000	Hs.70823	KIAA1077 protein	1.57	1.29
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	1.57	1.17
30	428471	X57348	Hs.184510	stratillin	1.57	1.55
	429249	X81479	Hs.2375	egf-like module containing, mucin-like,	1.57	1.19
	407966	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	1.57	2.12
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	1.57	1.05
35	430469	AW603667	Hs.288742	Homo sapiens cDNA: FLJ22712 fis, clone H	1.56	1.56
	445511	AA846512		Homo sapiens cDNA FLJ14459 fis, clone HE	1.55	2.08
	404501			nucleoside phosphorylase	1.55	2.54
	429107	AI470451	Hs.99075	ESTs	1.55	2.05
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	1.55	1.45
40	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	1.54	2.61
	458091	AF150286		gb:AF150286 Human mRNA from cd34 stem ce	1.54	1.54
	439280	AI125436	Hs.123654	ESTs	1.54	2.06
	428096	AW291771	Hs.42239	Homo sapiens, clone IMAGE:3868989, mRNA,	1.53	1.55
	414221	AW450979		gb:U1-H-B13-ala-a-12-O-U1s1 NCLCGAP_Su	1.53	1.39
45	451712	AA019290	Hs.110489	ESTs	1.53	1.99
	402487			Target Exon	1.53	2.02
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	1.53	1.29
	452887	AI702223	Hs.107253	hypothetical protein DKFZp761F241	1.53	1.21
	410253	T51823		ESTs	1.52	2.03
50	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	1.52	1.37
	432985	T92363	Hs.178703	ESTs	1.51	1.48
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	1.51	1.15
	429259	AA420450	Hs.292911	Plakophilin	1.51	1.31
	429289	AI400746	Hs.62187	phosphatidylinositol glycan, class K	1.51	1.19
55	441457	AW996651	Hs.43838	ESTs	1.51	2.08
	433365	AF026944	Hs.293797	ESTs	1.51	2.74
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	1.51	1.21
	424386	BE146577	Hs.285132	ESTs	1.50	1.53
	429655	U48959	Hs.211582	myosin, light polypeptide kinase	1.50	1.29
60	442391	AW450544	Hs.220751	ESTs	1.50	1.65
	414341	D80004	Hs.75909	KIAA0182 protein	1.50	2.10
	436222	AI208737	Hs.122810	Homo sapiens cDNA FLJ11489 fis, clone HE	1.50	2.16
	442264	AI278777	Hs.263455	ESTs, Weakly similar to ALU1_HUMAN ALU S	1.50	1.50
	443878	AW292499	Hs.139709	hypothetical protein FLJ12572	1.50	1.37
65	430152	AB001325	Hs.234642	aquaporin 3	1.50	1.43
	447752	M73700	Hs.105938	lactotransferrin	1.49	0.91
	404455			opioid receptor, kappa 1	1.49	1.36
	424106	AA412442	Hs.98132	ESTs	1.49	1.30
	433095	AK001092	Hs.302480	Homo sapiens cDNA FLJ10230 fis, clone HE	1.49	2.02
70	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	1.48	1.50
	456256	AB000450	Hs.82771	vaccinia related kinase 2	1.48	1.42
	439310	AF086120	Hs.102793	ESTs	1.48	1.48
	407102	AA007629		glycerol-3-phosphate dehydrogenase 1 (so	1.48	1.15
	437981	AA774445	Hs.145365	ESTs, Weakly similar to KIAA1397 protein	1.48	2.36
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	1.47	1.21
75	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	1.47	1.25
	453864	AW021407	Hs.21068	hypothetical protein	1.47	2.18
	401067			ENSP00000252105*:CDNA FLJ12240 fis, clon	1.47	1.81
	456054	BE313241		gb:601151545F1 NIH_MGC_19 Homo sapiens c	1.47	1.99
80	402324			C19001982:glj3043638[dbj]BAA25483.1[AB	1.47	2.03
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	1.47	1.29
	457734	BE394365	Hs.38750	hypothetical protein FLJ11526	1.47	2.26
	402013			Target Exon	1.46	2.42
	429295	AA682377	Hs.99216	ESTs, Moderately similar to ALU8_HUMAN A	1.46	2.09

5	430920	U96402	Hs.248132	gooseoid-like	1.46	2.46
	409368	AA071059		gb:zm66a10.r1 Stratagene neuroepithelium	1.46	2.02
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	1.46	1.43
	427719	AI833122	Hs.134726	ESTs	1.46	1.46
	433430	AI863735		ESTs	1.46	1.15
10	423790	BE152393		gb:CM2-HT0323-171199-033-a08 HT0323 Homo	1.46	2.36
	444083	AI123195		gb:oo17a10.x1 Soares_NSF_F8_9W_OT_PA_P_S	1.45	2.29
	433256	AW604447	Hs.339408	ESTs, Weekly similar to S26689 hypothe	1.45	1.50
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	1.45	1.17
	456664	AW963354	Hs.334409	metallothionein 1G	1.45	2.20
15	438158	AI796556	Hs.187884	ESTs	1.45	1.18
	409883	AW452419	Hs.296098	ESTs	1.45	2.00
	452316	AA298484	Hs.61265	ESTs, Moderately similar to G786_HUMAN P	1.45	1.27
	413048	M93221	Hs.75182	mannose receptor, C type 1	1.45	1.36
	457462	AI133573	Hs.272312	Homo sapiens mRNA; cDNA DKFZp434J2235 (f	1.45	2.08
20	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	1.44	1.28
	401116			Target Exon	1.44	2.19
	419618	AA528295		gb:nh26e06.s1 NCI_CGAP_Pr3 Homo sapiens	1.44	2.30
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	1.44	2.03
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	1.43	1.48
25	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	1.43	1.51
	418742	AW451197	Hs.113418	ESTs	1.43	1.24
	418335	R63267	Hs.28399	ESTs	1.43	1.14
	408404	AW192518		gb:xl45h08.x1 NCI_CGAP_Pan1 Homo sapiens	1.43	2.08
	448175	BE296174	Hs.225160	hypothetical protein FLJ13102	1.43	2.29
30	431846	BE019924	Hs.271580	uropod 1B	1.43	2.12
	459557	N58315		gb:yv68g06.s1 Soares fetal liver spleen	1.43	2.00
	449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	1.43	1.33
	442321	AF207664	Hs.8230	a disintegrin-like and metalloprotease (1.43	1.10
	454843	AW834536	Hs.258549	gb:MR2-TT0014-241199-012-f06 TT0014 Homo	1.43	1.55
35	410281	AF076612	Hs.166186	Homo sapiens clone 23928 mRNA sequence	1.43	1.38
	402998			NM_002463*:Homo sapiens myxovirus (influ	1.42	2.16
	443709	AI082692	Hs.134662	ESTs	1.42	2.22
	435259	AA152106	Hs.4859	cyclin L ania-6a	1.42	2.01
	454407	AW578420	Hs.118843	gb:RC1-CT0249-120100-022-b04 CT0249 Homo	1.42	1.76
40	453359	AA448787	Hs.24872	ESTs	1.42	1.33
	434126	AI138589	Hs.118205	ESTs	1.41	2.06
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	1.41	1.46
	442316	Z75331	Hs.8217	stromal antigen 2	1.41	2.20
	438330	AW450572	Hs.257316	ESTs	1.41	2.20
45	410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	1.41	2.02
	455885	BE153524		gb:PMO-HT0339-241199-002-C03 HT0339 Homo	1.41	1.33
	405550			C7001981*:gij565157[gb]AAB31881.1 T-cal	1.41	1.24
	451385	AA017656		gb:ze39h01.r1 Soares retina N2b4HR Homo	1.41	1.99
	424925	NM_002432	Hs.153837	myeloid cell nuclear differentiation ant	1.40	2.64
50	431022	AA490815	Hs.208351	ESTs	1.40	1.26
	439781	AA845538		glial cells missing (Drosophila) homolog	1.40	2.72
	429379	NM_014840	Hs.200598	KIAA0537 gene product	1.40	1.05
	435310	AA705075	Hs.169536	Rhesus blood group-associated glycoprote	1.40	1.26
	430702	U56979	Hs.278568	H factor 1 (complement)	1.39	1.18
55	451331	AK002039		Homo sapiens cDNA FLJ11177 fis, clone PL	1.39	1.26
	459198	AI086347	Hs.151138	ESTs	1.39	1.22
	442344	AI022925	Hs.79368	epithelial membrane protein 1	1.39	1.35
	402917			ENSP00000202587*:Bicarbonate transporter	1.39	1.44
	418211	BE244746	Hs.247474	hypothetical protein FLJ21032	1.39	2.08
60	437158	AW090198		KIAA1150 protein	1.38	2.07
	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	1.38	1.24
	433911	AI923092	Hs.8899	ESTs	1.38	2.15
	402504			C1003823*:gij4826521[emb]CAB42853.1 (AL	1.38	1.38
	409465	AW393810	Hs.78054	gb:QV4-TT0008-251099-016-e11 TT0008 Homo	1.37	2.22
65	449426	T92251	Hs.198882	ESTs	1.37	2.38
	405491			Target Exon	1.37	2.74
	406685	M18728		gb:Human nonspecific crossreacting anti	1.37	1.34
	442410	AW996503	Hs.197680	ESTs	1.37	1.56
	407701	AW375009	Hs.164407	ESTs	1.36	2.02
70	400818			Target Exon	1.36	2.10
	406475			C15000508*:gij2558825[gb]AAC53387.1 (AF	1.36	2.78
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	1.36	1.41
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	1.36	2.20
	444195	AB002351	Hs.10587	KIAA0353 protein	1.35	0.94
75	447918	AI129320	Hs.115175	ESTs, Highly similar to JC5818 gamma-act	1.35	1.22
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	1.35	1.40
	412992	AI423369	Hs.75111	protease, serine, 11 (IGF binding)	1.35	1.24
	401025			NM_004055*:Homo sapiens calpain 5 (CAPN5	1.35	1.30
	452862	AW378065	Hs.8687	ADAMTS2 (a disintegrin-like and metallo	1.34	2.12
80	425308	M97639	Hs.155585	receptor tyrosine kinase-like orphan rec	1.34	1.02
	402308			Target Exon	1.34	1.21
	428415	AA337211	Hs.184222	Down syndrome critical region gene 1	1.34	1.40
	407242	M18728		gb:Human nonspecific crossreacting anti	1.34	1.22
	410741	Z11695	Hs.324473	mitogen-activated protein kinase 1	1.34	2.05
	439335	AA742697	Hs.62492	NM_052863:Homo sapiens secretoglobulin, la	1.34	1.12
	431254	NM_006069	Hs.251385	murine retrovirus integration site 1 hom	1.33	1.21
	405213			Target Exon	1.33	2.03

5	447990	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy	1.33	1.05
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synthetase	1.33	2.09
	453914	NM_000607	Hs.574	fructose-1,6-bisphosphatase 1	1.33	1.32
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	1.33	1.18
	430385	AA113437		N-myc downstream-regulated gene 3	1.32	1.48
	447731	AA373527	Hs.19385	CGI-58 protein	1.32	2.22
	400740			hypothetical protein FLJ14280	1.32	2.01
	410481	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 2	1.32	1.32
10	440274	R24595	Hs.7122	scrapie responsive protein 1	1.32	1.32
	406867	AA157857	Hs.182265	keratin 19	1.32	1.42
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Drosophila)	1.32	2.30
	443144	BE246335		hypothetical protein MGC14797	1.32	2.03
	432810	AA863400		ESTs	1.32	4.01
15	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	1.31	1.24
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	1.31	2.17
	440099	AL080058	Hs.6909	DKFZP564G202 protein	1.31	1.53
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	1.31	1.31
	436874	H02780		gbvj41a1.1.1 Soares placenta Nb2HP Homo	1.31	2.03
20	402825			Target Exon	1.31	1.24
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danlos)	1.31	1.45
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	1.31	1.19
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	1.31	1.12
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	1.30	2.06
25	407409	AF060168		gb:Homo sapiens AS10 protein mRNA, partial	1.30	2.16
	400221			NM_002082:Homo sapiens G protein-coupled	1.30	2.02
	437751	AA767373		ESTs, Moderately similar to ALU1_HUMAN A	1.30	2.44
	450008	H52970	Hs.36688	WAP four-disulfide core domain 1	1.30	1.19
	441591	AF055992	Hs.183	Duffy blood group	1.29	1.03
30	405973			Target Exon	1.29	1.32
	424604	AW865388	Hs.151076	KIAA1243 protein	1.29	0.92
	410899	AW809716		gb:MR4-ST0124-241199-025-h09 ST0124 Homo	1.29	2.06
	405818			CX001073:gi4176497[emb]CAA20116.1[AL0	1.29	2.05
	402621			Target Exon	1.29	3.06
35	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	1.28	2.35
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subunit)	1.28	1.44
	453331	AJ240665		ESTs	1.28	2.36
	439791	H77774	Hs.35755	ESTs	1.28	2.00
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	1.28	3.00
40	407266	AJ235664		gb:Homo sapiens mRNA for immunoglobulin	1.28	1.28
	446526	H89616		Homo sapiens cDNA FLJ13357 fis, clone PL	1.28	1.28
	455577	BE006341		gb:RC2-BN0127-240300-011-b05 BN0127 Homo	1.28	1.28
	418863	AL135743	Hs.25566	ESTs, Weakly similar to 2004399A chromos	1.28	2.10
	407711	AI085846	Hs.25522	KIAA1808 protein	1.28	1.23
45	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	1.28	1.19
	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	1.27	1.24
	418203	X54942	Hs.83758	CDC28 protein kinase 2	1.27	2.08
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	1.27	2.05
	444418	AL034417	Hs.11169	Gene 33/Mig-6	1.27	1.98
50	427809	M26380	Hs.180878	lipoprotein lipase	1.27	1.09
	414590	BE410103	Hs.12313	hypothetical protein FLJ14566	1.27	1.36
	439919	AA970710	Hs.128064	ESTs	1.27	2.28
	401311			Target Exon	1.27	2.05
	444235	AW207346	Hs.143202	ESTs	1.27	2.00
55	430858	AF007190		Homo sapiens SIB 297 intestinal mucin (M	1.26	1.23
	448186	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT	1.26	2.40
	400161			Eos Control	1.26	1.33
	444239	R57988	Hs.10706	epithelial protein lost in neoplasm beta	1.26	1.20
	438369	T77886	Hs.83428	nuclear factor of kappa light polypeptide	1.26	1.26
60	441944	AW855861	Hs.8025	Homo sapiens clone Z3767 and Z3782 mRNA	1.26	1.12
	431142	AA852596	Hs.250641	tropomyosin 4	1.26	1.23
	434229	R56378	Hs.181223	hypothetical protein PRO2801	1.26	2.04
	406733	AA976565	Hs.297753	vimentin	1.26	1.29
	422292	AI815733	Hs.114360	transforming growth factor beta-stimulat	1.25	1.16
65	424137	AA335769	Hs.16262	ESTs	1.25	1.27
	434868	R50032	Hs.159263	collagen, type VI, alpha 2	1.24	1.50
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	1.24	1.29
	433750	H15448	Hs.31330	Homo sapiens clone HQ0319	1.24	1.27
	447299	AF043897	Hs.18075	chromosome 9 open reading frame 3	1.24	1.13
70	438357	AI042101	Hs.294107	ESTs	1.24	2.04
	409959	BE349470		mucin 6, gastric	1.23	2.22
	439897	NM_015310	Hs.6763	KIAA0942 protein	1.23	2.44
	421982	AF206019	Hs.110347	REV1 (yeast homolog)-like	1.23	2.14
	407207	T03651	Hs.336780	tubulin, beta polypeptide	1.23	1.32
75	416956	AA810664	Hs.101660	hypothetical protein MGC5391	1.23	2.39
	413624	BE177019	Hs.75445	SPARC-like 1 (mest19, hev1)	1.23	1.08
	442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	1.23	1.51
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.23	1.01
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	1.22	1.41
80	452934	AA581322	Hs.4213	hypothetical protein MGC16207	1.22	1.17
	421341	AJ243212		deleted in malignant brain tumors 1	1.22	1.09
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	1.22	1.52
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	1.22	2.55
	423189	M59371	Hs.171596	EphA2	1.22	1.15

	401899		Target Exon	1.22	1.22
	403579		Target Exon	1.22	2.34
	415954	AA171850	ESTs	1.22	2.24
5	429171	AI743173	ESTs, Weakly similar to ARL2_HUMAN ADP-R	1.21	1.14
	444071	AI627808	ESTs	1.21	2.23
	424344	AF036973	HCGN-6 protein	1.21	2.15
	434051	AF116622	gb:Homo sapiens clone FLB4217 mRNA seque	1.21	1.25
	422311	AF073515	cytokine receptor-like factor 1	1.21	1.39
10	404600		Target Exon	1.21	1.29
	429751	M55210	laminin, gamma 1 (formerly LAMB2)	1.21	1.03
	430392	NM_000627	latent transforming growth factor beta b	1.21	1.21
	422687	AW068823	insulin-like growth factor binding prote	1.21	1.23
	424855	AW204725	ESTs	1.20	1.98
15	418690	AA232134	ESTs	1.20	1.33
	413232	BE073258	hypothetical protein FKSG28	1.20	2.18
	414154	AW205314	ESTs	1.20	1.34
	416784	AA334592	lumican	1.20	1.27
	410933	C15974	gb:C15974 Clontech human aorta polyA mRN	1.19	2.05
20	415388	AF018081	collagen, type XVIII, alpha 1	1.19	1.11
	406731	AI559131	gb:tg31g07.x1 NCI_CGAP_U11 Homo sapiens	1.19	1.19
	447563	BE536115	EST	1.19	1.14
	405531		Target Exon	1.19	2.02
25	400363	NM_001403	eukaryotic translation elongation factor	1.19	1.21
	426611	BE178050	catenin (cadherin-associated protein), b	1.19	1.18
	427676	AA394062	tropomyosin 2 (beta)	1.18	1.16
	413929	BE501689	collagen, type IV, alpha 2	1.18	1.20
	413856	D13639	cyclin D2	1.18	1.20
	427111	AA351026	serine (or cysteine) proteinase inhibito	1.18	1.12
30	422287	F16365	cytochrome c oxidase subunit VIIa polype	1.18	1.05
	412758	Y07818	dihydropyrimidine-like 3(ULP)	1.18	1.06
	446668	AV660737	ESTs	1.18	1.18
	417613	AV654351	desmin (actin depolymerizing factor)	1.18	1.17
	405542		Target Exon	1.18	1.98
35	419908	AW971327	ESTs	1.17	2.02
	434095	AA011117	milk fat globule-EGF factor 8 protein	1.17	1.19
	407230	AA157857	keratin 19	1.17	1.35
	448413	AI746379	ESTs	1.17	2.87
	426653	AA530892	dual specificity phosphatase 1	1.17	1.39
40	424572	M19650	2',3'-cyclic nucleotide 3' phosphodiester	1.17	2.08
	440109	AK001138	hypothetical protein FLJ10276	1.17	1.06
	405131		C1002509.gi 9938010 ref NP_064684.1 odo	1.17	2.22
	422354	U20882	insulin-like growth factor-binding prote	1.17	1.19
	442124	R66412	Homo sapiens cDNA FLJ14309 fis, clone PL	1.17	1.11
45	400080		Eos Control	1.16	2.53
	431924	AK000850	Homo sapiens cDNA FLJ20843 fis, clone AD	1.16	2.00
	412602	U41518	aquaporin 1 (channel-forming integral pr	1.16	1.30
	429207	AA447941	ESTs	1.16	1.27
	415149	X12451	cathepsin L	1.16	1.12
50	400231		Eos Control	1.16	1.17
	416653	AA788553	metallothionein 1E (functional)	1.16	1.16
	422813	AV556571	transmembrane 4 superfamily member 6	1.16	1.10
	439318	AW837046	G protein-coupled receptor 56	1.16	1.15
	422424	AI186431	prostate differentiation factor	1.16	1.21
55	432745	AI821926	gb:n178f05.x5 NCI_CGAP_Pr3 Homo sapiens	1.15	2.00
	412477	AA150864	microsomal glutathione S-transferase 1	1.15	1.23
	430361	AK033965	sterol-C4-methyl oxidase-like	1.15	2.31
	424512	X53002	Integrin, beta 5	1.15	1.15
	449924	W30681	Homo sapiens cDNA: FLJ22130 fis, clone H	1.15	1.24
60	414682	AL021154	inhibitor of DNA binding 3, dominant neg	1.15	1.07
	456076	BE243877	ATPase, Na ⁺ transporting, beta 3 polypep	1.15	2.00
	403026		Target Exon	1.15	2.32
	422545	X02761	fibronectin 1	1.15	1.17
65	412719	AW016610	ESTs	1.15	1.05
	421848	X15880	collagen, type VI, alpha 1	1.15	1.14
	422087	X58968	matrix metalloproteinase 2 (gelatinase A	1.15	1.16
	413936	AF113676	serine (or cysteine) proteinase inhibito	1.14	1.13
	449845	AW971183	DnaJ (Hsp40) homolog, subfamily C, membe	1.14	2.07
	430202	T85775	gb:yd60g02.r1 Soares fetal liver spleen	1.14	1.14
70	418806	AA485970	ESTs	1.14	2.14
	424017	AA333789	gb:EST37925 Embryo, 9 week Homo sapiens	1.14	2.16
	422003	AA361760	ESTs	1.14	1.17
	437272	AW975957	gb:EST388066 MAGE resequences, MAGN Homo	1.14	2.17
	438357	N79588	ras homolog gene family, member B	1.14	1.23
75	453152	AK001933	hypothetical protein FLJ11071	1.13	2.36
	406849	AA454809	collagen, type I, alpha 1	1.13	1.33
	422110	AI376736	secreted protein, acidic, cysteine-rich	1.13	1.06
	425335	BE394327	folistatin-like 1	1.13	1.08
	434795	BE620794	translocating chain-associating membrane	1.13	1.09
80	417426	NM_002291	laminin, beta 1	1.13	1.11
	452924	AW580939	complement component C1q receptor	1.13	1.01
	416379	N38857	ESTs	1.12	1.12
	421464	AA291553	ESTs	1.12	2.01
	442420	AI024834	ESTs	1.12	1.15

	405369			NM_005569*:Homo sapiens LIM domain kinase	1.12	1.99
	421730	AW449808	Hs.334534	glucosamine (N-acetyl)-6-sulfatase [Sanf	1.12	2.08
	405932			C15000305:gil3806122[gb]AAC69198.1] (AF0	1.11	2.01
5	453542	AW836724		Homo sapiens mRNA expressed only in plac	1.11	2.00
	437585	AW976857		ESTs	1.11	2.01
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	1.11	1.05
	449931	AW875786	Hs.25734	ESTs, Weakly similar to BING1 [H.sapiens	1.11	1.03
	407085	Z70759		gb:H.sapiens mitochondrial 16S rRNA gene	1.10	1.12
10	447191	NM_014521	Hs.17667	SH3-domain binding protein 4	1.10	1.04
	406713	U02629	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.10	1.07
	432675	AJ791855	Hs.105884	ESTs	1.10	2.30
	432731	R31178	Hs.287820	fibronectin 1	1.09	2.12
	430763	AA485468		DNA fragmentation factor, 45 kD, alpha p	1.09	2.10
15	438855	AW946276	Hs.6441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr	1.09	1.04
	405156			NM_003213*:Homo sapiens TEA domain fami	1.09	2.19
	409031	AA376836		ESTs	1.09	2.22
	422608	AW160644	Hs.118695	potassium voltage-gated channel, subfam	1.09	2.26
	440704	M69241	Hs.162	insulin-like growth factor binding prote	1.09	1.28
20	410577	X91911	Hs.64639	glioma pathogenesis-related protein	1.08	2.64
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	1.07	1.02
	452219	AA024860	Hs.61224	ESTs	1.07	2.08
	430108	AA465294		ESTs	1.07	2.11
	402174			Target Exon	1.07	2.11
25	416952	AJ767736	Hs.290070	gelsolin (amyloidosis, Finnish type)	1.07	1.00
	410199	AW377424	Hs.205126	Homo sapiens cDNA: FLJ22667 fs, clone H	1.07	1.13
	442670	BE410050	Hs.11859	hypothetical protein FLJ13188	1.07	2.21
	442310	AF033199	Hs.8198	zinc finger protein 204	1.06	2.04
	405536			NM_005805:Homo sapiens 26S proteasome-as	1.06	2.20
30	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	1.06	1.06
	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibito	1.06	1.06
	425371	D49441	Hs.155981	mesothelin	1.06	1.27
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	1.06	2.37
	406711	N25514	Hs.77385	myosin, light polypeptide 6, alkali, smo	1.06	1.05
35	409407	AW967370	Hs.342655	Homo sapiens cDNA FLJ13289 fs, clone OV	1.05	2.00
	406109			Target Exon	1.05	2.04
	418597	AK001678	Hs.86337	similar to DNA-directed RNA polymerase I	1.05	2.67
	403162			C2000231*:gil9802031[gb]AAF95597.1]AF239	1.05	2.07
40	411020	NM_005770	Hs.67726	macrophage receptor with collagenous str	1.05	1.07
	407225	J04617		eukaryotic translation elongation factor	1.05	1.02
	416955	AW889150	Hs.80595	NM_004552*:Homo sapiens NADH dehydrogena	1.05	1.10
	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	1.04	2.12
	410276	AJ554545		angiopoietin-2	1.04	1.04
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	1.04	1.04
45	406712	M31212	Hs.77385	myosin, light polypeptide 6; alkali, smo	1.03	1.05
	406773	AA812424	Hs.76067	heat shock 27kD protein 1	1.03	1.10
	452082	N51905	Hs.125133	hypothetical protein FLJ22501	1.03	2.01
	419150	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	1.03	2.24
	417204	N81037	Hs.1074	surfactant, pulmonary-associated protein	1.02	1.00
50	408339	R97502	Hs.30443	sentrin/SUMO-specific protease	1.02	2.19
	400247			Eos Control	1.02	2.04
	430030	BE300094	Hs.227751	lectin, galactoside-binding, soluble, 1	1.01	1.01
	442275	AW449467	Hs.54795	ESTs	1.01	1.04
	406786	AW161678	Hs.111334	femlin, light polypeptide	1.01	1.06
55	439403	BE265745		ESTs, Weakly similar to ALUC_HUMAN !!!!	1.01	2.11
	428043	T92248	Hs.2240	uteroglobin	1.00	1.06
	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	1.00	1.02
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.00	2.16
	450724	R55428		gb:yl79b05.r1 Soares breast 2NbHst Homo	1.00	0.99
60	424125	M31669	Hs.1735	inhibin, beta B (activin AB beta polypep	1.00	1.08
	432077	AL134685		gb:DKFZp547M126_r1 547 (synonym: htfb1)	1.00	2.05
	427687	AW003867	Hs.1570	histamine receptor H1	1.00	1.00
	435256	AF193766	Hs.13872	cytokine-like protein C17	1.00	1.00
	420026	AI831190	Hs.166676	ESTs	1.00	1.00
65	455128	AW861555	Hs.314372	EST	1.00	1.00
	410685	AA497117	Hs.58893	ESTs, Moderately similar to ALU1_HUMAN A	1.00	1.00
	401404			Target Exon	1.00	1.00
	449625	NM_014253		odt (odd Oz/ten-m, Drosophila) homolog 1	1.00	1.00
	443458	R05385	Hs.143509	hypothetical protein FLJ21924	1.00	1.00
70	452744	AJ267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	1.00	1.00
	418355	L42563	Hs.1165	ATPase, H7 transporting, nongastric, alp	1.00	1.00
	447947	N33033	Hs.270215	ESTs	1.00	1.00
	419236	AA330447	Hs.135159	Homo sapiens cDNA FLJ11481 fs, clone HE	1.00	1.00
	455047	AW852530		gb:PM1-CT0243-071099-001-g06 CT0243 Homo	1.00	1.00
75	440400	AA94364	Hs.125594	ESTs, Weakly similar to T25472 hypothe	1.00	1.00
	444963	AJ916973	Hs.213603	ESTs	1.00	1.00
	410834	AW811114		gb:MR2-ST0131-111199-016-a04 ST0131 Homo	1.00	1.00
	442849	R10099	Hs.269805	ESTs	1.00	1.00
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	1.00	1.00
80	454600	AW810001		gb:MR4-ST0124-270300-005-b11 ST0124 Homo	1.00	1.00
	418454	AA315308	Hs.195870	hypothetical protein FLJ14991	1.00	1.00
	459045	N69101	Hs.40730	ESTs	1.00	1.00
	455500	AW963582		gb:EST375655 MAGE resequences, MAGH Homo	1.00	1.00
	411745	AW867826		gb:MR0-SN0039-300300-001-c02 SN0039 Homo	1.00	1.00

429932	AI095005	Hs.21586	ESTs	1.00	1.00
432365	AK001106	Hs.274419	hypothetical protein FLJ10244	1.00	1.00
415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	1.00	1.00
431374	BE258532	Hs.251871	CTP synthase	1.00	1.00
443162	T49951	Hs.9029	DKFZP434G032 protein	1.00	1.00
432128	AA127221	Hs.296502	ESTs	0.99	2.33
451838	AW005866	Hs.193969	ESTs	0.98	3.26
438414	AA806794	Hs.131511	ESTs	0.97	3.61
435872	AA701357	Hs.192759	ESTs	0.97	0.96
425211	M18657	Hs.1867	progastricsin (pepsinogen C)	0.97	1.08
424001	W67883	Hs.137476	paternally expressed 10	0.96	2.25
418869	AW516565		gb:qx01d05.x1 Soares_NHCEC_cervical_tumo	0.96	2.07
458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	0.94	2.18
418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	0.94	1.31
432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	0.94	2.12
432093	H28383		gb:yf52c03.r1 Soares breast 3NbHbSt Homo	0.94	2.19
452239	AW379378		protein tyrosine phosphatase, receptor t	0.94	0.79
403167			Target Exon	0.94	2.06
402209			Target Exon	0.92	2.04
453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	0.92	0.74
424090	X99699	Hs.139262	XIAP associated factor-1	0.91	2.11
432816	N38913	Hs.221575	ESTs	0.91	2.15
451779	AW368616	Hs.296234	ESTs, Weakly similar to T31613 hypothi	0.91	2.14
406851	AA609784		major histocompatibility complex, class	0.89	1.04
427698	AW972594	Hs.335499	ESTs	0.89	0.90
440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-li	0.88	2.42
427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	0.87	1.14
426024	Z43405	Hs.75668	Homo sapiens, Similar to RIKEN cDNA 1700	0.87	2.04
400986			NM_024085*-Homo sapiens hypothetical pro	0.87	2.10
430353	AW952337		citrate synthase	0.86	2.28
404975			uncharacterized hypothalamus protein HTO	0.86	2.50
406673	M34996	Hs.198253	major histocompatibility complex, class	0.86	1.94
431323	AW970623		gb:EST382705 MAGC resequences, MAGK Homo	0.80	2.08
404926			Target Exon	0.79	2.01
432297	AW663632	Hs.285625	Homo sapiens mRNA; cDNA DKFZp434A119 (fr	0.77	0.86
437601	AA761546	Hs.248844	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.77	2.10
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	0.76	2.66
406646	M33600	Hs.308026	major histocompatibility complex, class	0.76	1.09
442195	NM_001430		endothelial PAS domain protein 1	0.76	2.00
415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	0.76	0.78
413916	N49813	Hs.75615	apolipoprotein C-II	0.73	2.06
453716	AA037675	Hs.152675	ESTs	0.73	2.10
437802	AI475995	Hs.122910	ESTs	0.70	2.08
422282	AF019225	Hs.114309	apolipoprotein L	0.68	2.95
410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	0.54	2.11
424917	AI636208	Hs.96901	hypothetical protein FLJ23049	0.53	0.53

TABLE 34B:

50 Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
442006	1239046_1	AW975183 AA973583 AI355103 AI699495 AI301787
420195	28714_1	AK002039 AL117524 AV714494 AW964901 AL045243 BF955185 AU137860 AW880615 AW880496 AA256290 BE767078 N44348 AI886676 AA455877 N66571 AA998864 AU157344 AI817146 R54821 BE223107 AA455880 AI355752 BF589210 N63487 AI924033 AI923020 AI306145 AI919421 AI584169 AI250173 AI440227 AA669696 AW244040 AI358104 AI570333 AI418315 N94787 R72348 N94780 BF944396 BF754698 AW005707 N98831 BF001047 BF588691 AA318076 AW601474 AW883910 H10056 N63481 BE838574 BF909132 BI084973 BG257295 BG818471 BE348449 AI420623 AW271213 BE048764 W44682 AI887849 AW903942 AA975919 AA312915 BF948057 R55120 H10110 BI045196 AW880645 AW976930 AW292808 AW451796 BF514112 AI806378 AI658903 AI769457 AW593455 AI625525 AI538551 AI660509 AA761825 AA973287 AA861483 W73065 AI735361 W60499 W76653 BG959557 AW044647 AI670953 AI656180 AA484715 AI659205 BF923472 BE088101 T05990 AW872477 AF231512 AW300273 BG779015 AW510935 AI989816 AA137069 AI748876 AW150861 AI862628 AI805872 AI675382 BE855437 AW044703 AI677769 AA886718 AI753144 AA626885 AI018092 AI263010 AW026173 BE221138 AA256268 AW571932 AW276137 AI634216 AW296259 AA977716 AI302589 AA348340 AI720838 AI311733 AA015867 N73713 AL047586 AW840354 AA256196 AW840357 AW840504 T35664 Z36755 AW954421 AA247424 AI056930 T31380 BI910428 H88489 BG675223 AA443427 BE879501 AA478530 R72977 AA298568 BF792417 AA356982 BF922499 BE764808 BE565636 BF903986 BF331881 N42207 BG623760 BG611090 BF735387 BE697757 BE697755 BE718853 N78560 AI984095 AA137140 AA053711 N59865 AI078134 AA643796 T57803 AA018642 N66799 AI004600 BG896323 BF895104 N73684 N73806 N73811 AW900287 AA018641 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354 AA203701 R66895 BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826 BE091833 BE091874 BE091871 BE063078 BE151503 BE151498 AW872732 AW827432 AA199662 AA610519 R54983 BG207209 BE166299 AI204995 BF199355 AW969908 AA528756 AW440776 BI044354 AI90640 AI380016 BM273298 BM273060 BI017968 BE044740 BI017768 AW827360 BF380597 BI017970 BF746974 BF380582 BF380592 BF908552 BF907924 BF380784 BF380651 BF380634 BE166581 BE161439 BF908606 BI017961 BE044718 AW827623 BF907758 BI017967 AW827621 AA653908 BI017765 BI017955 BI017960 BI017798

411010	1066474_1	AW813381 AW816094 AW813357 AW814469 AW813293 AW816099 AW813295 AW813425 AW813331 AW813325 AW813351 AW813427 AW813339
449780	31099_2	BG721806 BG623574 AA367501 BG436403 BG619828 BG570704 BF086115 BF086118 R78932 BG620860 BG571920 BF997723 AA368244 BG620531 BG621967 BG435818 BG620442 BG621518 H12650 BG573175 H61600 R67494 H01715 D78811 BG435953 BF107266 D79043 R67255 H01310 BG570941 BG570693 R21776 AA327133 R32578 R30775 BG570963 T86946 H61601 W86279 BF991104 R21732 BF990905 BG622861 BE929694 AI090290 BE929277 BE929284 AA367783 AA082581 D78839 H78318 N91085 BE929344 D63217 BE929334 H53536 R80360 H54070 C17064 AW962470 R00900 BG619698 BG623946 H94918 BE929345 AA04267 BF957177 BG620685 BF086421 T87029 C17044 H60972 BG573514 AA131924 D78838 BG003560 C18615 W86323 R09737 R02529 AA367502
406641	0_0	AJ235667 AJ235668 AJ235669 AJ235670
454565	1061836_1	BE141160 BE141231 BE141793 BE141791 BE141167 BE141807 BE141806 BE141805 AW807591 AW807590 AW807586 AW807583 BE141803 AW845918 BE141207 BE141158
455657	1490185_1	BE065209 BE065364 BE065110 BE065111
459189	MH1945_5	AV683451 AK057494 BG718853 BM152866 BG390826 BE709644 AJ864727 BI045181 BI459637 AI909102 AI909090 BG722507 BI023834
454824	1073655_1	AW833783 AW833646 AW833525 AW833351 AW833526 AW833825
444986	704733_1	AW268472 AI204197 AW592537
413524	1518859_1	BE145894 BE145837 BM263472
422259	140437_1	BF821471 AW795791 BF844843 BF821371 AA307584 AW795790 BF833724 BE154067 BE064709
456034	685586_1	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
426603	1299162_1	AA994657 AA382291
456235	1979764_1	AA203637 AA832266 H67452
433930	19851_15	AW873618 AA620338
413464	415532_1	AL527514 AI732432 AA133309 AI225224 AV700997 BF589361 AW291763 AL121500 AA129708
411188	1072487_1	AW821260 BE162466 BE161168
410295	2817_1	BG402852 BG545086 AA150252 AL036760 AA452480 AI033256 W68776 W93372 N31248 AI052219 AI367635 W69374 N88610 R58194 B1524854 BI497111 BF940043 AI129268 AI359798 AI056480 AA121421 AI042150 AW449003 AI418180 AI419420 AI356058 BF832243 AI349330 AI359448 W76647 BF477170 AA099163 BF994549 AW608256 AA045418 H03770 AL574791 AW069455 BE302148 AW022281 AW960273 AA121268 AI336371 AI989381 AI131425 AI147483 AI311537 AW338638 AI141649 AA709414 AI187177 AA780884 AI333805 AA045312 AI623918 AI349421 W63753 W70299 AA557276 AA299007 N98212 W74064 N24823 T54892 AA054724 W73059 AI869152 N93462 N71889 AI537432 R71628 AA303089 AI498550 T60941 AV706417 AW067848 AI150677 AW338118 AI336313 AA826256 AI139518 AA662948 AA902723 AI970175 W68682 AI089380 AI148372 H99951 AW183001 AI270317 AA532767 AA044727 AA931652 R82469 AA150261 W67788 H67495 R80715 AW149812 H78914 AB62034 W61122 AW023118 W69375 T88917 T47984 N21531 R35646 AA055544 H15534 AA688295 AA090586 AA044764 BF994641 R79547 N21313 BF674610 H02874 AW975323 R16904 AA328030 AA054671 R79546 BF832310 AI249109 Y08200 NM_004581 BC003093 BE733834 BI753321 BG773890 BF091906 BI917541 AI023762 AA587230 BF435086 AI264262 AI687392 AI810536 AW589885 AI244419 AA749261 AA535435 AW205689 AI765770 AI765431 C02465 AW305347 AI818456 AA322111 AW381845 AW381829 AV749407 AA811636 AU159893 AA603065 AA652542 AI468678 R49616 AW381863 BE389867 BE182397 BF087771 AA527551 AA134051 AA831504 AA134052 AI871759 AW089048 BI913532 AA367709 BG628155 BF093014 BM471219 BE093160 BG171761 BI254009 AI905474 AA453162 AA829759 AI086559 AA776022 AI377446 BF589018 AA452822 AW614566 AA443880 AA476733 AW970674 AI393291 AA988283 AI905528 AW384956 D78656
400279	2140_1	AF150286 AV739062 AA835857
445511	9560_8	AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
458091	452694_1	AA774785 AA584875 AA577705 AA683178 AA083204 AW362057 T92332 T51823 T02858 AA083375 T92391
414221	685586_1	AW945170 BF930905 F33652 BG057818 AI368018 AI421485 AI300352 AI378525 AI264177 AI276281 AI245302 AI281050 AI190036 AW451438
410253	132134_1	AW242903 AA910870 F22289 F19647 F22375 AW473816 BF445785 AA774528 F33447 C01077 AW772227 F17759 H42812 R09701 AA349096
407102	7177_2	R48772 H42832 H42537 R47898 N28263 H25721 F32386 H43971 R48205 F21390 H45809 AA007629 R47897 R83734 H45844 AW983653 H43970 H42536 H24495 R48875 H42961 H22079 R66018 BF314481 BE313241 BI196333 BE383148
458054	1263570_1	AA071059 AA085201 AA085020
409368	110612_1	AA961586 AI863735 AA588325
433430	2181751_1	BE152393 AA330984 BE073904 BF176271
423790	886344_1	BI836699 AI123195
444083	10908_12	BG168298 AA247945 AA528295 AW971284
419618	252691_1	BF308898 BE298629 BE298765 AW192518 BE298614 BE300025 BF307463
408404	658475_1	BG623239 N58315 AI524952
459557	859794_1	BE153524 BE153576 BE153583
455885	1524553_1	AA019761 AA017656 AA017374
451385	85022_1	AA845538 AA890229
439781	2592493_1	AK002039 AL117524 AV714494 AW954901 AL045243 BF955185 AI137860 AW880615 AW880496 AA256290 BE767078 N44348 AI886676
451331	28714_1	AA455877 N66571 AA998864 AU157344 AI817148 R54821 BE223107 AA455880 AI355752 BF589210 N63487 AI924033 AI923020 AI306145 AI919421 AI584169 AI250173 AI440227 AA669696 AW244040 AI358104 AI570333 AI418315 N94787 R72348 N94780 BF944396 BF754698 AW005707 N98831 BF001047 BF588691 AA318076 AW601474 AW883910 H10056 N63481 BE838574 BF909132 BI084973 BG257295 BG818471 BE348449 AI420623 AW271213 BE048764 W44682 AI887849 AW903942 AA975919 AA312915 BF948057 R55120 H10110 BI045196 AW880645 AL050068 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 AA630766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057 AW516069 AI582546 BF221924 BF222543 AI801808 AW468599 AW000735 AI866625 AW235356 BM021837 AA911956 AI680606 W86516 T03370 AW611634 H41653 AI468349 H19588 AW090198 AW043993 R39847
406685	0_0	M18728
430385	MH497_8	NM_032013 AB044943 AF308609 BI769254 AI819262 AA845639 AI289073 BE670187 AA207127 T33098 AA633492 BE328324 AI083620 AI204945 AA903471 AI372602 AI049836 AI049737 BF000101 AI686167 BF436896 AI659189 T32971 AA311302 AW733149 AI435981 T03438 AA879206 AI972177 T33083 AA613910 AI971019 AI027140 AA853739 AI620528 AI637519 AI972307 BF054861 AK027665 BF082751 AIS98127 T33663 AA204743 BE086660 F12132 T26372 BF765338 AA323106 AA322907 BI037062 BE315235 AV772868 BE254381 T66212 BE566142 T09034 AA405202 BF843940 AI743855 AA113356 BG990683 BE086729 BE535539
443144	16112_3	AB058726 AI651414 BE245990 BE245765 BF439734 AA648422 AA040639 AI340155 AA255928 AA278365 BE766296 AA280771 AL555562 AI474638 AI863068 BI250946 AK027039 BG615852 AI698039 AA252016 AA258886 BE905205 AW501167 BF514117 BI857400 AW297001 AI624923 AA125900 AW272165 AA190967 AA280729 AA035532 AW129692 AA125899 BG528645 BE614599 BE464693 AI560128 AA551511 AI351149 AL555561
432810	101919_1	BG292389 C06094 AI668930 AW104534 AA310513 AA830127 AW134897 AA046953 AW965490 AI810530 BF092924 AA334151 AA334725 D31302 R20723 AA263003 BI824635 AI276287 AI684428 AI524234 AI335035 AW014704 AI911443 AA972102 AI367512 AI126670 AW016017 AI286003 AI147163 AA626033 AI539156 AA565542 AI094253 AW512612 BE889628 AA744752 BE646306 AW471324 AA999975 AA853400 H17550 AI991439 R46187 BE929954 AA33976 D63102 BF744491
438874	52147_1	AF075017 R66779 R22453 H02780
400221	9287_3	NM_002082 L16862 BG828886 BE795217 BE904064 BE294526 BE297283 BE394617 BE935127 BE935106 F12351 BG823182 H16710
437751	643238_1	AW978796 AA767373 AW173343 AA836163 N27583 AA905328 R97032

410899	1063474_1	BF374577 AW809840 AW809996 AW809798 AW809695 AW809646 AW809738 BF374582 AW809716 AW809826 AW809802 AW809747
453331	16559_1	AW810152 BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999
5		T49904 R75732 B1057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157457 AW663674 AA190993
		H01542 BF510304 AA626915 AA746952 AI161014 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620
		AA909684 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF959484 AI240655
		BF989591 B1056086 BG001590 BF107035
446526	11131_17	AK023419 BE464935 BE221668 AI148885 B1859909 AI374780 AA766892 AI347967 AI582917 AA477117 AA229236 AA652637 AA636109
10	455577	AU134580 F21298 BF802607 BE769124 AV658891 H89616 AV658953
430858	1475566_1	BE006307 BE006341 BE006311
400161	2656_2	AF007190 AW820705 BE168488 AF007192 BF753303 BG978971 BG978568
15		U44839 NM_004651 BC000350 B1458316 AU117940 BG759024 BG749694 BE799505 BG831537 AI816335 AA325352 AL547005 AW157038
		AI859331 AI816186 AU150786 AL043549 AW162880 AU159233 AI143169 T03478 BE727648 AA764725 BE206603 AI369814 AI984369 AW157545
		BE221486 H99016 AU159025 AI074496 AI494516 BE245950 AA704385 AA280862 AI479595 AI369776 BE671398 T05538 AA682249 B1677303
		BE645335 AI359434 H92868 D52599 D53609 D54715 T06015 BE222174 AI954706 D53218 D53787 R69889 W68696 AI497670 R70771 BF309414
		BE620147 BC910697 AW964968 BE836120 AL579715 H56512 D59566 B1044097 AL555239 BF220278 AA081991 AI819544 AW001573 AW131600
		AI858764 D52367 W22034 BG818979 BG024561 BE702779 B1458863 B1910399 BG707755 BF348284 H10055 E1086315 BE620574 H41088
		BG119517 W23267 W21941 AA328817
20	409959	AW513804 BE179199 BE179195 BE179198 BE179204 BE162686
421341	1407_1	NM_007329 AF159456 AJ243212 AJ297935 AA295769 NM_017579 AJ243224 AI492875 AI796676 B1479838 AA918144 AI814590 AI923531
		BF513992 AI720725 AI150879 AI279072 AW612904 AI492104 AI284510 AI141231 AA613554 AW662148 AW769047 AA565985 AW612888
		AU100513 BG955585 BG955588 AA295763 BE829414 BF760645 BG954398 AA295332 AA295795 BE932867 AW769569 T89953 BE934311
	434051	AF116622 AI114507 AA640834 BF111602 AA377999
25	410933	C16024 C15974 AW811066 AW811052 AW811020
406731	73505_1	AI559131
446868	1064624_1	AK074473 BC017997 B1831060 BF971101 AI886394 AI082824 AV708785 W86073 W07772 AV660737 AI816793 R52250 BG183529 AA633473
	0_0	AI191256 R44763 R19947 BF571346 W86267
	15525_1	BC011310 AF261085 BC004109 AY007133 BC009081 BC001601 NM_002046 M33197 BC020308 J02642 M36164 BE794233 AV721080 BE255459
400231	MH494_5	BG926429 BG389312 BG477333 AI031799 B1763443 AI260432 AA989106 AV728576 B1091380 AA402499 AI200513 AI284734 AI223995 AI289749
30		BG283291 BM013814 AW438544 BM450203 F35435 F33262 BE890952 AA401181 BG939668 F35525 B1088182 F34674 F33506 BM471326
		F34677 AW276712 AA187508 F34866 AA114245 AA522581 N23935 AI076923 AI018505 BE879774 BM465637 AI753078 BG222169 AA595947
		BF970917 B1094125 AA719841 BE893087 BG775178 BE793983 BE797071 BF339134 BE409272 BE266456 BE796770 BE745957 BG756835
		BE266758 BE259342 BM450181 BG748174 BE259322 BM423587 BM467637 BM452667 BM479516 BM452420 BE273297 BM466364 BM450640
		BM478743 BM459094 BM455306 BM472001 BM478247 BM478771 BM480379 BM459071 BM450106 BM467584 BM464548 BM465044 BM450176
35	432745	BF569359 BM462924 BM455329 BM471815 B1862301 BG331736 H04903 AA374894 BE902964
412477	112643_1	AA658826 AI821926 AI791191 AA635129 AA584492
	8669_2	AI220117 AI857837 AI218371 BM091400 AI304964 AI198508 AI400738 AW571549 AW950042 AI089943 AA437280 AU150878 BF197070 AI267984
		BF594181 BF196688 AI433152 AI338921 AI620364 AI280197 AA652531 AI674938 AI342447 AI620350 AI281295 AI148621 N54787 AI338121
		AI281153 N51899 AI087072 AA954788 AW069054 AI346309 BG529629 AI340135 BF083036 AI167365 AW819657 AA935468 AI467868 AW148701
		AI383720 BE047685 AW015498 AA937149 AA708346 AW771478 AW802508 H53334 AW389204 AW798230 AI539222 AI560688 AW950043
		AI961682 AV706506 R01853 AI216514 N62757 AI536893 AI926052 AI418720 N99964 AI568933 AI915737 AI080691 AI185358 N48996 N68575
		H82824 H60037 AI247247 T95684 BF593863 AI749637 AW088541 AA991294 AA887452 AI073726 AA629674 AA629649 AA629656
		AA576595 AI168758 AA804572 AI085786 AA994396 AA991209 AA948663 AA929054 AA927952 T87001 AA928210 AA629296 AW802267
		AW384129 BF744400 AA194110 AI382839 AA194837 AA406284 AI250750 R37035 AI255586 W01244
45	456076	BG210376 BG217800 BE925778 W39114 BG682395 N70644 BE709097 AW275615 BC001469 AL564888 AI088126 AW003852 BF792438
	8455_1	AA161295 AW970131 AI127310 AW029307 AW192534 AA843144 AW606235 BE221641 AW008111 AA224203 AA604507 AW794761 AA134005
		AA126850 N99165 AW769391 AW818302 AI269871 BE503027 AW401627 AA486231 AA486417 AI191542 AA028128 AA159991 AI498090
		AI241024 BM145449 AA774661 AI626021 C18251 BE185811 AA291517 N38896 N59222 AI245611 AA169207 AI298572 AA169585 AI131139
		AA157960 AI439983 AI208276 AA938061 W67305 AW337587 AI357055 W04739 AI214517 AA617789 AW241277 AI880213 AI582789 AI143995
		BE814848 N49964 AI936222 AI817819 F09976 AA039349 AW805002 T35117 N94388 AI689530 AW384573 AW584555 AW384539 AW384473
		AI129709 AW384466 BG194342 BG204579 BG027536 AL578075 AA399553 AW794949 T88866 AW511211 R26588 R36111 BG170598 BE937009
		BG678833 AA862899 H56612 H02273 AA768487 BF211173 N32570 AA088287 R68451 AA297563 H16847 R80665 AA421891 W68402 R28379
		R64119 R70109 R77661 R67963 BG701844 H68870 AA169864 AA114111 BE715243 R69317 BE715252 BE713804 BG336586 NM_001679
		BC011835 U51478 BM463117 AU119746 B1462090 B1277086 BG706303 BF059073 BG706532 B1544716 AI568735 BE858747 AI122881
		AU126210 AI186547 AU134705 BE281323 AI147220 BE263820 AW973937 BG281863 BE858367 BE278941 AI262814 AI001194 AI391616
		AI200862 N32564 AI161064 AI089818 BF514359 AI370916 AI341797 BE263168 AI218416 AI131098 AI285310 AI928440 AI066642 AI375442
		AW028327 AI217792 AI161020 AI342854 AI221544 AI304700 AI343005 BM148839 AA831536 AW074258 BF940569 AI149876 AI914574 AA298442
		AI241343 AA668385 AW272172 AI160537 BG209220 AA028152 AA025989
	430202	AW968345 AA468998 T85775
60	424017	AW956107 AA334317 AA333789
437272	1233214_1	AB075828 BG107783 AW021313 B1492345 AW385707 AW580860 AW296117 BE072066 AW580775 BF679498 AW580828 BE003666 BE003672
	888651_1	AW580851 AW580908 B1037146 AW580894 AW580864 H17858 N50343 N54223 F05579 F07386 F05578 AA73248 AA354359 AA330257 C20685
	176_2	BE548300 AW968728 AW968554 AA777644 AA706898 AA682517 AA832267 BG165087 N51087 N51567 R95837 BE256603 W89042 R95835
		R97364 AW975957 AA747943 AA811289
65	453542	BF568186 BF899745 AW836724 BE243668
	885_22	AW976857 AI809001 AA769369 AW102732 AA761235
	596988_1	AL578301 AI337389 AI671302 AA978185 BF591738 AI765912
	1400_7	BF036043 AW190446 BG194731 AW662036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112068 AV721682 H16423 AI270167
	9531_1	AI857345 AA937302 AW818444 BE929780 BG498678 BF155010 B1598271 B1598811 BE161728 AW578737 AW753711 AW379707 AW381918
70		BG506608 AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AI018009 N42850 AW573242 AI417258
		AA463483 AI676131 AI167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 B1043239 AW474342 BG708553
		AW362423 BF090028 BE827256 R16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405
		AW994425 D81879 BE093545 AW901107 AA383529 B1021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW367006 BF358697
		BF366318 AA663856 BE702099 BF035969 AI267384 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074
		AW954476 AW954472 AA376836 AV724531 D53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057
		D53502 AW373300 AL118798 BM128728 AA193411 AA444709 AW952455 AI887612 BF431948 B1496876 AI264159 BM128481 AI624657
		AI689301 AI969467 AA861685 AA251595 AA625761 AA872090 AI826790 AA328366 BE827416 R75951 D56918 R58122 BE827384 AL118797
		AI184164 AA164411 B1495332 BE858113 AI863860 H00660 T69849 AW780389 C14667 BE934995 B1018652 R92801 AA164410 H00752
		AW373305 AW373299 AW373302
80	430108	AA298810 AW968393 AA65294 AA811301
410276	1233254_1	AA083514 AI554545 AW169852 AI363822 AI633826 AI656026 AI765624 AA147545 AA147552
400247	641443_1	BC022339 BC009610 BC010537 X79805 NM_006713 U12979 BM467814 BM450743 AU132951 AU137129 BG493425 AV758819 BG708412
	2764_1	BG705885 BG702217 AV716638 BG777009 B154569 B1552153 BM476712 BG770858 BG527656 BG528277 BG391388 AV716861 B1602926

5			BG290073 BI667399 BM451469 BI667173 BI602139 BG532171 BI669216 BI544727 BG721852 AV716503 AV701327 BM090738 BI492000 AJ308856 BI544904 AL599813 AV715829 AV716505 AV714587 AV717902 BF668072 AV716385 BI461927 BM090954 AV717826 BG503676 AV647719 BG501392 BG428433 BE895629 BM313117 AW021050 BG435032 BM152910 AA313503 AA872377 BG574714 AV712054 AV732696 AA252476 AV712759 AL599643 BE790872 BG654930 W73337 AW675377 AV760376 AV725139 AV716379 AA887165 BE830003 AW023795 AL599291 AI902948 BG944042 F00781 AA352483 BG217897 N33888 AW581924 BG654730 D31410 AA353088 D31288 AA285029 H95170 BE935104 AU139980 BG772963 BG776470 BG532512 BG105449 BI545421 AV715456 AW386083 BG699714 AL535832 AL514940 BG190861 BG210593 AW999254 H95138 AA353863 BE764809 N50375 BE091363 BG701255 BI860846 BI832485 BG168150 BG028647 BE546301 BG900321 BI909737 BG702363 BG614141 BG611137 BG700121 BF031492 N85802 AV715940 N51590 BG993478 BE172016 AW893522 AK056692 AF066220 AI375065 AA284293 W32566 AW797961 AA960897 AA504145 BF060834 BI019048 AW862002 AK056737 AA429538 AW063311 AW440655 AW231970 AA428584 AA995028 AW854593 AA984131 AA552874 AA564758 AA528743 BG927275 BE045117 AW975234 AA664937 BF749390 BG928948 AA984546 BE009153 AV732487 BE078167 AW872716 AW063245 AA578441 AI820704 AI732283 R55428 BF999154 BF880485 AL134685 AW972760 AA525319 AA526644 AA525342 AA526632 AA525296 AV739423 AW972755 BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360 AW852530 AW852526 AW852527 AL597969 AW811114 AW811095 AW811094 AW811124 AW811157 AW811054 AW811087 AW810001 BF374633 AW809694 AW809672 BF374748 BF374562 AW810209 AW810092 AW809786 AW810428 AW810429 AW809884 BF374650 BF374641 BF374764 BF374744 AW810552 BF374578 BF374653 BF374579 AW810168 AW810170 BF374611 BF374676 BF374667 AW810353 BF374682 AW810154 BF374688 BF374565 BF374757 BF374637 BF374743 BF374719 AW809664 BF374643 BF374680 BF374714 BF374708 BF374716 AW810432 BF374691 BF358066 AW810006 AW810345 AW809960 AW963582 BE054192 BE054169 BE152580 AW963587 AV704306 BF368780 AW867826 AW859896 AA229762 AA230035 AW972670 AA525808 H28359 H28383 BG034853 AW173315 AW303375 BG190225 BG939153 BF057308 AA600736 AI751258 AI090486 BE939504 AW631492 AI768270 AI862133 AA417652 BE378218 AA599207 AW794702 AA024968 AA446024 AI148235 AI191710 BI493797 AI272646 BI493796 AA634323 AI754332 AA258414 C05155 AI218226 AI039656 AI350380 AI084698 AI754989 AI673545 AI432010 AI751035 AA375571 AA446297 BG216743 AA609784 R97304 BC010106 AL560552 AU133296 AU133086 BE268567 BE268523 BI544879 BE398161 BG473088 BI544445 BE258021 BE296339 BE255040 BE263020 BG706790 AL598627 AW952337 BG758113 AW512753 BE267666 BE253415 BI225718 BE268350 BE258245 BI224965 AW772605 BG723903 BE397282 BI196341 BG702880 AI878949 AL600437 AA416759 BE259917 AI031582 BF512142 AI088248 BE560328 AI802623 AI288613 AL597585 AW768553 AI816352 BF732831 BI225687 AA833686 AA722593 AA807750 AW068064 AA405187 AI923236 N51593 AL527710 BG282576 AL525927 AL525971 BI869547 AI064725 R91856 H46814 H20112 W01682 AW848870 AW848585 AW376662 AW848985 AW848937 AW848862 AW848581 AW848512 AW848176 AW752623 AW752618 AW376822 AW376821 AW376684 AW376623 AW376622 BE706047 AW752602 AW752691 AW752674 AW752652 AA379167 AW752610 AW752684 AW752613 AW752660 AW848709 AW848576 AW849155 AW848981 AW848980 AW848979 AW848978 AW848973 AW848916 AW848713 AW848708 AW848642 AW848641 AW848639 AW848573 AW848493 AW848492 AW848489 AW848488 AW848487 AW848353 AW848352 AW848220 AW752698 AW752697 AW752682 AW752681 AW752680 AW752679 AW752664 AW752651 AW752638 AW752637 AW752636 AW752628 AW752626 AW752624 AW752619 AW752596 AW752608 AL582019 BE875587 AL529175 AW965868 BG686208 AA259073 BE696973 AA459543 AA358314 W40564 BF926427 AW849000 AW848718 AW848515 AW848507 AW848444 AW848440 AW848232 AW848222 AW752657 AW376786 AW376781 AW376615 AW376614 BI752581 AA534520 AI748906 AA047799 AI014753 AL514460 AL581982 BG743145 W24171 H20102 H11227 AW752607 AW006596 AW130378 BE716519 AW752661 AW848289 BF349557 AW752612 AW752632 AW848910 NM_004077 AF047042 AL560606 BI765896 BI196831 BI855656 BE906674 BG749937 BE535486 BE019810 AA313713 AA92542 AA332541 AA682985 AA356125 BE140478 BG750945 BI457548 BG025661 BF326302 AA325019 BG980676 AA337465 AA321974 BG949285 BG427585 R23979 BG611485 BE560678 W16977 N50379 BG824101 BG471750 BI453171 W04691 AU099360 BG471590 BM011999 BE262945 BE559801 BF756438 BE881957 BE314546 BG911831 BG150811 BG112017 AA157518 T92368 AW752620 AW970623 AA502839 AA502819 U81984 NM_001430 BE907085 BI333232 AI021986 AU138476 C18601 U51626 AU100517 BI054387 AU076970 BE786454 BG010080 AW377189 BF998789 AA368139 R11396 T83613 BG006324 BI012404 BG001643 BF757957 AL549361 AL544018 BE002870 BE929314 BE090199 AL046650 BI053717 BE929315 BI054967 BF960655 BF925432 R05421 BF922073 T70331 BI004403
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TABLE 34C:

55

Pkey:

Ref:

Strand:

NL_position:

Unique number corresponding to an Eos probeset

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

60

Pkey

Ref

Strand

NL_position

405443

7408143

Plus

90716-90887,101420-101577

401645

7657839

Minus

34986-35133

401673

7689903

Minus

122587-122705,122765-123047

65

405120

8099940

Plus

140176-140340

401785

7249190

Minus

165776-165996,166189-166314,166408-16656

402333

8844110

Minus

165693-165856

404942

7382153

Plus

92095-92252

403362

8571772

Plus

64099-64260

70

402641

9958129

Minus

122596-125136

405600

5923540

Plus

26662-27225

405061

7656744

Minus

132492-132932

402327

7656695

Minus

108575-108770,109801-109910

404342

9838093

Plus

115854-116033

75

404429

7407979

Plus

31352-31498

403344

8569726

Plus

70823-70990

401593

7230957

Plus

10368-10572,11293-12356

406461

9756020

Minus

158842-159136

400609

9887571

Minus

92037-92247

80

402674

8077108

Minus

39290-39502

401677

9965537

Minus

62856-63086,63603-63884

405579

6456174

Plus

100996-101542

405797

1934909

Minus

5599-5681,5821-6104

5	405159	9966252	Plus	79659-79804
	403520	7684483	Minus	97621-98084
	402538	9801137	Minus	96314-96539
	404151	7534014	Minus	69038-69399
	400496	9743564	Plus	41515-41695
	403010	3132346	Plus	78385-79052
	406387	9256180	Plus	116229-116371,117512-117651
	402885	9926751	Plus	71919-72049
10	404501	7229859	Minus	37270-37526
	402487	9797538	Plus	75677-75843
	404455	7677926	Minus	26927-27611
	401067	5764724	Minus	153366-153509
	402324	7630361	Plus	26052-26803
15	402013	7407997	Plus	174540-174634,175449-175568
	401116	9966559	Plus	123579-124447
	402998	2996643	Minus	17175-17373
	405550	1552494	Plus	91720-92115
	402917	7406502	Minus	1034-1177,3143-3266
20	402504	9797871	Plus	12366-12614
	405491	5801645	Plus	81857-82045
	400818	8569994	Plus	172644-172765,173085-173200
	406475	9797684	Plus	125417-125563,128052-128180
	401025	8117518	Minus	179287-179483,181044-181166,181844-18203
25	402308	7340295	Minus	92080-93638
	405213	6692345	Minus	50267-51151
	400740	7329267	Minus	79920-80510,80576-80746
	402825	6165330	Minus	78572-78807
	405973	8247789	Plus	103859-104254
30	405818	4071056	Plus	29055-29196
	402621	9930950	Plus	130806-131036
	401311	9212516	Minus	180124-180754
	401899	7230209	Minus	155620-155815
	403579	8101179	Minus	36167-36365
35	404600	8705107	Plus	118354-118444,118649-118792
	405531	9665194	Plus	35602-35803
	405542	9857564	Plus	71331-72183
	405131	8516051	Minus	136764-137594
	403026	7670575	Plus	56521-56840
40	405369	2078469	Minus	34183-34357,35686-35751
	405932	7767812	Minus	123525-123713
	405156	9966228	Plus	145733-145860,147899-147961,153127-15325
	402174	8575912	Plus	253499-253674
	405536	9795661	Plus	164091-164162,164397-164516,166720-16679
45	405109	9127147	Minus	58328-58485
	403162	9838085	Plus	82652-83613
	401404	7710968	Plus	136474-136646
	403167	9838127	Plus	162599-162935
	402209	8576119	Minus	53315-53472
50	400986	8085497	Minus	63140-63319
	404975	3419864	Minus	86096-86605
	404926	7341919	Minus	150411-151484

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TABLE 35A: About 323 genes upregulated in hypersensitivity pneumonitis relative to idiopathic pulmonary fibrosis or non-specific interstitial pneumonitis

60	Pkey:	Unique Eos probeset identifier number				
	ExAccn:	Exemplar Accession number, Genbank accession number				
	UnigeneID:	Unigene number				
	Unigene Title:	Unigene gene title				
	R1:	90th percentile of HP AIs divided by 90th percentile of IPF AIs, where 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator. The minimum value for the numerator and denominator was set to 50.				
65	R2:	90th percentile of HP AIs divided by the median of IPF AIs, where the minimum value for the numerator and denominator was set to 50.				
	Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
70	402550			Target Exon	4.03	4.70
	421563	NM_006433	Hs.105806	granulysin	3.37	2.70
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	3.31	2.42
	417957	BE244373	Hs.11119	nuclear receptor subfamily 4, group A, m	3.09	1.51
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	2.99	1.28
75	416350	AF188625	Hs.189507	phospholipase A2, group IID	2.71	1.43
	406654	M90686	Hs.73885	HLA-G histocompatibility antigen, class	2.70	1.53
	459705	BE082764	Hs.270252	ESTs, Weakly similar to androgen recepto	2.70	1.14
	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	2.69	2.99
	452194	AI694413		olfactory receptor, family 2, subfamily	2.63	2.67
80	447709	U97145	Hs.19317	GDNF family receptor alpha 2	2.63	1.52
	410910	AW810204		gb:MR4-ST0125-021199-017-d08 ST0125 Homo	2.59	1.00
	454671	AW812929	Hs.338908	ESTs	2.50	2.34
	441859	AW194364	Hs.94814	interleukin-4 induced gene-1 protein (FI	2.45	1.90
	422398	AI476149	Hs.334489	hypothetical protein FLJ21992	2.45	1.36
	403244			C2002870:gij82698[ipr]UQ0985 hydroxypr	2.40	1.53

	415462	R52692	Hs.12698	ESTs	2.40	1.00
	447028	A1973128	Hs.167257	brain link protein-1	2.33	1.64
	412394	AW984150		gb:PM2-HN0008-170300-001-h09 HN0008 Homo	2.32	1.00
5	450165	AA007235	Hs.63931	ESTs	2.32	1.32
	431093	AB031038	Hs.301704	eomesoderm (Xenopus laevis) homolog	2.30	1.81
	444090	S69115	Hs.10306	natural killer cell group 7 sequence	2.28	1.69
	413682	BE156991		gb:RC3-HT0371-290100-013-e02 HT0371 Homo	2.27	1.59
	441320	A1768724		fibulin 1	2.27	1.87
10	456766	R87310	Hs.7740	oxysterol binding protein-like 1	2.27	1.35
	420340	NM_000734	Hs.97087	CD32 antigen, zeta polypeptide (TIT3 com	2.26	1.98
	459721	A1299050	Hs.143835	gb:qn14d12x1 NCI_CGAP_Lu5 Homo sapiens	2.25	1.82
	405452			Target Exon	2.25	1.29
	458079	A1796870	Hs.54277	DNA segment on chromosome X (unique) 992	2.25	5.80
	401447			Target Exon	2.25	1.55
15	423066	Y18264	Hs.123094	sal (Drosophila)-like 1	2.24	1.51
	441704	A1458766	Hs.192125	ESTs	2.24	1.00
	405097			ENSP00000175238*:A disintegrin and metal	2.24	1.00
	408544	AW293825		ESTs	2.22	1.95
20	413454	BE141162		gb:MR0-HT0076-021299-001-d03 HT0076 Homo	2.20	2.26
	444404	M31525		major histocompatibility complex, class	2.20	1.37
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	2.19	2.88
	436063	AK000028		ribosomal protein S24	2.19	1.42
	429212	NM_001504	Hs.198252	G protein-coupled receptor 9	2.18	1.22
25	400712			Target Exon	2.18	1.00
	417929	R27219	Hs.74647	Human T-cell receptor active alpha-chain	2.17	1.79
	403478			NM_022342:Homo sapiens kinesin protein 9	2.17	1.80
	418747	AJ249977	Hs.88049	protein kinase, AMP-activated, gamma 3 n	2.17	1.76
	429712	AW245825	Hs.211914	ENSP00000233627*:NADH-ubiquinone oxidore	2.16	1.44
30	451668	Z43948	Hs.326444	cartilage acidic protein 1	2.16	2.12
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	2.15	2.88
	456057	AA947457	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.15	2.50
	444346	A1142274		ESTs	2.15	2.38
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	2.14	1.93
35	451318	AA029888	Hs.95071	ESTs	2.14	1.16
	458935	Y16521	Hs.24812	CDP-diacylglycerol synthase (phosphatida	2.13	1.52
	417105	X60992	Hs.81226	CD6 antigen	2.13	2.61
	408219	BE061111	Hs.254211	gb:QV0-BT0041-011199-039-f02 BT0041 Homo	2.13	1.94
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	2.11	2.66
40	443711	N67861	Hs.49390	ESTs	2.10	1.00
	423234	AA323534	Hs.296162	AD037 protein	2.10	1.52
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	2.09	3.74
	425280	U31519	Hs.1872	phosphoenolpyruvate carboxykinase 1 (sol	2.08	1.84
	405827			Target Exon	2.08	1.00
45	406909	L20777	Hs.73885	gb:Human MHC class I HLA-G gene (HLA-A33	2.08	2.29
	437295	AW779318	Hs.88417	ESTs	2.07	1.72
	424281	AA766243		gb:oa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	2.07	1.00
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	2.07	2.16
	423901	AA333006		gb:EST37064 Embryo, 8 week 1 Homo sapien	2.07	1.50
50	405075			Target Exon	2.07	1.15
	457423	AK000642	Hs.265018	hypothetical protein FLJ20635	2.07	2.67
	406267			Target Exon	2.07	1.30
	423365	AA324992	Hs.257168	ESTs	2.06	1.70
	449970	A1678058	Hs.201227	ESTs	2.06	2.48
55	430733	AW976920	Hs.121036	ESTs	2.06	1.00
	446323	A1288274	Hs.345792	ESTs	2.06	1.00
	402240			Target Exon	2.05	1.94
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.05	1.44
	424463	AW196353	Hs.119903	ESTs	2.04	1.32
60	400107			Eos Control	2.04	2.42
	404811			NM_021096:Homo sapiens calcium channel,	2.03	2.18
	403589			Target Exon	2.03	1.57
	404088			Target Exon	2.03	1.00
	414991	C17898		gb:C17898 Human placenta cDNA (TFujiwara	2.03	2.04
65	429073	AA446167	Hs.47385	ESTs	2.03	3.10
	426274	D38122	Hs.2007	tumor necrosis factor (ligand) superfam	2.02	1.92
	401897			C17001987:gt[7303380]gb[AAF58438.1] (AE0	2.02	1.55
	431094	AW972276	Hs.116195	ESTs	2.02	1.00
	424899	AL119387	Hs.119062	ESTs	2.01	2.41
70	419711	C02621	Hs.159282	ESTs	2.01	1.92
	459019	AA017156	Hs.40719	hypothetical protein KIAA1164	2.01	1.76
	405453			NM_005748*:Homo sapiens YY1-associated f	2.01	1.24
	402516			Target Exon	2.01	1.00
	457365	AA577297	Hs.303249	EST	2.01	2.35
75	407928	NM_002262	Hs.41682	killer cell lectin-like receptor subfam	2.01	2.62
	436553	AW407157	Hs.8997	immunoglobulin lambda locus	2.00	1.64
	406266			Target Exon	2.00	2.46
	419409	AW297831	Hs.143792	hypothetical protein MGC2656	2.00	1.60
	435028	AW193035	Hs.187370	ESTs	2.00	1.55
80	404696			NM_013443:Homo sapiens CMP-NeuAC:(beta)-	2.00	1.21
	403533			Target Exon	2.00	1.17
	411673	BE064863		gb:RC1-BT0313-110300-015-f06 BT0313 Homo	2.00	1.00
	424148	BE242274	Hs.1741	integrin, beta 7	1.99	3.65
	419833	AA251131	Hs.220697	ESTs	1.99	1.89

	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	1.99	1.84
	426416	AW612744	Hs.169824	killer cell lectin-like receptor subfam	1.98	2.56
	449317	AW293413	Hs.132906	19A24 protein	1.98	2.44
5	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	1.97	2.51
	422109	S73265	Hs.1473	gastrin-releasing peptide	1.97	3.32
	424218	AF031824	Hs.143212	cystatin F (leukocystatin)	1.96	1.86
	406303			C16000922:gil7499103[pir]T20903 hypothe	1.96	2.16
	438676	AA813745	Hs.123446	ESTs	1.95	3.62
10	404240			NM_018950:Homo sapiens major histocompat	1.95	2.06
	404056			Target Exon	1.94	2.60
	425508	AA991551	Hs.97013	Homo sapiens, Similar to RIKEN cDNA 2310	1.93	3.24
	429819	AL133011	Hs.225108	Homo sapiens mRNA; cDNA DKFZp434P201 (fr	1.93	2.35
	416941	BE000150	Hs.48778	niban protein	1.92	2.24
15	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	1.92	5.44
	409153	W03754	Hs.50813	hypothetical protein FLJ20022	1.92	6.08
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	1.90	5.52
	446608	N75217	Hs.257846	ESTs	1.90	4.63
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	1.89	1.50
	414812	X72755	Hs.77367	monokine induced by gamma interferon	1.89	4.93
20	422994	AW891802	Hs.296276	ESTs	1.88	3.30
	424517	AI539443	Hs.137447	Homo sapiens cDNA FLJ12169 fis, clone MA	1.88	2.17
	433671	AW138797	Hs.132906	19A24 protein	1.88	1.83
	412116	AW402166	Hs.784	Epslein-Barr virus induced gene 2 (lymph	1.86	3.12
25	447656	NM_003726	Hs.19126	src kinase-associated phosphoprotein of	1.86	1.88
	432468	AW402155	Hs.3003	CD3E antigen, epsilon polypeptide (TIT3	1.84	1.65
	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	1.83	2.46
	427527	AI809057	Hs.153261	immunoglobulin heavy constant mu	1.82	2.07
	431574	AW572659	Hs.261373	hypothetical protein dJ434O14.3	1.82	2.63
	436485	X59135	Hs.156110	immunoglobulin kappa constant	1.82	2.75
30	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.81	4.56
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	1.80	5.10
	448569	BE382657	Hs.21486	signal transducer and activator of trans	1.79	1.89
	429570	L01087	Hs.211593	protein kinase C, theta	1.78	3.34
	412584	X54870	Hs.74085	DNA segment on chromosome 12 (unique) 24	1.78	3.55
35	413869	NM_000878	Hs.75596	interleukin 2 receptor, beta	1.78	1.97
	406672	M26041	Hs.198253	major histocompatibility complex, class	1.76	2.12
	452203	X57522		transporter 1, ATP-binding cassette, sub	1.75	1.55
	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	1.73	2.04
40	447131	NM_004585	Hs.17466	retinoic acid receptor responder (lazarus	1.73	1.56
	414512	AL044336	Hs.6831	golgi phosphoprotein 1	1.73	2.00
	426752	X69490	Hs.172004	lilin	1.73	2.62
	444793	U89281	Hs.11958	oxidative 3 alpha hydroxysteroid dehydro	1.72	2.30
	452334	D60471	Hs.13390	gb:HUM111D09B Clontech human fetal brain	1.72	2.12
45	446227	AI281459	Hs.270114	ESTs	1.72	2.48
	407830	NM_001086	Hs.587	arylacetylamine deacetylase (esterase)	1.72	2.72
	423799	AW026300	Hs.132906	19A24 protein	1.71	2.40
	458332	AI000341		ESTs	1.70	3.71
	408380	AF123050	Hs.44532	diubiquitin	1.70	2.71
50	437644	AA748575	Hs.135748	lectin-like NK cell receptor	1.70	2.58
	402736			NM_024852:Homo sapiens hypothetical prot	1.69	2.10
	438866	U44385	Hs.325495	tissue inhibitor of metalloproteinase 2	1.69	1.39
	422846	BE513934	Hs.1583	neutrophil cytosolic factor 1 (47kD, chr	1.68	2.02
	426202	BE266484	Hs.82916	chaperonin containing TCP1, subunit 6A (1.68	2.14
55	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	1.68	3.30
	420440	NM_002407	Hs.97644	mammaglobin 2	1.67	2.42
	416967	BE616731	Hs.80645	Interferon regulatory factor 1	1.67	1.49
	415823	R81864	Hs.205103	ESTs	1.65	2.16
	421924	BE514514	Hs.109606	coronin, actin-binding protein, 1A	1.65	1.58
60	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	1.63	1.94
	444929	AI685841	Hs.161354	ESTs	1.63	2.16
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	1.63	1.74
	418196	AI745649	Hs.26549	KIAA1708 protein	1.62	2.76
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	1.62	4.42
65	438568	R98865	Hs.11135	major histocompatibility complex, class	1.62	1.74
	430308	BE540865	Hs.238990	cyclin-dependent kinase inhibitor 1B (p2	1.62	1.85
	433934	AW273261	Hs.216292	ESTs	1.62	2.00
	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	1.61	2.00
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	1.61	1.46
70	415349	AI766697	Hs.13231	ESTs	1.60	2.00
	405556	M16714	Hs.89643	major histocompatibility complex, class	1.60	1.47
	456974	M12529	Hs.169401	apolipoprotein E	1.60	1.63
	416401	N80139	Hs.268916	ESTs	1.59	1.68
	439372	AF088033	Hs.159225	ESTs	1.59	2.04
	434666	AF151103	Hs.112259	T cell receptor gamma locus	1.59	4.08
75	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	1.58	3.06
	417427	M90391	Hs.82127	interleukin 16 (lymphocyte chemoattracta	1.58	2.37
	431903	AB029488	Hs.272100	SMS3 protein	1.57	2.14
	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	1.57	2.28
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	1.56	1.46
80	412472	AW975398	Hs.293836	ESTs	1.56	2.26
	451405	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	1.56	2.38
	412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.55	1.67
	449835	AW979300	Hs.293813	ESTs	1.55	2.16

	405545		Target Exon	1.55	2.64	
	435299	AI745458	Hs.343026	ESTs, Weakly similar to T20593 hypotheti	1.55	3.81
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	1.54	2.14
5	424243	AI949359	Hs.143600	ESTs, Highly similar to cis Golgi-locali	1.53	2.62
	457500	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	1.53	2.04
	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	1.53	2.00
	439039	AI656707	Hs.48713	ESTs	1.53	2.38
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	1.52	2.65
10	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	1.52	2.06
	415198	AW009480	Hs.943	natural killer cell transcript 4	1.52	1.40
	431594	AI823999		ESTs	1.52	2.12
	432656	NM_000246	Hs.3076	MHC class II transactivator	1.52	2.20
	422426	W79117	Hs.58559	ESTs	1.52	2.22
15	414372	AA143654		gbz065a02r1 Stratagene pancreas (93720	1.51	2.80
	427247	AW504221	Hs.174103	Integrin, alpha L (antigen CD11A (p180),	1.50	1.67
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	1.49	3.12
	406621	X57809	Hs.6997	immunoglobulin lambda locus	1.49	1.78
	419166	AA234638	Hs.293584	ESTs	1.49	2.10
20	418323	NM_002118	Hs.1162	major histocompatibility complex, class	1.49	1.47
	435304	H10709	Hs.269524	ESTs	1.48	2.96
	452834	AI638627	Hs.105885	KIAA1688 protein	1.48	2.14
	446616	R65964	Hs.334873	ESTs, Weakly similar to ALU8_HUMAN ALU S	1.48	1.38
	429272	W25140	Hs.110667	ESTs	1.48	3.19
25	428379	X06026	Hs.2259	CD3G antigen, gamma polypeptide (TIT3 co	1.48	1.66
	433231	AB040926	Hs.143552	KIAA1493 protein	1.47	2.16
	408947	AW290997	Hs.30348	ESTs	1.46	2.08
	405441			Target Exon	1.46	2.99
30	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	1.45	1.56
	459644	AW197203		gbxm38b01.x1 NCI_CGAP_GC6 Homo sapiens	1.45	2.44
	431433	X65018	Hs.253495	surfactant, pulmonary-associated protein	1.45	1.70
	422934	BE244189	Hs.122492	hypothetical protein	1.44	1.27
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	1.44	3.46
	406698	X03068	Hs.73931	major histocompatibility complex, class	1.44	1.71
35	421407	T82331	Hs.182278	ESTs, Weakly similar to CGHU6C collagen	1.43	1.56
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	1.43	1.25
	400269			Eos Control	1.43	2.02
	420973	AA743415	Hs.291368	ESTs	1.42	2.06
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	1.42	2.20
40	430015	AW768399		ESTs	1.41	2.06
	427648	AI376722	Hs.180062	proteasome (prosome, macropain) subunit,	1.41	1.31
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	1.40	1.72
	437479	R61866	Hs.101277	ESTs	1.40	2.52
	425345	AU077297	Hs.155894	protein tyrosine phosphatase, non-recept	1.40	2.17
45	416030	H15261	Hs.21948	ESTs	1.40	2.62
	419886	AA251562	Hs.146168	ESTs, Weakly similar to AF118023 1 SH3 d	1.40	1.68
	443951	F13272		ferritin, light polypeptide	1.40	1.64
	414875	H42679	Hs.77522	major histocompatibility complex, class	1.40	1.42
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platel	1.40	1.34
50	428782	X12830	Hs.193400	interleukin 6 receptor	1.40	2.30
	400680			NM_014207:Homo sapiens CD5 antigen (p56-	1.39	1.93
	428289	M26301	Hs.2253	complement component 2	1.39	1.39
	441410	AA932689	Hs.233304	ESTs, Weakly similar to I38022 hypotheti	1.39	1.42
	406645	M57466	Hs.814	major histocompatibility complex, class	1.39	1.45
55	441379	AW175787	Hs.334841	selenium binding protein 1	1.38	1.32
	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	1.38	2.04
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	1.38	1.35
	423526	AB011086	Hs.129739	KIAA0514 gene product	1.37	1.41
	424168	L29277	Hs.321677	signal transducer and activator of trans	1.37	1.33
60	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (I	1.37	1.74
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	1.35	1.38
	446566	H95741	Hs.17914	membrane-spanning 4-domains, subfamily A	1.35	1.54
	452353	C18825	Hs.29191	epithelial membrane protein 2	1.34	1.47
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	1.31	1.77
65	435106	AA100847	Hs.5978	ESTs, Highly similar to AF174600 1 F-box	1.31	1.53
	444633	AF111713	Hs.286218	junctional adhesion molecule 1	1.30	1.37
	430998	AF128847	Hs.204038	indolethylamine N-methyltransferase	1.29	1.49
	419092	J05581	Hs.89603	mucin 1, transmembrane	1.28	1.36
	451864	N20370	Hs.69547	ESTs	1.28	1.42
70	421140	AA298741	Hs.102135	signal sequence receptor, delta (translo	1.28	1.31
	412790	NM_014767	Hs.74583	KIAA0275 gene product	1.28	1.63
	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	1.28	1.38
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	1.28	1.36
	435822	T95594	Hs.187435	ESTs	1.27	1.82
75	455863	AA907305	Hs.36475	ESTs	1.27	1.36
	404277			NM_019111:Homo sapiens major histocompa	1.27	1.52
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	1.27	1.54
	441835	AB036432	Hs.184	advanced glycosylation end product-speci	1.27	1.53
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	1.26	1.27
80	434747	AA837085		ESTs	1.26	1.60
	425320	U29344	Hs.83190	fatty acid synthase	1.25	1.35
	452363	AI582743	Hs.94953	Homo sapiens, Similar to complement comp	1.25	1.41
	434644	H98071	Hs.4055	chromosome 21 open reading frame 50	1.25	1.30
	404854			Target Exon	1.25	1.57

5	406973	M34996	Hs.198253	major histocompatibility complex, class	1.25	1.57
	421071	AJ311238	Hs.104476	ESTs, Weakly similar to CGHU1E collagen	1.24	1.26
	431779	AW971178	Hs.268571	apolipoprotein C-I	1.24	1.39
	416047	BE435894	Hs.78991	DNA segment, numerous copies, expressed	1.23	2.08
	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	1.23	1.20
	426836	N41720	Hs.172684	vesicle-associated membrane protein 8 (e	1.22	1.24
	415561	AF057307	Hs.78575	prosaposin (variant Gaucher disease and	1.22	1.16
	405824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	1.22	1.17
10	420679	X57152	Hs.99853	fibrillarin	1.22	1.30
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	1.22	1.58
	418090	U57059	Hs.83429	tumor necrosis factor (ligand) superfam	1.21	1.33
	430250	NM_016929	Hs.283021	chloride intracellular channel 5	1.21	1.60
	406825	AJ982529	Hs.84298	CD74 antigen (invariant polypeptide of m	1.20	1.20
15	436906	H95990	Hs.181244	major histocompatibility complex, class	1.19	1.27
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor I	1.19	1.62
	408279	AF216965	Hs.44095	Homo sapiens, clone MGC:12617, mRNA, com	1.18	1.25
	411372	AJ147861	Hs.213289	low density lipoprotein receptor (famili	1.17	1.33
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	1.16	1.49
20	406906	Z25424		gb:Hsapiens protein-serine/threonine ki	1.16	1.15
	451558	NM_001089	Hs.26530	ATP-binding cassette, sub-family A (ABC1	1.16	1.38
	432805	X94630	Hs.3107	CD97 antigen	1.16	1.22
	427383	NM_005411	Hs.177582	surfactant, pulmonary-associated protein	1.16	1.41
	438086	AA336519	Hs.83623	nuclear receptor subfamily 1, group I, m	1.16	1.36
25	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	1.15	1.27
	429832	AW293301	Hs.288472	ESTs, Weakly similar to UBPF_HUMAN UBIQU	1.15	1.72
	438183	BE263252	Hs.6101	hypothetical protein MGC3178	1.15	1.21
	432680	T47364	Hs.278613	Interferon, alpha-inducible protein 27	1.14	1.21
	406782	AA430373		gb:zw20f11.1.s1 Soares ovary tumor NbHOT H	1.14	1.41
30	414662	AL036058	Hs.76807	major histocompatibility complex, class	1.12	1.25
	452547	AA335295	Hs.74120	adipose specific 2	1.11	1.39
	414803	X03100	Hs.914	Human mRNA for SB classII histocompatibi	1.11	1.22
	430280	AA361258	Hs.237858	interleukin 7 receptor	1.10	1.73
	441384	AA447849	Hs.288660	retinoic acid induced 3	1.09	1.22
35	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibitor	1.09	1.14
	419200	AW966405		EST	1.08	1.64
	416511	NM_006762	Hs.79356	Lysosomal-associated multispinning membr	1.08	1.18
	409428	M33680	Hs.54457	CD81 antigen (target of antiproliferativ	1.07	1.12
	447023	AA356764	Hs.17109	integral membrane protein 2A	1.07	1.71
40	421481	AW391972	Hs.104696	KIAA1324 protein	1.07	1.58
	406868	AA505445	Hs.300697	immunoglobulin heavy constant gamma 3 (G	1.07	1.23
	412819	T25829	Hs.24048	FK506 binding protein precursor	1.06	1.45
	418253	AA215539	Hs.283643	Homo sapiens cDNA FLJ11606 fis, clone HE	1.06	1.24
	431243	U46455	Hs.252189	syndecan 4 (amphiglycan, ryudocan)	1.05	1.17
45	448133	AA723157	Hs.73769	folate receptor 1 (adult)	1.04	1.21
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	1.04	9.14
	418156	W17056	Hs.83623	nuclear receptor subfamily 1, group I, m	1.03	6.65
	438089	W05391		nuclear receptor subfamily 1, group I, m	1.03	8.00
	429615	AF258627	Hs.211562	ATP-binding cassette, sub-family A (ABC1	1.01	1.25
50	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	1.00	1.18
	438091	AW373062		nuclear receptor subfamily 1, group I, m	0.99	12.84
	407018	U49869		NM_018955:Homo sapiens ubiquitin B (UBB)	0.99	1.07
	412896	AW804157	Hs.308026	major histocompatibility complex, class	0.98	1.57
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	0.97	1.40
55	426530	U24578	Hs.278625	complement component 4A	0.96	1.28
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	0.95	1.29
	407241	M34516		gb:Human omega light chain protein 14.1	0.94	1.11
	425371	D49441	Hs.155981	mesothelin	0.92	1.45
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (0.91	1.28

TABLE 35B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
411089	5597_6	BI009308 BI009893 BF922023 BF922909 BF922913 BF922096 BF957733 BE701791 AA456454 AA579876 BF933710 AA091294 BI007291 AW905577 AW975593 AA713730 AW836781 AA666384 AA551106 BF594606 AJ082382 AJ955808 AJ679895 AJ679386 BF435555 AA586369 AA551351 AA595822 AA565188 BF808855 AA584921 N86077 AA501031 AA633188 AA514764 AA454562 AA551297 AA936109 BI009389 AW897806 BE815442 BF739374 BI009310 BF925422 BF933709 BF922034 BF925465 BI009680 AI694413 AW994700 AJ912946 N73548 AJ082035 AW271652 W24189 W24182 AJ719718 AAD24658 AW810120 AW015394 T79755 AA988043 AJ709339
452194	90339_1	AW810196 AW810555 AW810507 AW810204 AW810619 AW810534 AW947794 AW947793 AW947802 AW947798 AW947792 AW984150 AW984166 AW984167 AW984168 AW984179 AW984134 AW984160 AW984180 AW984194 AW984202 AW984190 BE156943 BE157375 BE156965 BE156949 BE156956 AJ346734 AJ377971 BG193341 BG548376 AA928353 AJ768724 BG215700 AA449370 BI462157 BI060283 BG677508 AA318802 BG719160 AW293825 AW235391
410910	1063929_1	BE141291 BE141306 BE141288 BE141283 BE141162 BE141168 BE141290 BE141161 BE141165
412394	1174616_1	BC013183 AW408658 NM_002119 M31525 M26039 BM456399 BF732381 BM152457 AW407685 BM193161 AW407778 BI819141 AA702254 BF855074 BI761232

436063	5483_1	AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593 AI147991 AI142274 AI198553 AA338252 AA338213 AW962691 AA333006 AA332289 D78831 C17898 D78863 BF330730 BF350539 BE153665 BE065062 BE064650 BE064853 BF330763 BE153820 BE064737 BE155079 BE064651 AW856751 AW856622 BE064691 BE153674 BE153698 BE064730 BE153536 BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW973295 AI361433 AA564644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783361 T57198 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AA75626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI660216 BI753586 AI000341 AI766341 AW873274 AI823999 AA970060 AA508176 AW972585 AI873427 AW972389 BI093452 AW970865 BG118285 AA569075 AA492132 AW753140 AA213770 AA143654 W03900 AW197203 AW753300 X65018 BC022318 NM_003019 BE465060 AI732255 BF446634 AI820677 AI002217 AI924488 BI821373 BI770406 BI823937 BI820265 BI489632 BG482911 AA617783 AI807697 AW205576 T94427 AA487101 T94513 BI819407 BI822450 BI820618 BI824619 BG542824 BG537862 BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG784420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 BI769980 BG395998 BM048875 BE881070 BE313689 BE879144 BM009834 AW245847 AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 H08534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA863395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H05091 AI334106 R63583 AI028079 AI140098 AI911625 AI890637 F34815 T65959 N0935 W52768 AA854747 AA861945 AA878472 AA778270 W32249 AA026061 W52662 W15352 W79670 W95384 T94283 AA002155 R82052 BE825493 BE825520 BE177651 H06215 BE144709 BE144829 AW976537 AI033582 AA837085 AA745261 AA548395 AA430373 AA968771 BF036043 AW190446 BG194731 AW662036 AI445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AI270167 AI857345 AA937302 AW818444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608 AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AI018009 N42850 AW573242 AI417258 AA463483 AI676131 AI167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 BI043239 AW474342 BG708553 AW362423 BF090028 BE827256 R16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405 AW994425 D81879 BE093545 AW901107 AA383529 BI021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW357006 BF386997 BF366318 AA663856 BE702099 BF035969 AI267384 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 AV724531 D53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 AL118798 BM128728 AA183411 AW444709 AW952455 AI887612 BF431948 BI496876 AI264159 BM128481 AI624657 AI683301 AI969467 AA861685 AA251595 AA625761 AA872090 AI826790 AA328366 BE827416 R75951 D56918 R68122 BE827384 AL118797 AI184164 AA164411 BI495332 BE858113 AI863860 H00660 T69849 AW780389 C14667 BE394995 BI018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302 BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009112 BG899664 H91240 R60548 N41701 AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510598 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581
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TABLE 35C:

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Pkey: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NL_position: Indicates nucleotide positions of predicted exons.

80

Pkey	Ref	Strand	NL_position
402550	7652009	Minus	80413-80573
403244	7637828	Plus	175792-176144
405452	7656638	Minus	93876-94275

5	401447	8574299	Minus	65053-65283
	405097	8072599	Plus	171191-171360
	400712	8118874	Plus	36087-36268
	403478	9958258	Plus	116458-116554
	405827	7109593	Plus	10279-10972
	405075	7770506	Minus	124680-125321
	406267	7528342	Minus	2570-2731
	402240	7690131	Plus	104382-104527,106136-106372
10	404811	3702428	Plus	26424-26596,28854-28987
	403589	8101229	Plus	5-330
	404088	9958257	Plus	184131-184295
	401897	8569218	Plus	604-767
	405453	7656675	Minus	83710-83980
15	402516	9798099	Minus	195342-195511
	406266	7528342	Minus	2365-2518
	404696	9800109	Minus	60037-60144,62675-63081
	403533	8076874	Plus	162922-163658
	406303	8575868	Plus	173622-173786
20	404240	5002624	Minus	116132-116407,116653-116922
	404056	3548785	Plus	75843-76980,77146-78263
	402736	9212044	Minus	66876-67010
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	405441	7408124	Plus	100952-101283
25	400680	8118752	Plus	118343-118684,120720-121013
	404277	1834458	Minus	91665-91946
	404854	7143420	Plus	14260-14537

30 TABLE 36A: About 52 genes upregulated in non-specific interstitial pneumonitis relative to hypersensitivity pneumonitis or idiopathic pulmonary fibrosis

	Pkey:	Unique Eos probeset Identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
35	Unigene Title:	Unigene gene title			
	R1:	90th percentile of NSIP AIs divided by 90th percentile of HP AIs, where the minimum value for the numerator and denominator was set to 50.			
	R2:	90th percentile of NSIP AIs divided by 90th percentile of IPF AIs, where the minimum value for the numerator and denominator was set to 50.			
40	Pkey	ExAccn	UnigeneID	Unigene Title	R1 R2
	435140	AA668123	Hs.134170	ESTs	2.76 2.76
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3) (NGAL)	2.57 1.00
	435375	A1733510		ESTs	2.55 2.55
45	420813	X51501	Hs.99949	prolactin-induced protein	2.55 1.35
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	2.52 0.73
	421296	NM_002666	Hs.103253	perilipin	2.50 2.45
	419290	A1128114	Hs.112885	spinal cord-derived growth factor-B	2.43 1.79
	408882	H12084	Hs.31110	ESTs, Weakly similar to MAGE-B4 [Hsapie	2.42 1.77
50	437318	AW362939	Hs.120721	ESTs	2.36 1.61
	421823	N40850	Hs.28625	ESTs	2.29 0.56
	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	2.28 0.89
	430536	A1809163	Hs.9908	nitrogen fixation cluster-like	2.25 2.80
	414009	R67516		ESTs	2.19 1.86
55	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	2.19 0.33
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	2.18 1.24
	413722	BE247354	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	2.14 1.95
	433874	AW204429	Hs.155033	ESTs	2.13 1.72
	429609	AF002246	Hs.210863	cell adhesion molecule with homology to	2.12 0.91
60	414290	A1568801	Hs.71721	ESTs	2.11 0.81
	451678	AA374181	Hs.26789	DKFZP564D0764 protein	2.11 1.01
	408785	AA588061		gbnkl10d03.s1 NCI_CGAP_Co2 Homo sapiens	2.10 1.61
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	2.08 0.85
	444179	W35132	Hs.267442	ESTs	2.08 1.13
65	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	2.05 0.80
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	2.04 0.79
	439134	AA830599		ESTs	2.04 1.89
	418512	AW498974		diacylglycerol kinase, zeta (104kD)	2.02 2.02
	457311	A1497811	Hs.172753	Homo sapiens chromosome 19, BAC 41195 (C	2.00 1.45
70	402274			C[9000498"gi4567179]gb AAD23607.1 AC00	1.88 2.24
	453222	AA033929	Hs.19156	ESTs	1.77 2.00
	447261	NM_006691	Hs.17917	extracellular link domain-containing 1	1.73 2.02
	427297	AW292593	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com	1.69 1.69
	406714	A1219304	Hs.266959	hemoglobin, gamma G	1.62 2.47
75	418333	W92113		gbzh48e01.r1 Soares_fetal_liver_spleen_	1.59 2.04
	404090			Target Exon	1.48 2.03
	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fs, clone K	1.39 2.06
	414386	X00442	Hs.75990	haploglobin	1.09 1.44
	439372	AF088033	Hs.159225	ESTs	1.05 2.13
80	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	1.01 2.08
	412472	AW975398	Hs.293836	ESTs	1.00 2.26
	432894	AW167668	Hs.279772	brain specific protein	0.97 1.19
	422060	R20893	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	0.96 2.06
	416971	R34657	Hs.80658	uncoupling protein 2 (mitochondrial, pro	0.95 1.08

5	424310	AA338648	Hs.50334	testes development-related NYD-SP22	0.93	1.47
	422109	S73265	Hs.1473	gastrin-releasing peptide	0.92	3.05
	420440	NM_002407	Hs.97644	mammaglobin 2	0.91	2.11
	418196	A1745649	Hs.26549	KIAA1708 protein	0.90	2.25
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	0.89	1.11
	419231	AL046294	Hs.136245	ESTs, Weakly similar to T17227 hypotheti	0.85	1.74
	446608	N75217	Hs.257846	ESTs	0.82	2.10
	418918	X07871	Hs.89476	CD2 antigen (p50), sheep red blood cell	0.73	1.32
10	412610	X90908	Hs.74126	fatty acid binding protein 6, ileal (gas	0.70	1.76

TABLE 36B:

15	Pkey:	Unique Eos probeset identifier number				
	CAT number:	Gene cluster number				
	Accession:	Genbank accession numbers				
	Pkey	CAT Number	Accession			
20	435375	130020_1	A1733610 A1049989 AA678769			
	414009	438978_1	BE221268 R67515 AV730582 R67516			
	406785	0_0	AA588061			
	439134	2581476_1	AAB30599 AA970659 AA883802			
	418512	12225_6	BM046773 AA224297 T33786 T08951 T09274 T08592 T30936 AA350905			
25	418333	73080_1	AF264624 AW668618 AV731446 R93353 AA584550 AV732728 BF802614 BF434359 AA077092 BI027317 AA199812 AW629027 AA831618 AJ124782 AA765804 AA055698 AA677404 AA055366 AA889402 AA765530 BE503126 BE467367 AW139964 W81697 AJ887846 W81696 AA447817 AA447667 F13631 BF055573 AW268271 AW088477 BF677839 AL601859 AW502118 AW502624 AA574189 BI020104			

TABLE 36C:

30	Pkey:	Unique number corresponding to an Eos probeset			
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.			
35	Strand:	Indicates DNA strand from which exons were predicted.			
	NL_position:	Indicates nucleotide positions of predicted exons.			

40	Pkey	Ref	Strand	NL_position
	402274	2935596	Plus	5604-6527
	404090	9967460	Minus	100815-100966

TABLE 37A: About 206 genes downregulated in lung fibrosis relative to normal lung

50	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigenelD:	Unigene number		
	Unigene Title:	Unigene gene title		
	R1:	90th percentile of normal lung AIs divided by the median of IPF AIs, where the minimum value for the numerator and denominator was set to 50.		

55	Pkey	ExAccn	UnigenelD	Unigene Title	R1
	454229	AW957744	Hs.278469	lacrimal proline rich protein	11.67
	432128	AA127221	Hs.296502	ESTs	9.86
	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	7.69
60	453310	X70697	Hs.553	solute carrier family 6 (neurotransmitte	7.32
	420958	AA309431	Hs.66	interleukin 1 receptor-like 1	7.13
	402608			Homo sapiens defensin, alpha 1, myeloid-	6.67
	406714	A1218304	Hs.266959	hemoglobin, gamma G	5.40
	406673	M34996	Hs.198253	major histocompatibility complex, class	5.22
	416539	Y07909	Hs.79368	epithelial membrane protein 1	5.04
65	418021	M15881	Hs.1137	uromodulin (uromucoid, Tamm-Horsfall gly	4.77
	409385	AA071267		gbzm61g01.r1 Stralagene fibroblast (937	4.74
	450847	NM_003155	Hs.25590	stanniocalcin 1	4.46
	404518			CD83 antigen (activated B lymphocytes, i	4.36
70	413951	AW051200	Hs.75640	natriuretic peptide precursor A	4.32
	407570	Z19002	Hs.37096	zinc finger protein 145 (Kruppel-like, e	4.25
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.23
	429509	AW614420	Hs.204354	ras homolog gene family, member B	4.14
	445769	A1741471	Hs.23666	ESTs	4.10
75	414002	NM_005732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.06
	425571	AJ007292	Hs.158306	ephrin-A2	3.92
	423168	R34385	Hs.124940	GTP-binding protein	3.80
	401234			mitogen-activated protein kinase 8 inter	3.78
	402181			Target Exon	3.77
80	403479			NM_007064:Homo sapiens serine/threonine	3.68
	435424	AW083883	Hs.37696	Homo sapiens cDNA FLJ13510 fis, clone PL	3.68
	402911			NM_021158:Homo sapiens protein kinase d	3.66
	442195	NM_001430		endothelial PAS domain protein 1	3.65
	400089			Eos Control	3.60

5	413948	C05145	Hs.75636	myosin light chain 2a	3.56
	438564	AA381553	Hs.198253	major histocompatibility complex, class	3.54
	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	3.54
	431319	AA873350	Hs.302232	ESTs	3.52
	434292	AF124368	Hs.306551	Homo sapiens IMAGE Consortium ID 839832,	3.48
	401540			NM_002675:Homo sapiens promyelocytic leu	3.46
	426477	AA379464	Hs.154073	gb:EST92386 Skin tumor I Homo sapiens cD	3.43
	402328			Target Exon	3.42
10	401590			Target Exon	3.42
	403645			NM_024513:Homo sapiens FYVE and coiled-	3.37
	403376			Target Exon	3.36
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.35
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	3.28
15	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	3.27
	401126			NM_006856:Homo sapiens activating trans	3.27
	408243	Y00787	Hs.624	interleukin 8	3.23
	412429	AV650262	Hs.75765	GRO2 oncogene	3.22
	426420	BE383808	Hs.322430	NDRG family, member 4	3.21
20	449338	H73444	Hs.394	adrenomedullin	3.19
	401904			Target Exon	3.16
	401919			NM_012448:Homo sapiens signal transduce	3.14
	406443			ENSP00000236574:Hypothetical 21.8 kDa p	3.14
	458232	BE217872	Hs.279537	ESTs	3.12
25	406016			Target Exon	3.12
	450912	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	3.11
	451831	NM_001674	Hs.460	activating transcription factor 3	3.08
	450562	AW136468	Hs.202199	ESTs	3.07
	405938			Target Exon	3.04
30	451029	AA852097	Hs.25829	ras-related protein	3.02
	421201	AW241940	Hs.102500	hypothetical protein FLJ20481	2.98
	439839	AA889354		ESTs	2.98
	439891	AL389940	Hs.109968	ESTs	2.96
	418935	T28499	Hs.89485	carbonic anhydrase IV	2.95
35	418853	NM_005236	Hs.89296	excision repair cross-complementing rode	2.95
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.94
	410326	AI368909	Hs.47650	ESTs	2.88
	407244	M10014		fibrinogen, gamma polypeptide	2.85
40	459721	AI299050	Hs.143835	gb:gn14d12.x1 NCI_CGAP_Lu5 Homo sapiens	2.84
	416212	R40290	Hs.124685	ESTs	2.84
	426686	AA431801	Hs.98764	ESTs, Weakly similar to A29861 actin gam	2.83
	437508	AI204354	Hs.121347	ESTs	2.82
	437990	AI686579	Hs.121784	ESTs	2.82
	443709	AI082692	Hs.134662	ESTs	2.81
45	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor I	2.80
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	2.79
	404231			Target Exon	2.78
	434305	AI018260	Hs.130189	ESTs	2.77
	445493	AI915771		metallothionein 1E (functional)	2.76
50	418056	AA524886		gb:nh3402.s1 NCI_CGAP_Pr3 Homo sapiens	2.76
	404102			Target Exon	2.75
	440206	AI762232	Hs.46794	ESTs	2.75
	403031			cathepsin D (lysosomal aspartyl protease	2.75
	413164	BE068494		gb:MR1-BT0371-050500-009-a12 BT0371 Homo	2.74
55	459330	C16931		gb:C16931 Clontech human aorta polyA mRNA	2.74
	456967	AW004056	Hs.168357	T-box 2	2.74
	427602	AI375258	Hs.98005	ESTs	2.74
	431367	Z20964	Hs.323817	DKFZP547E1010 protein	2.72
	406059			Target Exon	2.71
60	420575	BE263301	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	2.71
	457275	AA463422	Hs.209431	ESTs	2.71
	432559	AW452948	Hs.257631	ESTs	2.71
	402483			NM_020389:Homo sapiens putative capacita	2.70
	416069	R37101	Hs.20982	ESTs	2.70
65	445445	AF238870	Hs.275706	Homo sapiens clone GLSH-3 similar to gll	2.69
	436232	AA707006	Hs.187863	ESTs	2.68
	418773	T39748	Hs.325474	Target CAT	2.67
	434038	AA622104		ESTs	2.67
	405448			Homo sapiens mRNA; cDNA DKFZp58612022 (f	2.66
70	404439			ENSP00000067222:Mitochondrial 28S ribos	2.65
	435724	N39308	Hs.117898	ESTs	2.65
	404026			Target Exon	2.65
	400881			NM_025080:Homo sapiens hypothetical prot	2.64
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	2.62
75	405429			Target Exon	2.62
	402642			C1002295:gi5677817ref[NP_033126.1] rep	2.61
	438575	BE304709	Hs.146550	myosin, heavy polypeptide 9, non-muscle	2.61
	449293	AA001088	Hs.29739	ESTs, Weakly similar to C34323 GTP-bindi	2.61
	416157	NM_003243	Hs.342874	transforming growth factor, beta recepto	2.60
80	446122	AI362790	Hs.278639	KIAA1684 protein; likely homolog of mous	2.59
	433291	AF007191		gb:Homo sapiens SIB 276 intestinal mucin	2.59
	426795	AI810474	Hs.196945	ESTs	2.58
	423503	M92843	Hs.343586	zinc finger protein homologous to Zfp-36	2.58
	430768	AB030207	Hs.247888	guanine nucleotide binding protein 13, g	2.58